

GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus.p2n model

Run on: January 8, 2003, 05:14:09 ; Search time 37.454 Seconds
(without alignments)
1359.222 Million cell updates/sec

Title: US-09-813-775c-18

Perfect score: 843
Sequence: 1 APPRLICDSRVLEERYILEAK.....NFLRGLKLYTGACRTGDR 166

Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-DB=Issued_Patents_NA -OPMT=fastap -SUFFIX=p2n.rni -MINMATCH=0.1 -LOOPEXT=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blomsu62 -TRANS=human40.cdi
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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_NA:*

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- 2: /cgn2_6/ptodata/1/lna/5B.COMB.seq:*
- 3: /cgn2_6/ptodata/1/lna/6A.COMB.seq:*
- 4: /cgn2_6/ptodata/1/lna/6B.COMB.seq:*
- 5: /cgn2_6/ptodata/1/lna/PCTUS.COMB.seq:*
- 6: /cgn2_6/ptodata/1/lna/Backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	825	97.9	508	1	US-08-318-193-69 Sequence 69, Appl
2	825	97.9	725	1	PCT-US94-04361-21 Sequence 21, Appl
3	825	97.9	788	2	US-08-883-795A-35 Sequence 35, Appl
4	825	97.9	823	2	US-08-883-795A-35 Sequence 35, Appl
5	825	97.9	823	4	US-09-205-337-1 Sequence 1, Appl
6	825	97.9	1011	4	US-08-750-128-12 Sequence 12, Appl
7	822	97.5	1239	4	US-09-366-009-39 Sequence 39, Appl
8	802	95.1	945	2	US-08-750-128-7 Sequence 7, Appl
9	802	95.1	969	2	US-08-750-128-4 Sequence 4, Appl
10	743.5	88.2	5107	4	US-08-910-647-3 Sequence 3, Appl
11	743.5	88.2	5107	4	US-08-910-647-3 Sequence 3, Appl
12	741.5	88.0	681	5	PCT-US94-04361-22 Sequence 22, Appl

13	695	82.4	681	5	PCT-US94-04361-27	Sequence 27, Appl
14	692	82.1	678	5	PCT-US94-04361-24	Sequence 24, Appl
15	676	80.2	679	5	PCT-US94-04361-23	Sequence 23, Appl
16	665.5	78.9	687	5	PCT-US94-04361-25	Sequence 25, Appl
17	665	78.9	688	5	PCT-US94-04361-26	Sequence 26, Appl
18	590.5	70.0	3601	3	US-09-017-631-23	Sequence 23, Appl
19	590.5	70.0	3602	2	US-08-883-795A-33	Sequence 33, Appl
20	590.5	70.0	3602	2	US-09-018-138-1	Sequence 1, Appl
21	106	12.6	65	2	US-08-883-795A-6	Sequence 24, Appl
22	105	12.5	58	2	US-08-883-795A-22	Sequence 6, Appl
23	105	12.5	58	2	US-08-883-795A-5	Sequence 22, Appl
24	97	11.5	61	2	US-08-883-795A-8	Sequence 8, Appl
25	97	11.5	61	2	US-08-883-795A-27	Sequence 27, Appl
26	96	11.4	996	4	US-08-875-533-59	Sequence 59, Appl
27	96	11.4	996	4	US-08-875-533-60	Sequence 60, Appl
28	95	11.3	996	4	US-08-875-533-58	Sequence 58, Appl
29	93	11.0	465	3	US-08-469-318-180	Sequence 180, Appl
30	93	11.0	465	3	US-08-468-609A-180	Sequence 180, Appl
31	93	11.0	465	3	US-08-471-045-54	Sequence 54, Appl
32	93	11.0	465	3	US-08-469-318-180	Sequence 54, Appl
33	93	11.0	465	3	US-08-469-318-180	Sequence 54, Appl
34	93	11.0	465	4	US-08-446-871-54	Sequence 54, Appl
35	93	11.0	465	4	US-08-446-872A-180	Sequence 180, Appl
36	93	11.0	465	4	US-08-468-910-54	Sequence 54, Appl
37	93	11.0	465	4	US-08-761-907-54	Sequence 54, Appl
38	93	11.0	465	4	US-08-762-227A-180	Sequence 180, Appl
39	93	11.0	465	5	PCT-US95-01185-180	Sequence 180, Appl
40	93	11.0	498	1	US-08-413-803-28	Sequence 28, Appl
41	93	11.0	605	1	US-08-388-779A-3	Sequence 3, Appl
42	93	11.0	605	1	US-08-591-070A-3	Sequence 3, Appl
43	93	11.0	605	2	US-08-927-855-3	Sequence 3, Appl
44	93	11.0	852	3	US-08-469-318-185	Sequence 185, App
45	93	11.0	852	3	US-08-468-609A-185	Sequence 185, App

ALIGNMENTS

RESULT 1
US-08-318-193-69
Sequence 69, Application US/08318193
Patent No. 5641663
GENERAL INFORMATION:
APPLICANT: GARVIN, Robert T.
TITLE OF INVENTION: AN EXPRESSION SYSTEM FOR THE SECRETION
OF BIOACTIVE HUMAN GRANULOCYTE MACROPHAGE COLONY
STIMULATING FACTOR (GM-CSF) AND OTHER HETEROLOGOUS
PROTEINS FROM STREPTOCOCCI
TITLE OF INVENTION: STIMULATING FACTOR (GM-CSF) AND OTHER HETEROLOGOUS
PROTEINS FROM STREPTOCOCCI
NUMBER OF SEQUENCES: 91
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 diagonal Road, Suite 500
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/318,193
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,314
FILING DATE:
APPLICATION NUMBER: US 07/224,568
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 18740/116 CACO

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703)836-9300
 TELEFAX: (703)683-4109
 TELEX: 899149
 INFORMATION FOR SEQ ID NO: 69:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 508 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: Other nucleic acid;
 DESCRIPTION: Synthetic DNA oligonucleotide
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 5..502
 US-08-318-193-69

Alignment Scores:
 Pred. No.: 5.06e-101 Length: 508
 Score: 825.00 Matches: 162
 Percent Similarity: 97.59% Conservative: 0
 Best Local Similarity: 97.59% Mismatches: 4
 Query Match: 97.86% Indels: 0
 DB: 1 Gaps: 0

US-09-813-775C-18 (1-166) x US-08-318-193-69 (1-508)

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QY 1 AAlaProPtoAArgLeuIleCysAspSerArgValLeuGluArgTyrLeuLeuGluAlaLys 20
DB 5 GCCCCCCCGCGCTCATCTGCGACAGCCGCTCTCGAGCGGTACTGTCGAGAGCCAG 64
QY 21 GUAlaGluAsnIleThrThrlGlyCysAlaGluHisCysSerLeuAsnGluAsnIleThr 40
DB 65 GAGGGGAGAAATATACGACGGGGTGGCCGACACTGCTCCCTCAACGAGAACTACACC 124
QY 41 ValProAspThrLysValAsnPhetYrAlaTrpLysArgAsn***Ser**GlnGlnAla 60
DB 125 GTCGCCGACACCAAGTCACTTACGCTTGAAGCCGATGAGATGGGCCAGCAGCGG 184
QY 61 ValGluValITrPGlnGlyLeuAlaLeuLeuSerGluAlaValLeuArgGlyGlnAlaLeu 80
DB 185 GTGAGAGTCTGGCAGGGGCTCGCGTCTCTCGAGGGGGTCTCGGGGAGGAGCCCTC 244
QY 81 LeuValAsnSerSerGlnProTrpGluProLeuGlnLeuHisValAspLysAlaValSer 100
DB 245 CTGGTGAACCTGCTCCAGCGCGTGGAGCGCGCTGCCAGCTGCACAGGACGCGCTCTCC 304
QY 101 GlysLeuArgSerLeuThrlThrlLeuArgAlaLeuGlyAlaGlnLysGlnAlaLysSer 120
DB 305 GGGCTCCGGTCTTACACACGCTGCTGCGCGCTCGGTGCGCCAGAGAGGAGCCATCTCG 364
QY 121 ProProAspAlaAlaSerAlaAlaProLeuArgThrIleThrlAlaAspThrPheArgLys 140
DB 365 CCCCCGAGCGCGCAGCGCGCGCGCTGCGGAGCATCAGCGGAGACCTTCGCGAAG 424
QY 141 LeuPheArgValTyrSerAsnPhleuArgGlyLysLeuLysLeuTyrThrlGlyAla 160
DB 425 CTGTTCGCGGGTCTTACTTCAACTTCTTGGCGGGAAGTGAACCTTACACCGCGAGGCC 484
QY 161 CysArgThrGlyAspArg 166
DB 485 TGCCGCGAGCGGAGCGG 502

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RESULT 2
 PCT-US94-04361-21
 Sequence 21, Application PC/TUS9404361
 GENERAL INFORMATION:
 APPLICANT: Brigham and Women's Hospital
 APPLICANT: 75 Francis Street
 APPLICANT: Boston, MA 02115
 APPLICANT: Bunn, H. Franklin
 APPLICANT: Wen, Danyi
 APPLICANT: Showers, Mark O.

TITLE OF INVENTION: Erythropoietin Mutelins With Enhanced
 TITLE OF INVENTION: Activily
 NUMBER OF SEQUENCES: 59
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Sterne, Kessler, Goldstein & Fox
 STREET: 1100 New York Avenue, Suite 600
 CITY: Washington
 STATE: D.C.
 COUNTRY: U.S.A.
 ZIP: 20005-3934
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US94/04361
 FILING DATE: Herewith
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/049,802
 FILING DATE: 21-APR-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Cimbala, Michele A.
 REGISTRATION NUMBER: 33,851
 REFERENCE NUMBER: 0627,336PC01
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 371-2600
 TELEFAX: (202) 371-2540
 INFORMATION FOR SEQ ID NO: 21:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 725 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: both
 PCT-US94-04361-21

Alignment Scores:
 Pred. No.: 8.77e-101 Length: 725
 Score: 825.00 Matches: 162
 Percent Similarity: 97.59% Conservative: 0
 Best Local Similarity: 97.59% Mismatches: 4
 Query Match: 97.86% Indels: 0
 DB: 5 Gaps: 0

US-09-813-775C-18 (1-166) x PCT-US94-04361-21 (1-725)

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QY 1 AAlaProPtoAArgLeuIleCysAspSerArgValLeuGluArgTyrLeuLeuGluAlaLys 20
DB 92 GCCCCACACAGCGCTCATCTGTGACAGCCGAGTCTCGGAGAGTACTCTTGGAGGCCAAG 151
QY 21 GUAlaGluAsnIleThrThrlGlyCysAlaGluHisCysSerLeuAsnGluAsnIleThr 40
DB 152 GAGGCGGAGAAATATACGACGGGCTGTGTAACCTGACAGCTTGAAGAGAAATATCTCT 211
QY 41 ValProAspThrLysValAsnPhetYrAlaTrpLysArgAsn***Ser**GlnGlnAla 60
DB 212 GTCCGAGACACCAAGTAAATTTCTATGCTGGAAGAGATGAGATGAGCGGAGAGGCC 271
QY 61 ValGluValITrPGlnGlyLeuAlaLeuLeuSerGluAlaValLeuArgGlyGlnAlaLeu 80
DB 272 GTAGAAAGTCTGGCAGGGGCTGCGCTGCTGTGGAAAGTGTCTGCGGGGCGAGGCGCTG 331
QY 81 LeuValAsnSerSerGlnProTrpGluProLeuGlnLeuHisValAspLysAlaValSer 100
DB 332 TTGGTCAACTCTTCCACAGCGGTGGAGGCCCTGCGAGCTGCACTGTGATTAAGCCGTCACT 391
QY 101 GlysLeuArgSerLeuThrlThrlLeuArgAlaLeuGlyAlaGlnLysGlnAlaLysSer 120
DB 392 GGGCTTCCAGCCTTCACACTCTGCTGCGGCTCTGGAGGCCAGAAAGAGCCATCTCC 451
QY 121 ProProAspAlaAlaSerAlaAlaProLeuArgThrIleThrlAlaAspThrPheArgLys 140

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DB 452 CCTCCAGATGGGCTGCTGCTCCACTCCGAACAATCATCTGCTGACACTTCCGCAA 511

QY 141 LeuPheargValtyrSerasnPheluArglyLysleuLysleuTyrrThrglyGluAla 160
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DB 512 CTTCTCCGAGTCTACTCCAAATTTCTCTCCGGGAAAGCTGAAGCTGTACACAGGGGAGGCC 571

QY 161 CysargThrglyAsparg 166
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DB 572 TGCAGGACAGGGGACAGA 589

RESULT 3

US-08-883-795A-35
Sequence 35, Application US/08883795A
Patent No. 5985607
GENERAL INFORMATION:
APPLICANT: Delcive, Genevieve
APPLICANT: Awang, Gregor
TITLE OF INVENTION: Recombinant DNA Molecules and Expression
TITLE OF INVENTION: Vectors for Tissue Plasmidogen Activator
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: BERESKIN & PARR
STREET: 40 King Street West
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5H 3Y2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/883,795A
FILING DATE: 27-JUN-1997
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Gravelle, Micheline
REGISTRATION NUMBER: 40,261
REFERENCE/DOCKET NUMBER: 7841-062
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 364-7311
TELEFAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 788 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: EPOlong

US-08-883-795A-35

Alignment Scores:

Pred. No.:	9,98e-101	Length:	788
Score:	825.00	Matches:	162
Percent Similarity:	97.59%	Conservative:	0
Best Local Similarity:	97.59%	Mismatches:	4
Query Match:	97.86%	Indels:	0
DB:	2	Gaps:	0

US-09-813-775C-18 (1-166) x US-08-883-795A-35 (1-788)

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DB 161 GCCCCACACGGCTCATCTCTGACACCGAGTCTGAGAGGTACTCTTGAGGAGCCAA 220

QY 21 GluAlaGluAsnIleThrThrglyCysAlaGluHisCysSerLeuAsnGluAsnIleThr 40
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DB 221 GAGGCCGAGATATCATCAGACGGGCTGTGCTGAACAATTGCAAGCTTGAAATGAAATATCACT 280

QY 41 ValProAspThrLysValAsnPhetyrAlaTrpLysArgAsn***Ser***GlnGlnAla 60
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DB 281 GTCCACAGACACCAAGTAAATTCTATGCTCGAGAGAGATGAGGTGCGGAGAGGCC 340

QY 61 ValGluValTrpGlnGlyLeuAlaLeuLeuSerGluAlaValLeuArgGlyGlnAlaLeu 80
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DB 341 GTAGAAAGTCTGGCAGGGCCCTGGCCCTGCTGCTCGAAGAGTCTCTCGGGGAGGCCCTG 400

QY 81 LeuValAsnSerSerGlnProTrpGluProLeuGlnLeuHisValAspLysAlaValSer 100
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DB 401 TTGGTCAACTCTTCCACAGCGGTGGAGCCCTCAGCTGATGTGATTAAGCGTCAGT 460

QY 101 GlyLeuArgSerLeuThrTrpLeuLeuArgAlaLeuGlyAlaGlnLysGluAlaIleSer 120
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DB 461 GGCCTTCGACGCTCACCACATCTGCTTGCGGCTCTGGAGAGCCAGAAAGCATCTCC 520

QY 121 ProProAspAlaAlaSerAlaAlaProLeuArgThrIleThrAlaAspThrPheArgLys 140
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DB 521 CCTCCAGATGGGCTCAGCTGCTCCACTCCGAACAATCATCTGCTGACACTTCCGCAA 580

QY 141 LeuPheargValtyrSerasnPheluArglyLysleuLysleuTyrrThrglyGluAla 160
|||||

DB 581 CTTCTCCGAGTCTACTCCAAATTTCTCTCCGGGAAAGCTGAAGCTGTACACAGGGGAGGCC 640

QY 161 CysargThrglyAsparg 166
|||||

DB 641 TGCAGGACAGGGGACAGA 658

RESULT 4

US-08-785-750-1
Sequence 1, Application US/08785750
Patent No. 5846528
GENERAL INFORMATION:
APPLICANT: PODSAKOFF, GREGORY M.
APPLICANT: KURTZMAN, GARY J.
TITLE OF INVENTION: METHODS OF TREATING ANEMIA USING
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROBINS & ASSOCIATES
STREET: 90 MIDDLEFIELD ROAD, SUITE 200
CITY: MENLO PARK
STATE: CA
COUNTRY: USA
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/785,750
FILING DATE: 16-JAN-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/588,355
FILING DATE: 18-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: MCCracken, THOMAS P.
REGISTRATION NUMBER: 38,548
REFERENCE/DOCKET NUMBER: 0800-0009.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 325-7812
TELEFAX: (415) 325-7823
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 823 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

US-08-785-750-1

Alignment Scores:

Pred. No.: 1.07e-100 Length: 823
Score: 825.00 Matches: 162
Percent Similarity: 97.59% Conservative: 0
Best Local Similarity: 97.59% Mismatches: 4
Query Match: 97.86% Indels: 0
Gaps: 2

US-09-813-775c-18 (1-166) x US-08-785-750-1 (1-823)

OY 1 AAlaProProAArgLeuIleCysAspSerArgValLeuGluArgTyrLeuLeuGluAlaLys 20
Db 133 GCCCAGACAGCCCTCATGTGTACAGCCGAGCTCGAGAGGTACTCTTGGAGGCCAAG 192
OY 21 GluAlaGluAsnIleThrThrGlyCysAlaGluHisCysSerLeuAsnGluAsnIleThr 40
Db 193 GAGGCCGAGAAATATACAGAGGGGCTGTGCTGAACTGCACTTGAATGAGAAATTCAC 252
OY 41 ValProAspThrLysValAsnPhetYrAlaTrpLysArgAsn***Ser***GlnGlnAla 60
Db 253 GTCCAGACACCAAGTTAATTCTATGCTGAGAGAGATGAGAGTGGCAGCAGGCC 312
OY 61 ValGluValITrpgInGlyLeuAlaLeuLeuSerGluAlaValLeuArgGlyGlnAlaLeu 80
Db 313 GTAGAAGTCTGGCAGGGCTGGCCCTGCTGTGGAAGCTGCTCGGGGCCAGGCCCTG 372
OY 81 LeuValAsnSerSerGlnProTrpGluProLeuGlnLeuHisValAspLysAlaValSer 100
Db 373 TTGGTCACACTCTCCAGCCGCGGAGCCCTGCACTGCACTGATGATTAAGCCGTCAGT 432
OY 101 GlyLeuArgSerLeuThrThrLeuLeuArgAlaLeuGlyAlaGlnLysGlnAlaIleSer 120
Db 433 GGCCTTCCAGAGCTCACACCTGCTGCGGCTGTGGAGCCCAAGAGCAATCCATCTCC 492
OY 121 PropProAspAlaIleSerAlaIleProLeuArgThrIleThrAlaAspThrPheArgLys 140
Db 493 CTTCCAGATGGGCTCAGCTGCTCCTCAGCAATCATCTGCTGACCTTTCGCGAAA 552
OY 141 LeuPheArgValITyrSerAsnPhetLeuArgGlyLysLeuLysLeuTyrThrGlyGlnAla 160
Db 553 CTCTCCGAGTCTACTCCAAATTTCTCCGGGGAAGCTGAACCTGTACACAGGGAGGCC 612
OY 161 CysArgThrGlyAspArg 166
Db 613 TGCAGACAGGGGACAGA 630

RESULT 5

US-09-205-337-1
Sequence 1, Application US/09205337
Patent No. 632598

GENERAL INFORMATION:

APPLICANT: PODSAKOFF, GREGORY M.
KURTZMAN, GARY J.

TITLE OF INVENTION: METHODS OF TREATING ANEMIA USING
RECOMBINANT ADENO-ASSOCIATED VIRUS VARIANTS

NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:

ADDRESSEE: ROBINS & ASSOCIATES
STREET: 90 MIDDLEFIELD ROAD, SUITE 200
CITY: MENLO PARK

STATE: CA
COUNTRY: USA

ZIP: 94025

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/205,337

FILING DATE: 04-Dec-1998

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/785,750

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: MCCracken, THOMAS P.

REGISTRATION NUMBER: 38,548

REFERENCE/DOCKET NUMBER: 0800-0009.21

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 325-7812

TELEFAX: (415) 325-7823

INFORMATION FOR SEQ. ID NO. 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 823 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Alignment Scores:

Pred. No.: 1.07e-100 Length: 823
Score: 825.00 Matches: 162
Percent Similarity: 97.59% Conservative: 0
Best Local Similarity: 97.59% Mismatches: 4
Query Match: 97.86% Indels: 0
Gaps: 2

US-09-813-775c-18 (1-166) x US-09-205-337-1 (1-823)

OY 1 AAlaProProAArgLeuIleCysAspSerArgValLeuGluArgTyrLeuLeuGluAlaLys 20
Db 133 GCCCAGACAGCCCTCATGTGTACAGCCGAGCTCGAGAGGTACTCTTGGAGGCCAAG 192
OY 21 GluAlaGluAsnIleThrThrGlyCysAlaGluHisCysSerLeuAsnGluAsnIleThr 40
Db 193 GAGGCCGAGAAATATACAGAGGGGCTGTGCTGAACTGCACTTGAATGAGAAATTCAC 252
OY 41 ValProAspThrLysValAsnPhetYrAlaTrpLysArgAsn***Ser***GlnGlnAla 60
Db 253 GTCCAGACACCAAGTTAATTCTATGCTGAGAGAGATGAGAGTGGCAGCAGGCC 312
OY 61 ValGluValITrpgInGlyLeuAlaLeuLeuSerGluAlaValLeuArgGlyGlnAlaLeu 80
Db 313 GTAGAAGTCTGGCAGGGCTGGCCCTGCTGTGGAAGCTGCTCGGGGCCAGGCCCTG 372
OY 81 LeuValAsnSerSerGlnProTrpGluProLeuGlnLeuHisValAspLysAlaValSer 100
Db 373 TTGGTCACACTCTCCAGCCGCGGAGCCCTGCACTGCACTGATGATTAAGCCGTCAGT 432
OY 101 GlyLeuArgSerLeuThrThrLeuLeuArgAlaLeuGlyAlaGlnLysGlnAlaIleSer 120
Db 433 GGCCTTCCAGAGCTCACACCTGCTGCGGCTGTGGAGCCCAAGAGCAATCCATCTCC 492
OY 121 PropProAspAlaIleSerAlaIleProLeuArgThrIleThrAlaAspThrPheArgLys 140
Db 493 CTTCCAGATGGGCTCAGCTGCTCCTCAGCAATCATCTGCTGACCTTTCGCGAAA 552
OY 141 LeuPheArgValITyrSerAsnPhetLeuArgGlyLysLeuLysLeuTyrThrGlyGlnAla 160
Db 553 CTCTCCGAGTCTACTCCAAATTTCTCCGGGGAAGCTGAACCTGTACACAGGGAGGCC 612
OY 161 CysArgThrGlyAspArg 166
Db 613 TGCAGACAGGGGACAGA 630

RESULT 6

US-08-750-128-12
Sequence 12, Application US/08750128
Patent No. 5915773

GENERAL INFORMATION:

APPLICANT: MELE Antonio,
APPLICANT: DE SANTIS Rita,

APPLICANT: CARLONI Cristina,
APPLICANT: COSCARELLA Annamaria
TITLE OF INVENTION: Hybrid molecule of formula GM-CSF-L-EPO or
TITLE OF INVENTION: EPO-L-GM-CSF for hematopoietic stimulation
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: LOWE, PRICE, LEBLANC & BECKER
STREET: 99 Canal Center Plaza, Suite 300
CITY: Alexandria
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk, 3.50 inch.
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/750,128
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IT FI 94 A 000106
FILING DATE: 27-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Robert L. Price
REGISTRATION NUMBER: 22,685
REFERENCE/DOCKET NUMBER: 2879-007
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-684-1111
TELEFAX: 703-684-1124
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1011 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
US-09-750-128-12

Alignment Scores:
Pred. No.: 1.47e-100 Length: 1011
Score: 825.00 Matches: 162
Percent Similarity: 97.59% Conservative: 0
Best Local Similarity: 97.59% Mismatches: 4
Query Match: 97.86% Indels: 0
Gaps: 0
DB: 2

US-09-813-775C-18 (1-166) x US-08-750-128-12 (1-1011)

QY 1 AAlAPROARgLeuilecysAspSerArgValIleuGluuArgTyrLeuIleuGluuAlaLys 20
DB 82 GCGCCACACAGCGCTCATCTGTGTGACAGCCAGTCTGAGAGAGTACTCTTGAGGCCAAG 141
QY 21 GluAlaGluAsnIleThrThrGlyCysAlaGluHisCysSerLeuAsnIleThr 40
DB 142 GAGGCCGAGAAATATACAGAGCGGCTGTGCTGAACTGACAGTGTGAATGAGAAATACACT 201
QY 41 ValProAspThrLysValAsnIlePheTyrAlaTPrLysArgAsn***Ser***GlnGlnAla 60
DB 202 GTGCCAGACACAAAGTAAATTTCTATGCTGTGAGAGAGAGTGGAGTCCGGCAGCAGGCC 261
QY 61 ValGluValTPrGlnGlyLeuAlaLeuLeuSerGluAlaValLeuArgGlyGlnAlaLeu 80
DB 262 GTAGAGAGTCTGGAGGCGCTGCGCCCTGCTGTGCGAAGCTGTCTCGGGGGCCAGGCCCTG 321
QY 81 LeuValAsnSerSerGlnProTPrGluProLeuGlnLeuHisValAspLysAlaValSer 100
DB 322 TTGGTCAACTCTCCAGCGCGTGGAGAGCCCTGACATGTGATTAAGCGCTCAGT 381
QY 101 GlyLeuArgSerLeuThrThrLeuLeuArgAlaLeuGlyAlaGlnLysGluAlaIleSer 120

DB 382 GGCCTTCGACGCTCACCACTTCGTCGGGCTCTGGAGACCCAGAGAACCATCTCC 441
QY 121 ProProAspAlaIleSerAlaIleProLeuArgThrIleThrAlaAspThrPheArgLys 140
DB 442 CCTCCAGATCGGCTCGCTGCTCTCCAGTCAATCTCTGACACTTCCGAA 501
QY 141 LeuPheArgValTyrSerAsnIleLeuArgGlyLysLeuLysLeuTyrThrGlyGluAla 160
DB 502 CTCTCCAGACTTACTCCATTTCTCCGGGAAAGCTGAAGCTGACACAGGGAGGCC 561
QY 161 CysArgThrGlyAspArg 166
DB 562 TGCAGGACAGCGACAGA 579

RESULT 7
US-09-366-009-39
Sequence 39, Application US/09366009
Patent No. 6426042
GENERAL INFORMATION:
APPLICANT: Asada, Kiyozo
Uemori, Takashi
Koyama, No. 6426042uto
Hashino, Kimikazu
Kato, Ikunoshin
TITLE OF INVENTION: METHOD FOR GENE TRANSFER INTO TARGET
CELLS WITH RETROVIRUS
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: WEISER & ASSOCIATES
STREET: 230 South Fifteenth Street, Suite 500
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/366,009
FILING DATE: 02-Aug-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/809,156
FILING DATE: <Unknown>
APPLICATION NUMBER: JP 294382/1995
FILING DATE: 13-NOV-1995
APPLICATION NUMBER: JP 051847/1996
FILING DATE: 08-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Weiser, Gerard J.
REGISTRATION NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 977,6507P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-875-8383
TELEFAX: 215-875-8394
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 1239 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-09-366-009-39

Alignment Scores:
Pred. No.: 5.05e-100 Length: 1239
Score: 822.00 Matches: 161
Percent Similarity: 97.59% Conservative: 1
Best Local Similarity: 96.99% Mismatches: 4

Query Match: 97.51% Indels: 0
DB: 4 Gaps: 0
US-09-813-775C-18 (1-166) x US-09-366-009-39 (1-1239)
QY 1 AAlaProPrtArgLeuIleCysAspSerArgValLeuGluArgTyrLeuLeuGluAlaLys 20
DB 697 GCCCACCACCGGCTCTGTCAGCAGCCAGTCTGCGAGAGGTACCTCTTGAGAGGCGCAAG 756
QY 21 GluAlaGluAsnIleThrThrGlyCysAlaGluHisCysSerLeuAsnGluAsnIleThr 40
DB 757 GAGGCCGGAATATACAGCAGCGGCTGCTGAACACTGACGCTTGATGAGATATACACT 816
QY 41 ValProAspThrLysValAsnPhenylalanylArgAsn***Ser***GlnGlnAla 60
DB 817 GTCCAGACACCAAGATTATTTCTATGCTGGAAGAGATGAGAGCTCGGCGACGAGGCC 876
QY 61 ValGluValIleTrpGlnGlyLeuValLeuLeuSerGluAlaValLeuArgGlyGlnAlaLeu 80
DB 877 GTAGAAAGTCTGCGAGGCGCTGCGCTGCTGCTGGAAGCTGCTCGGGGCGAGGCGCTG 936
QY 81 LeuValAsnSerSerGlnProTrpGluProLeuGlnLeuHisValAspLysAlaValSer 100
DB 937 TTGCTCACTCTTCCACGCGCTGCGAGGCCCTGCGAGCTGATGATTAACCGCTCACT 996
QY 101 GlyLeuArgSerLeuThrThrLeuLeuArgAlaLeuGlyAlaGlnLysGluAlaIleSer 120
DB 997 GCCCTTCGAGGCTCACACACTCTGCTGCGGCTGCGGAGCCAGAGAGGACCAATCTCC 1056
QY 121 ProProAspAlaAlaSerAlaAlaProLeuArgThrIleThrAlaAspThrPheArgLys 140
DB 1057 CCTCCAGATGCGGCGCTCAGCTCTCCACTCCGACAAATCATCTGACACTTCCGCGCAA 1116
QY 141 LeuPheArgValTyrSerAsnPhenylalanylLysLeuLysLeuTyrThrGlyGluAla 160
DB 1117 CTTCTCCGAGTCTACTCCAAATTTCTCCGCGGAAAGCTGAACCTGACAGAGGAGGCC 1176
QY 161 CysArgThrGlyAspArg 166
DB 1177 TGCAGAGACAGGGGACAGA 1194
RESULT 8
US-08-750-128-7
Sequence 7, Application US/08750128
Patent No. 5916773
GENERAL INFORMATION:
APPLICANT: MELE Antonio,
APPLICANT: DE SANTIS Rita,
APPLICANT: CARLONI Cristina,
APPLICANT: COSCARRELLA Annamaria
TITLE OF INVENTION: Hybrid molecule of formula GM-CSF-L-EPO or
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: LOWE, PRICE, LeBLANC & BECKER
STREET: 99 Canal Center Plaza, Suite 300
CITY: Alexandria
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk, 3.50 inch.
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/750,128
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IT FI 94 A 000106
FILING DATE: 27-MAY-1994
ATTORNEY/AGENT INFORMATION:

NAME: Robert L. Price
REGISTRATION NUMBER: 22,685
REFERENCE/DOCKET NUMBER: 2879-007
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-684-1111
TELEFAX: 703-684-1124
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 945 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHEetical: NO
US-08-750-128-7
Alignment Scores:
Pred. No.: 1.55e-97 Length: 945
Score: 802.00 Matches: 158
Percent Similarity: 97.53% Conservative: 0
Best Local Similarity: 97.53% Mismatches: 4
Query Match: 95.14% Indels: 0
DB: 2 Gaps: 0
US-09-813-775C-18 (1-166) x US-08-750-128-7 (1-945)
QY 5 LeuIleCysAspSerArgValLeuGluArgTyrLeuLeuGluAlaLysGluAlaLys 24
DB 457 CTCATCTGTGACAGCGAGAGTCTCTGAGAGAGTACTCTTGAGAGGCCAAGAGGCCAGANT 516
QY 25 IleThrThrGlyCysAlaGluHisCysSerLeuAsnGluAsnIleThrValProAspThr 44
DB 517 ATCAGAGCGGGCTGTGCTGGAACATCTGAAATGAAATATCATCTCCAGACACC 576
QY 45 LysValAsnPhenylalanylArgAsn***Ser***GlnGlnAlaValGluValIleTrp 64
DB 577 AAGCTTAATTTCTATGCTCGAAGAGAGATGAGAGTCTGCGGCGACAGCCCTGACAACTCTG 636
QY 65 GlnGlyLeuAlaLeuLeuSerGluAlaValLeuArgGlyGlnAlaLeuLeuValAsnSer 84
DB 637 CAGGCGCTGCGGCTCTGCTGCGAAGCTGCTGCGGCGCGAGCCCTGTGTCAACTCT 696
QY 85 SerGlnProTrpGluProLeuGlnLeuHisValAspLysAlaValSerGlyLeuArgSer 104
DB 697 TCCAGCGCGTGGAGCCCTGCACTGATGATGATTAAGCCGTCAAGTCTGCGACGC 756
QY 105 LeuThrThrLeuLeuArgAlaLeuGlyAlaGlnLysGluAlaIleSerProProAspAla 124
DB 757 CTCACCACTCTGCTCTCGGCGCTCTGGAGCCCGAAGAGCAATCTCCCTCCAGATGCG 816
QY 125 AlaSerAlaAlaProLeuArgThrIleThrAlaAspThrPheArgLysLeuPheArgVal 144
DB 817 GCCTCAGCTGCTCCACTCCGAACATCATCTGACACTTCCGCAACTCTTCGAGTGC 876
QY 145 TyrSerAsnPhenylalanylLysLeuLysLeuTyrThrGlyGluAlaCysArgThrGly 164
DB 877 TACTCAATTTCTCTCGGGGAAAGCTGAAGCTGTACACAGGAGGCGCTGACGAGAGG 936
QY 165 AspArg 166
DB 937 GACAGA 942
RESULT 9
US-08-750-128-4
Sequence 4, Application US/08750128
Patent No. 5916773
GENERAL INFORMATION:
APPLICANT: MELE Antonio,
APPLICANT: DE SANTIS Rita,
APPLICANT: CARLONI Cristina,
APPLICANT: COSCARRELLA Annamaria
TITLE OF INVENTION: Hybrid molecule of formula GM-CSF-L-EPO or
EPO-L-GM-CSF for hematopoietic stimulation

NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: LOWE, PRICE, LEBLANC & BECKER
STREET: 99 Canal Center Plaza, Suite 300
CITY: Alexandria
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk, 3.50 inch.
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/750,128
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IT FI 94 A 000106
FILING DATE: 27-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Robert L. Price
REGISTRATION NUMBER: 22,685
REFERENCE/DOCKET NUMBER: 2879-007
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-684-1111
TELEFAX: 703-684-1124
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 969 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
US-08-750-128-4

Alignment Scores:
Pred. No.: 1,61e-97 Length: 969
Score: 802.00 Matches: 158
Percent Similarity: 97.53% Conservative: 0
Best Local Similarity: 97.53% Mismatches: 4
Query Match: 95.14% Indels: 0
Gaps: 0

US-09-813-775c-18 (1-166) x US-08-750-128-4 (1-969)

QY 5 LeuilecysaspserrargValleuGluarGtyrleuGluAlaIysGluAlaAsn 24
|||||
Db 481 CTGATCTGTACAGCCGAGTCTGGAGAGGTACTCTTGGAGGCCCAAGAGCCGAGAAAT 540
QY 25 IleThrThrglycysAlaGluHisCysSerleuAsnGluAsnIleThrValProAspThr 44
|||||
Db 541 ATCAGCAGCGGGCTGTGCTGAACACTGCAGCTTGAAATATCACTGTGCCAGACACC 600
QY 45 LysValAsnDheTyralATrPlySAIrgAsn***Ser**GlnGlnAlaValGluValTyr 64
|||||
Db 601 AAAGTTAATTCTATGCTCGAAGAGGTGAGGTCTGGGAGCAGCGCCGTGAAGTCTGG 660
QY 65 GlnGlyleuAlaIleuSerGluAlaValleuArgGlyGlnAlaIleuValAsnSer 84
|||||
Db 661 CAGGGCCCTGGCCCTGCTGCGAAGCTGCTCGCGGGCCAGGCCCTGTGCTCAACTCT 720
QY 85 SerGlnProTrpGluProleuGlnLeuHisValAspLysAlaValSerGlyLeuArgSer 104
|||||
Db 721 TCCCAAGCCGTGGAGCCCTCGACCTCATGTGATAAAGCCGTCACTGGCCTTCGACAC 780
QY 105 LeuThrThrleuLeuArgAlaIleuGlyAlaGlnLysGluAlaIleSerProProAspAla 124
|||||
Db 781 CTCACCACTCTGCTTGGGCTTGGGAGCCAGAAAGAACCATCTCCCTCCGATGCG 840
QY 125 AlSerIleAlaProleuArgThrIleThrAlaAspThrPheArgLysLeuPheArgVal 144
|||||

Db 841 GCCCTACCTGCTCCACTCCGAAACAATCACTGCTGACACTTTCGGCAACTCTTCGAGTC 900
QY 145 TyrSerAsnDheLeuArgGlyLysLeuLysleuTyThrGlyGluAlaCysArgThrGly 164
|||||
Db 901 TACTCAATTCTCCCGGGGAAACCTGAAGCTGTACACAGGGAGGCGCTGACAGACAGG 960
QY 165 AspArg 166
|||||
Db 961 GACAGA 966

RESULT 10
US-08-910-647-3
Sequence 3, Application US/08910647
Patent No. 6251433
GENERAL INFORMATION:
APPLICANT: Zuckermann et al.
TITLE OF INVENTION: Compositions and Methods for
TITLE OF INVENTION: Polynucleotide Delivery
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
City: Emeryville
STATE: California
COUNTRY: U.S.A.
ZIP: 94608-2916
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/910,647
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Fujita, Sharon M.
REGISTRATION NUMBER: 38,459
REFERENCE/DOCKET NUMBER: 1218.002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 923-2706
TELEFAX: (510) 655-3542
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5107 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-910-647-3

Alignment Scores:
Pred. No.: 1,35e-88 Length: 5107
Score: 743.50 Matches: 148
Percent Similarity: 93.37% Conservative: 7
Best Local Similarity: 89.16% Mismatches: 10
Query Match: 88.20% Indels: 1
Gaps: 1

US-09-813-775c-18 (1-166) x US-08-910-647-3 (1-5107)

QY 1 AlaProProArgleuilecysAspserrargValleuGluarGtyrleuGluAlaIys 20
|||||
Db 1791 GCCCAGACAGCCCTCATCTGTGACAGCGAGTCTGGAGAGTACCTCTTGAGAGCCAG 1850
QY 21 GluAlaGluAsnIleThrThrglyCysAlaGluHisCysSerleuAsnGluAsnIleThr 40
|||||
Db 1851 GAGCCGAGAAATGTCACAGATGGGCTGTTCGAAAGCTGCAATGAAATATCACC 1910
QY 41 ValProAspThrLysValAsnDheTyralATrPlySAIrgAsn***Ser**GlnGlnAla 60
|||||
Db 1911 GTCCAGACACCAAGTTAATTCTATGCTCGAAGAGATGAGGTGCGGCGACAGGCT 1970

QY 61 ValGluValTrrPcInGlyLeuAlaLeuLeuSerGluAlaValLeuArgGlyGlnAlaLeu 80
 DB 1971 GTAGAAAGTCTGGCAGGGGCTGGCCCTGCTCTCAGAAAGTCTGGCGGGGAGGCCGTG 2030
 QY 81 LeuValAsnSerSerGlnProTrrPgluProlLeuGlnLeuHisValAspLysAlaValSer 100
 DB 2031 TTGGCCCAACTCTTCCAGGCTTTCGAGCCCTCCAGCTCCACATGATGAACCCATCACT 2090
 QY 101 GlyLeuArgSerLeuThrThrLeuLeuArgAlaLeuGlyAlaGlnLysGlnAlaIleSer 120
 DB 2091 GGCCCTCGCAGCATCACCACTGCTGGTGGGGGCTGGAGGCCAG---GAAGCCATCTCC 2147
 QY 121 ProProAspAlaIleSerAlaAlaProlLeuArgThrIleThrAlaAspThrPheArgLys 140
 DB 2148 CTCACAGATGCGGCTCGGCTGCTCCACTCCAGACCATCATGCTGACACTTCTTCGAAA 2207
 QY 141 LeuPheArgValTrrSerAsnPheLeuArgGlyLysLeuLysLeuThrGlyGlnAla 160
 DB 2208 CTCTTCGAGTCTACTCCCAATTTCCTCCGGGAAAGCTGAAGCTGTACAGGGGAGGCC 2267
 QY 161 CysArgThrGlyAspArg 166
 DB 2268 TGCAGAGAGGGGACAGA 2285
 RESULT 11
 US-09-620-925-3
 : Sequence 3, Application US/09620925
 : Patent No. 6468986
 : GENERAL INFORMATION:
 : APPLICANT: Zuckermann et al.
 : TITLE OF INVENTION: Compositions and Methods for
 : Polynucleotide Delivery
 : NUMBER OF SEQUENCES: 4
 : CORRESPONDENCE ADDRESSES:
 : ADDRESSEE: Chiron Corporation
 : STREET: 4560 Horton Street
 : CITY: Emeryville
 : STATE: California
 : COUNTRY: U.S.A.
 : ZIP: 94608-2916
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: PatentIn Release #1.0, Version #1.30
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/09/620,925
 : FILING DATE: 21-Jul-2000
 : CLASSIFICATION: <Unknown>
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: 08/910,647
 : FILING DATE: <Unknown>
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Fujita, Sharon M.
 : REGISTRATION NUMBER: 38,459
 : REFERENCE/DOCKET NUMBER: 1218.002
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: (510) 923-2706
 : TELEFAX: (510) 655-3542
 : INFORMATION FOR SEQ ID NO: 3:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 5107 base pairs
 : TYPE: nucleic acid
 : STRANDEDNESS: single
 : TOPOLOGY: linear
 : MOLECULE TYPE: DNA (genomic)
 : SEQUENCE DESCRIPTION: SEQ ID NO: 3:
 US-09-620-925-3
 Alignment Scores:
 Pred. No.: 1,35e-88 Length: 5107
 Score: 743.50 Matches: 148
 Percent Similarity: 93.37% Conservative: 7

Best Local Similarity: 89.16% Mismatches: 10
 Query Match: 88.20% Indels: 1
 DB: 4 Gaps: 1
 US-09-813-775c-18 (1-166) x US-09-620-925-3 (1-5107)
 QY 1 AlaProProArgLeuIleCysAspSerArgValLeuGluArgTyrLeuGlnAlaLys 20
 DB 1791 GCCCCACACGCTCATCTGTGACAGCCGAGTCTGGAGAGGTACTCTTGGAGGCCAAG 1850
 QY 21 GluAlaGlnAsnIleThrThrGlyCysAlaGlnHisCysSerLeuAsnGlnAsnIleThr 40
 DB 1851 GAGGCCGAGAAATGTCAGATGGGCTGTTCGAAAGCTGCAGCTTGAAATGATATACAC 1910
 QY 41 ValProAspThrLysValAsnPheTrrAlaTrrPlysArgAsn***Ser**GlnGlnAla 60
 DB 1911 GTCCAGACACCAAAAGTTAACTTATGCTTGAAAGAGATGAGGTGGGAGCAGAGCT 1970
 QY 61 ValGluValTrrPcInGlyLeuAlaLeuLeuSerGluAlaValLeuArgGlyGlnAlaLeu 80
 DB 1971 GTAGAAAGTCTGGCAGGGGCTGGCCCTGCTCTCAGAAAGTCTGGCGGGGAGGCCGTG 2030
 QY 81 LeuValAsnSerSerGlnProTrrPgluProlLeuGlnLeuHisValAspLysAlaValSer 100
 DB 2031 TTGGCCCAACTCTTCCAGGCTTTCGAGCCCTCCAGCTCCACATGATGAACCCATCACT 2090
 QY 101 GlyLeuArgSerLeuThrThrLeuLeuArgAlaLeuGlyAlaGlnLysGlnAlaIleSer 120
 DB 2091 GGCCCTCGCAGCATCACCACTGCTGGTGGGGGCTGGAGGCCAG---GAAGCCATCTCC 2147
 QY 121 ProProAspAlaIleSerAlaAlaProlLeuArgThrIleThrAlaAspThrPheArgLys 140
 DB 2148 CTCACAGATGCGGCTCGGCTGCTCCACTCCAGACCATCATGCTGACACTTCTTCGAAA 2207
 QY 141 LeuPheArgValTrrSerAsnPheLeuArgGlyLysLeuLysLeuThrGlyGlnAla 160
 DB 2208 CTCTTCGAGTCTACTCCCAATTTCCTCCGGGAAAGCTGAAGCTGTACAGGGGAGGCC 2267
 QY 161 CysArgThrGlyAspArg 166
 DB 2268 TGCAGAGAGGGGACAGA 2285
 RESULT 12
 PCT-US94-04361-22
 : Sequence 22, Application PC/TUS9404361
 : GENERAL INFORMATION:
 : APPLICANT: Brigham and Women's Hospital
 : APPLICANT: 75 Francis Street
 : APPLICANT: Boston, MA 02115
 : APPLICANT: Bunn, H. Franklin
 : APPLICANT: Wen, Danyl
 : APPLICANT: Showers, Mark O.
 : TITLE OF INVENTION: Erythropoietin Mutelins With Enhanced
 : TITLE OF INVENTION: Activity
 : NUMBER OF SEQUENCES: 59
 : CORRESPONDENCE ADDRESSES:
 : ADDRESSEE: Sterne, Kessler, Goldstein & Fox
 : STREET: 1100 New York Avenue, Suite 600
 : CITY: Washington
 : STATE: D.C.
 : COUNTRY: U.S.A.
 : ZIP: 20005-3934
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: PatentIn Release #1.0, Version #1.25
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: PCT/US94/04361
 : FILING DATE: Herewith
 : CLASSIFICATION:
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: 08/049,802

```

FILING DATE: 21-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Cimbalà, Michele A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 0627.336PC01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 681 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: both
PCT-US94-04361-22

Alignment Scores:
Pred. No.: 1, 116-89 length: 681
Score: 741.50 Matches: 147
Percent Similarity: 93.37% Conservative: 8
Best Local Similarity: 88.55% Mismatches: 10
Query Match: 87.96% Indels: 1
DB: 5 Gaps: 1

US-09-813-775C-18 (1-166) x PCT-US94-04361-22 (1-681)
QY 1 AlaProProArgLeuIleCysAspSerArgValLeuGluArgTyrLeuLeuGluAlaLys 20
Db 72 GCGCCAGCAGCGCTGCTGTGTGACAGCCGAGCTCTGGAGAGTACTCTTGGAGGCCAG 131
QY 21 GluAlaGluAsnIleThrThrGlyCysAlaGluHisCysSerLeuAsnGluAsnIleThr 40
Db 132 GAGGCCGGAAGTGTACGATGGCGCTTCCGAAAGCTGCAGTGTGATGAAATATCACC 191
QY 41 ValProAspThrLysValAsnPhetYrAlaTrpLysArgAsn***Ser***GlnGlnAla 60
Db 192 GTCCCGACAGACCAAGTAACTTCTATGCTGAGAGAGGATAGAGCTCGGCGACAGGCT 251
QY 61 ValGluValTrpGlnGlyLeuAlaLeuLeuSerGluAlaValLeuArgGlyGlnAlaLeu 80
Db 252 GTAGAAGTGTGGCAGGGCGCTGGCGCTGCTCGAAGAGTGTCTGGGGGCCAGGGCGTG 311
QY 81 LeuValAsnSerSerGlnProTrpGluProLeuGlnLeuHisValAspLysAlaValSer 100
Db 312 TTGGCCCAACTTCCAGGCTTTCGAGCCCTGCACCTGACATGATAAAGCCATCAGT 371
QY 101 GlyLeuArgSerLeuThrThrLeuLeuArgAlaLeuGlyValAlaGlnGlyAlaIleSer 120
Db 372 GGCCTTCGACAGATCACCACTGCTGCTGGCGCTGGAGCCAG--GAAGCCATCTCC 428
QY 121 ProProAspAlaAlaSerAlaAlaProLeuArgThrIleThrAlaAspThrPheArgLys 140
Db 429 CTCGCCAGATGGCGGCTCGGCTGCTCCAGTCGGAACCATCAGCTCTGACACTTCTGCAA 488
QY 141 LeuPheArgValItySerAsnPhelLeuArgGlyLysLeuLysLeuTyrThrGlyGluAla 160
Db 489 CTCCTCCGAGTACTACTCAATTCTCCGCGGGAAAGCTGAAGCTTAACGCGGGGAGGCC 548
QY 161 CysArgThrGlyAspArg 166
Db 549 TCCAGGACAGGGGACAGA 566

RESULT 13
PCT-US94-04361-27
Sequence 27, Application PC/TUS9404361
GENERAL INFORMATION:
APPLICANT: Brigham and Women's Hospital
APPLICANT: 75 Francis Street
APPLICANT: Boston, MA 02115
APPLICANT: Bunn, H. Franklin
APPLICANT: Men, Danyl
APPLICANT: Showers, Mark O.
TITLE OF INVENTION: Erythropoietin Mutains With Enhanced

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TITLE OF INVENTION: Activity
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/04361
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/049,802
FILING DATE: 21-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Cimbalà, Michele A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 0627.336PC01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 681 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: both
PCT-US94-04361-27

Alignment Scores:
Pred. No.: 1, 79e-83 length: 681
Score: 695.00 Matches: 137
Percent Similarity: 87.35% Conservative: 8
Best Local Similarity: 82.53% Mismatches: 21
Query Match: 82.44% Indels: 0
DB: 5 Gaps: 0

US-09-813-775C-18 (1-166) x PCT-US94-04361-27 (1-681)
QY 1 AlaProProArgLeuIleCysAspSerArgValLeuGluArgTyrLeuLeuGluAlaLys 20
Db 67 GCGCCCGCTCCGCTCATCTGTGTGACAGCCGAGCTCTGGAGAGTACTCTGAGAGGCCAGG 126
QY 21 GluAlaGluAsnIleThrThrGlyCysAlaGluHisCysSerLeuAsnGluAsnIleThr 40
Db 127 GAGGCCGGAAGTGTACAGATGGGCTGTGTGAGAGGCTGCAGCTTCACTGGAATATCACC 186
QY 41 ValProAspThrLysValAsnPhetYrAlaTrpLysArgAsn***Ser***GlnGlnAla 60
Db 187 GTCCAGACAGCAAGGTCAACTTCTATACCTGGAAGAGATGCAGCTCGGCGACAGAGCT 246
QY 61 ValGluValTrpGlnGlyLeuAlaLeuLeuSerGluAlaValLeuArgGlyGlnAlaLeu 80
Db 247 GTGGAAGTGTGGCAGGGCGCTGGCGCTGCTCCGAGAGCCATCTCGGGCGGCGGCGCTG 306
QY 81 LeuValAsnSerSerGlnProTrpGluProLeuGlnLeuHisValAspLysAlaValSer 100
Db 307 CTGGCCAACTCTCCAGCATGTGAGACCTCTGACGTGATGTGATAAAGCCGTCAGC 366
QY 101 GlyLeuArgSerLeuThrThrLeuLeuArgAlaLeuGlyValAlaGlnGlyAlaIleSer 120
Db 367 AGCCTGGAGGCTCACTCCCTGCTTGGGCGCTGGAGGCCAGGAAGGACCACTCC 426
QY 121 ProProAspAlaAlaSerAlaAlaProLeuArgThrIleThrAlaAspThrPheArgLys 140
Db 427 CTCGACAGGACCACTCTGCTGCTCCAGTCGGAACCATTCAGTGTGATCTTGTGCAA 486

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QY 141 LeupheargValTyrSerAsnPhelenuargLysLeuLysLeuTyrThrGlyAla 160
DB 487 CTCTCCGAATCTACTCCAACTCTCTCGGGGAGAGCTGACACAGGAGGCC 546
QY 161 CysArgThrGlyAspArg 166
DB 547 TCCGAGAGAGGAGCAGG 564

RESULT 14
PCT-US94-04361-24
Sequence 24, Application PC/TUS9404361
GENERAL INFORMATION:
APPLICANT: Brigham and Women's Hospital
APPLICANT: 75 Francis Street
APPLICANT: Boston, MA 02115
APPLICANT: Bunn, H. Franklin
APPLICANT: Men, Danyl
APPLICANT: Showers, Mark O.
TITLE OF INVENTION: Erythropoietin Mutens With Enhanced
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3934

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/04361
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/049,802
FILING DATE: 21-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Cimbal, Michele A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 0627,336PC01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 678 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: both
PCT-US94-04361-24

Alignment Scores:
Pred. No.: 4,46e-83 Length: 678
Score: 692.00 Matches: 135
Percent Similarity: 88.55% Conservative: 12
Best Local Similarity: 81.33% Mismatches: 19
Query Match: 82.09% Indels: 0
Gaps: 0

US-09-813-775c-18 (1-166) x PCT-US94-04361-24 (1-678)

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QY 21 GluAlaGluAsnIleThrThrGlyCysAlaGluHisCysSerLeuAsnGluAsnIleThr 40
DB 129 GAGCGAGAAATGTCAATGGGCTGTGCAGAAAGTCCCAAGACTGATGAGAAATTTACC 188

QY 41 ValProAspThrLysValAsnPhetYrAlaTrpLysArgAsn**Ser**GlnGlnAla 60
DB 189 GTCCAGATATACAAAGTCACTTACGCTTGAAAGATGAAAGTGAAGACAGGCT 248
QY 61 ValGluValTrpGlnGlyLeuAlaLeuSerGluAlaValLeuArgGlyGlnAlaLeu 80
DB 249 GTAGAAATTTGGCAAGGCTGTCTGCTCAGAAAGCATCTTCAGGCCAGCTCTG 308
QY 81 LeuValAsnSerSerGluProTrpGluProLeuGlnLeuHisValAspLysAlaValSer 100
DB 309 CAGGCCAATTCCTCCAGCCACAGAGAGTCTTACGCTTCATATGACAAAGCCATCAGT 368
QY 101 GlyLeuArgSerLeuThrThrLeuLeuArgAlaLeuGlyAlaGlnLysGluAlaIleSer 120
DB 369 GGGCTACGAGCGCTCATTCACTGCTGCGGTGCTGGAGAGCTCAGAAAGATGTATGTCG 428
QY 121 PropioAspAlaAlaSerAlaAlaProLeuArgThrIleThrAlaAspThrPheArgLys 140
DB 429 CCTCCAGAGCGCCAGCCGCTCCTCCTCCGACATCAGCGAGATCTTCTGCAAG 488
QY 141 LeupheargValTyrSerAsnPhelenuargLysLeuLysLeuTyrThrGlyAla 160
DB 488 CTCTCCGGGCTACTCCAACTTCTCTCGGGGAGAGTGAAGCTGTACACGGGGAGGCC 548
QY 161 CysArgThrGlyAspArg 166
DB 549 TCCAGCAGAGGAGCAGG 566

RESULT 15
PCT-US94-04361-23
Sequence 23, Application PC/TUS9404361
GENERAL INFORMATION:
APPLICANT: Brigham and Women's Hospital
APPLICANT: 75 Francis Street
APPLICANT: Boston, MA 02115
APPLICANT: Bunn, H. Franklin
APPLICANT: Men, Danyl
APPLICANT: Showers, Mark O.
TITLE OF INVENTION: Erythropoietin Mutens With Enhanced
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3934

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/04361
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/049,802
FILING DATE: 21-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Cimbal, Michele A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 0627,336PC01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 679 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: both
PCT-US94-04361-23

Alignment Scores:
Pred. No.: 6,11e-81 Length: 679
Score: 676.00 Matches: 130
Percent Similarity: 86.75% Conservative: 14
Best Local Similarity: 78.31% Mismatches: 22
Query Match: 80.19% Indels: 0
DB: 5 Gaps: 0

US-09-813-775C-18 (1-166) x PCT-US94-04361-23 (1-679)

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    |||
DB 69 GCTCCCCACGCCCTCATCTGCCGACAGTTCGTGAGAGTACATCTAGAGCCCAAG 128
    |||

QY 21 GluAlaGluAsnIleThrThrGlyCysAlaGluHisCysSerLeuAsnGluAsnIleThr 40
    |||
DB 129 GAGGCGAAGAAATGTCAGATGGGTGTGCAGAAAGTCCAGACTGAGTGAATAATATACA 188
    |||

QY 41 ValProAspThrLysValAsnPhenylAlaTyrLysArgAsn**Ser**GlnGlnAla 60
    |||
DB 189 GTCCCGATACCAACTCACTTCTATGCTTGAAAAAGATGAGAGTGGAGAGACAGGCC 248
    |||

QY 61 ValGluValTyrPglngIleuAlaLeuLeuSerGluAlaValLeuArgGlyGlnAlaLeu 80
    |||
DB 249 ATAGAAGTTGGCAAGCCTGTCCCTGCTCTCAGAAAGCATCCTGCAGGCCAGGCCCTG 308
    |||

QY 81 LeuValAsnSerSerGlnProTyrPgluProLeuGlnLeuHisValAspLysAlaValSer 100
    |||
DB 309 CTAGCCAAATTCCTCCACAGCCACCAGAGACCTTCACCTCATATAGACAAAGCCATCAGT 368
    |||

QY 101 GlyLeuArgSerLeuThrThrLeuLeuArgAlaLeuGlyAlaGlnLysGluAlaIleSer 120
    |||
DB 369 GGTCTACGTAGCCTCCTCCTCCTGCTTGGGTACTGGAGCTCAGAAAGATGATGTGC 428
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QY 121 ProProAspAlaAlaSerAlaAlaProLeuArgThrIleThrAlaAspThrPheArgLys 140
    |||
DB 429 CCTCCAGATACACCCACCCTGCTCCACATCCGAAACATCACAGTGTACTTCTGCAAG 488
    |||

QY 141 LeuPheArgValTyrSerAsnPhenLeuArgGlyLysLeuLysLeuTyrThrGlyGluAla 160
    |||
DB 489 CTCTTCGGGGTCTACGCCCAACTTCTCTCGGGGAAACTGAAGCTGTACAGGGAGAGGTC 548
    |||

QY 161 CysArgThrGlyAspArg 166
    |||
DB 549 TGCAGAGAGGGGACAGG 566
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Search completed: January 8, 2003, 05:36:48
Job time: 44.454 secs

GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 8, 2003, 05:18:00 : Search time 42.5404 Seconds
(without alignments)
1717.360 Million cell updates/sec

Title: US-09-813-775c-18

Perfect score: 843
Sequence: 1 APPRLICDSRYLERYLLEAK.....NFLRGLKLYTGECARTGDR 166

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Searched: 389086 seqs, 220051671 residues

Total number of hits satisfying chosen parameters: 778172

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters: -DEV=x1h
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-TRANS=human40.cdi -LIST=45 -DOCLIGN=200 -THR_SCORE=pct -THR_MAX=100
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database: Published_Applications_NA:

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2: /cgn2_6/ptodata/1/pubpna/PCF_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
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3	325	38.6	423	10	US-09-864-761-16087
4	284	33.7	191	10	US-09-864-761-32584

5	81.5	9.7	2863	9	US-10-136-224-2	Sequence 2, Appl1
6	81.5	9.7	3686	9	US-10-136-224-3	Sequence 3, Appl1
7	81.5	9.7	3940	9	US-10-136-224-1	Sequence 1, Appl1
8	79	9.4	1663	10	US-09-070-927A-277	Sequence 277, App
9	79	9.4	2022	10	US-09-782-980-69	Sequence 67, Appl
10	79	9.4	2815	10	US-09-782-980-67	Sequence 67, Appl
11	76.5	9.1	7419	10	US-09-815-242-4009	Sequence 4109, Ap
12	73	8.7	174424	10	US-09-967-768A-314	Sequence 314, App
13	72	8.5	1290	10	US-09-764-847-1605	Sequence 1605, Ap
14	71	8.4	1443	10	US-09-901-884-15	Sequence 15, Appl
15	71	8.4	2000	10	US-09-887-576-853	Sequence 853, App
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17	71	8.4	3885	10	US-09-815-242-9626	Sequence 9626, Ap
18	71	8.4	9500	10	US-09-901-884-21	Sequence 21, Appl
19	71	8.4	17286	10	US-09-764-877-3334	Sequence 3234, Ap
20	70.5	8.4	1379	9	US-09-974-300-2909	Sequence 2909, Ap
21	70.5	8.4	2332	9	US-09-764-904-136	Sequence 136, Appl
22	70.5	8.4	2332	10	US-09-764-860-1197	Sequence 1197, App
23	70	8.3	554	10	US-09-864-761-15332	Sequence 15332, A
24	70	8.3	1934	10	US-09-909-446-15	Sequence 1, Appl1
25	70	8.3	1934	10	US-09-909-325-1	Sequence 1, Appl1
26	70	8.3	1934	10	US-09-909-326-1	Sequence 1, Appl1
27	70	8.3	180557	12	US-10-003-806-6	Sequence 6, Appl1
28	70	8.3	180557	12	US-10-003-806-9	Sequence 9, Appl1
29	69.5	8.2	2322	9	US-10-045-815-7	Sequence 7, Appl1
30	69.5	8.2	2416	9	US-10-045-815-5	Sequence 5, Appl1
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32	69	8.2	1119	10	US-09-974-300-4290	Sequence 4290, Ap
33	69	8.2	13957	10	US-09-782-378A-22	Sequence 22, Appl
34	69	8.2	13957	10	US-09-880-107-2284	Sequence 2284, Ap
35	68.5	8.1	4695	10	US-09-801-368-243	Sequence 243, App
36	68.5	8.1	21423	10	US-09-764-877-2835	Sequence 2835, Ap
37	68.5	8.1	40392	10	US-09-954-456-44	Sequence 44, Appl
38	68.5	8.1	40392	10	US-09-954-456-687	Sequence 687, App
39	68	8.1	1149	9	US-09-938-842A-2167	Sequence 2167, Ap
40	68	8.1	1171	9	US-09-945-182-25	Sequence 25, Appl
41	68	8.1	2149	10	US-09-925-301-130	Sequence 130, App
42	68	8.1	7626	9	US-10-001-835-82	Sequence 82, Appl
43	68	8.1	8160	10	US-09-070-927A-159	Sequence 159, App
44	67.5	8.0	332	10	US-09-878-574-2932	Sequence 2932, Ap
45	67.5	8.0	4605	10	US-09-070-927A-315	Sequence 315, App

ALIGNMENTS

RESULT 1
US-09-975-063-1
Sequence 1, Application US/09975063
Patent No. US20020045255A1
GENERAL INFORMATION:
APPLICANT: POWELL, Jerry S.
TITLE OF INVENTION: HUMAN ERYTHROPOIETIN GENE: HIGH LEVEL
EXPRESSION IN STABLY TRANSFECTED MAMMALIAN CELLS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dorsey & Whitney, LLP
STREET: Suite 3400, 1420 Fifth Avenue, U.S. Bank Centre
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 6.7/78
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/975,063
FILING DATE: 10-Oct-2001
ATTORNEY/AGENT INFORMATION:
NAME: Roberts, Mark W.
REGISTRATION NUMBER: 46,160
REFERENCE/DOCKET NUMBER: 500582.03 (112893.109)

OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: MS-WORD
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/011,858
 FILING DATE: 05-NO. US20020137145A1-2001
 ATTORNEY/AGENT INFORMATION:
 NAME: Roderics, Mark W.
 REGISTRATION NUMBER: 46,160
 REFERENCE/DOCKET NUMBER: 500582.13
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 206-903-8728
 TELEFAX: 206-903-8820
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2426 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 US-10-011-858-1

Alignment Scores:
 Pred. No.: 1,02e-63 Length: 2426
 Score: 567.00 Matches: 160
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 Best Local Similarity: 31.94% Mismatches: 4
 Query Match: 67.26% Indels: 337
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 QY 26 ----- 26
 Db 826 GGGCTTCAGGCACTCTCTCCAGATCCAGGAACCTGGCACTTGGTTGGGGTGGAGTTGG 885
 QY 26 ----- 26
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 Db 946 AACTAGGCAAGAGCAAAAGCCAGACAGATCTACGCTGTGGCCAGGGCCAGAGCTTCAG 1005
 QY 27 ----- 35
 Db 1006 GCAACCTTGACGCCCGGGCTGTGTCAATTTCAGACGGGCTGTGTGAACACTGCAAGCTT 1065
 QY 35 uAsnGluAsnIleThrValProAspThrLysValAsnPhetyrAlaTrpLysArqAsn-- 54
 Db 1066 GAATGGAATATCAGTGTCCAGACACCAAAAGTTAATTTCTAAGCTGTGGAAGAGATGGA 1125
 QY 54 ----- 54
 Db 1126 GGTGAGTCTTTTTTTTTTTTTTTTCTTTTGTGAGAAATCATTTGCGAGCCTGAT 1185
 QY 54 ----- 54
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 Db 1546 GAAAAATATGAGGCGCTGTATGGAATAGTTTCATTTATTCACATCAGTCACTCACTCA 1605
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 Db 1666 CTTGGGGCTGTGAGGGGCGAGAGAGAGGTGACATCCCTCAGCTGACTCCACAGATTC 1725
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 Db 1785 GGAAGCTGTCTCTCGGGGGCCAGGCCCTGTGTGGAACCTCTCCAGCCGCGGAGGCCCT 1844
 QY 91 uGlnLeuHisValAspLysAlaValSerGlyLeuArqSerLeuThrleuLeuArqAl 111
 Db 1845 GCAGCTGCATGTGATAAAGCCGTGAGTCCGACAGCTCACCACATCTCTCTGGGGC 1904
 QY 111 AlauGlyAla----- 114
 Db 1905 TCTGGGAGC-CCAGGTAGTAGAGCGGACACTTCTGCTTCCCTTTCCTTAAGAAAGCG 1963
 QY 114 ----- 114
 Db 1964 AGAAGGTTCTGCTAAGAGTACAGAACTGCTCCGATTCCTTCTCTGTGGCAGTG 2023
 QY 115 ----- 126
 Db 2024 CACGACCTTCCTGTTCTCTCTTGGCAGAAAGCAAGCCATCTCCCTCCAGATCGCGCTC 2083
 QY 126 rAlaAlaProLeuArqThrIleThrAlaAspThrPheArqLysLeuPheArqValYrse 146
 Db 2084 AGCTGCTCCACTCCGAACAATCACTGCTGACACTTTCGCAAACTTTCGGAATCTTAC 2143
 QY 146 rAsnPheLeuArqGlyLysLeuLysLeuYrThrGlyAlaLysArqThrLysAspAr 166
 Db 2144 CAATTTCTCTCGGGGAAAGCTGAAGCTGTACACAGGGAGGCTGCGAGGACAGGACAG 2203
 QY 166 g 166
 Db 2204 A 2204
 RESULT 3
 US-09-864-761-16087/c
 Sequence 16087, Application US/09864761
 Patent No. US20020048763A1
 GENERAL INFORMATION:
 APPLICANT: Penn, Sharon G.
 APPLICANT: Rank, David R.
 APPLICANT: Hanzel, David K.
 APPLICANT: Chen, Wensheng
 TITLE OF INVENTION: HUMAN GENOME- DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO

```

: TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
: FILE REFERENCE: Aecm1ca-x-1
: CURRENT APPLICATION NUMBER: US/09/864,761
: CURRENT FILING DATE: 2001-05-23
: PRIOR APPLICATION NUMBER: US 60/180,312
: PRIOR FILING DATE: 2000-02-04
: PRIOR APPLICATION NUMBER: US 60/207,456
: PRIOR FILING DATE: 2000-05-26
: PRIOR APPLICATION NUMBER: US 09/632,366
: PRIOR FILING DATE: 2000-08-03
: PRIOR APPLICATION NUMBER: GB 24263.6
: PRIOR FILING DATE: 2000-10-04
: PRIOR APPLICATION NUMBER: US 60/236,359
: PRIOR FILING DATE: 2000-09-27
: PRIOR APPLICATION NUMBER: PCT/US01/00666
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00667
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00664
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00669
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00665
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00668
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00663
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00662
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00661
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00670
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: US 60/234,687
: PRIOR FILING DATE: 2000-09-21
: PRIOR APPLICATION NUMBER: US 09/608,408
: PRIOR FILING DATE: 2000-06-30
: PRIOR APPLICATION NUMBER: US 09/774,203
: PRIOR FILING DATE: 2001-01-29
: NUMBER OF SEQ ID NOS: 49117
: SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
: SEQ ID NO 16087
: LENGTH: 423
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: OTHER INFORMATION: MAP TO AF053356.1
: OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.93
US-09-864-761-16087

Alignment Scores:
Pred. No.: 1.96e-33 Length: 423
Score: 325.00 Matches: 77
Percent Similarity: 62.60% Conservative: 0
Best Local Similarity: 62.60% Mismatches: 1
Query Match: 38.55% Indels: 46
DB: 10 Gaps: 1

US-09-813-775c-18 (1-166) x US-09-864-761-16087 (1-423)
OY 58 GINGINALAVALGUAITTPGILNGLYLEUALLEULSERGIUALAVALLEUARGLY 77
DB 370 CAGCGGCCGAGAGAGTGTGGAGGCGCTGCTGTGTGGAGCTGTCTCGGGGCG 311
OY 78 GINALALEULVALASERSEGINPRTPGILUPROLEUINLEUHISSALPLYS 97
DB 310 CAGGCGCTGTGGTCACTCTTCCAGCGCGTGGAGCCCCCTGCACCTCATGTGGATAA 251
OY 98 AAlAValSerGlyLeuArgSerLeuThrThrLeuLeuArgAlaLeuGlyAla----- 114
DB 250 GCCGTCAATGGCGCTTCGACAGCTCACCACTCTGCTTCGGGCTCTGGAGGC-CCAGGTGAG 192
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OY 114 ----- 114
DB 191 TAGAGCGGACACTTCTGCTTCCCTTCTGTAGAGGAGGAGGCTTGTAGGA 132
OY 114 ----- 114
DB 131 GTACAGAACTGTCCGTAATTCCTTCTTCTGTGGCACTGCAGCGACCTCCTGTTTCT 72
OY 115 -----GlnLysGluAlaIleSerProPsaPalaIleSerAlaIleProLeuArgThr 132
DB 71 CCTTGCGAAGAGGAGCATCTCCCTCAGATGCGCTCATGCTCTCAGTCCGAGACA 12
OY 133 ILehrAla 135
DB 11 ATCACTGCT 3

RESULT 4
US-09-864-761-32584/C
: Sequence 32584, Application US/09864761
: Patent No. US20020048763A1
: GENERAL INFORMATION:
: APPLICANT: Penn, Sharon G.
: APPLICANT: Rank, David R.
: APPLICANT: Hanzel, David K.
: APPLICANT: Chen, Wensheng
: TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
: FILE REFERENCE: Aecm1ca-x-1
: CURRENT APPLICATION NUMBER: US/09/864,761
: CURRENT FILING DATE: 2001-05-23
: PRIOR APPLICATION NUMBER: US 60/180,312
: PRIOR FILING DATE: 2000-02-04
: PRIOR APPLICATION NUMBER: US 60/207,456
: PRIOR FILING DATE: 2000-05-26
: PRIOR APPLICATION NUMBER: US 09/632,366
: PRIOR FILING DATE: 2000-08-03
: PRIOR APPLICATION NUMBER: GB 24263.6
: PRIOR FILING DATE: 2000-10-04
: PRIOR APPLICATION NUMBER: US 60/236,359
: PRIOR FILING DATE: 2000-09-27
: PRIOR APPLICATION NUMBER: PCT/US01/00666
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00667
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00664
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00669
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00665
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00668
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00663
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00662
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00661
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00670
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: US 60/234,687
: PRIOR FILING DATE: 2000-09-21
: PRIOR APPLICATION NUMBER: US 09/608,408
: PRIOR FILING DATE: 2000-06-30
: PRIOR APPLICATION NUMBER: US 09/774,203
: PRIOR FILING DATE: 2001-01-29
: NUMBER OF SEQ ID NOS: 49117
: SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
: SEQ ID NO 32584
: LENGTH: 191
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
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Db 526 GAATTAGTCCTAAGTCTCTGGAACATATGTTTGTACTTAACCAAGCAAGTA----- 579
Qy 49 TYRATATPRLYSARGASN***Ser***GlnGlnAlaValaGluValTrrpGlnGlyLeuAla 68
Db 580 -----CTTCTGGAAACAGTGAAGAAAGCTGTTCAATTGATGAGATTTACTT 627
Qy 69 LeuLeuSerGluAlaValaLeuArgGlyGlnAlaLeuLeuValaSerSerGlnProTrrp 88
Db 628 TTACAAAGCAAGCAAGCAATTAAGTTAAATGCAATCTTATTGAATCAG----- 675
Qy 89 GluProLeuGlnLeuHisValaLaspLysAlaValaSerGlyLeuArgSerLeuThrThrLeu 108
Db 676 -----ATTGCGCTTTTCTGCAA-----ACAAAAATT 702
Qy 109 LeuArgAlaLeuGlyAlaGlnLysGluAlaIleSerProProAspAlaAlaSerAlaAla 128
Db 703 TTGGCTAACAGATGGCTATCAACAAGCAATATTGCT-----CATACATTAAAGCTTCAT 756
Qy 129 Pro-----LeuArgThrIleThrAlaAspThrPheArgLysLeuPhe 142
Db 757 CCTTATCGAGTCAGTACGCTTACAAACAGTCGACGATTTGAAATGTCCTCGATTAGAA 816
Qy 143 ArgValTyrSerAspPheLeuArgGlyLysLeuLysLeuTrrhrgLys 159
Db 817 AGACTTATGATGATTAGTTGAAAAATGATTACCGCATGAAACGGGCCAA 867

RESULT 9

US-09-782-980-69
; Sequence 69, Application US/09782980
; Patent No. US20020072089A1
; GENERAL INFORMATION:
; APPLICANT: Khodadoust, Mehran M.
; APPLICANT: Macbeth, Kyle J.
; APPLICANT: Busfield, Samantha J.
; APPLICANT: McCarthy, Sean A.
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: Gu, Wei
; APPLICANT: White, David
; TITLE OF INVENTION: NOVEL ITALY, LOR-2, STRIFE, TRASH, BDSF, LRSG, AND
; TITLE OF INVENTION: STIMST PROTEIN AND NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: MNI-121CP
; CURRENT APPLICATION NUMBER: US/09/782,980
; CURRENT FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: PCT/US00/02125
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: 09/448,076
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: 09/276,400
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: 60/117,580
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 09/014,195
; PRIOR FILING DATE: 1998-01-27
; PRIOR APPLICATION NUMBER: 09/014,348
; PRIOR FILING DATE: 1998-01-27
; PRIOR APPLICATION NUMBER: 09/086,892
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: 09/296,208
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: 09/063,950
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 09/561,381
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 09/561,810
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 09/087,121
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: 09/672,721
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 09/049,799
; PRIOR FILING DATE: 1998-03-27

; NUMBER OF SEQ ID NOS: 176
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 69
; LENGTH: 2022
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2019)
US-09-782-980-69

Alignment Scores:
Pred. No.: 1.59 Length: 2022
Score: 79.00 Matches: 32
Percent Similarity: 40.83% Conservative: 17
Best Local Similarity: 26.67% Mismatches: 65
Query Match: 9.37% Indels: 6
DB: 10 Gaps: 3

US-09-813-775c-18 (1-166) x US-09-782-980-69 (1-2022)

Qy 19 AlalysgluAlaGlnAsnIleThrThrGlyCysAlaGluHisCysSerLeuAsnGluAsn 38
Db 458 AGCTCAAGCTGCCAGACATGACCTTGGGTGTGCCCCCATTTGACCTTGGCCGCTGC 517
Qy 39 IleThrValProAspThrLysValaAspPheTyrAlaTrrpLys-ArgAsn***Ser***G1 58
Db 518 TGCGTGTGACGTCAGCCAGCAACAGCATCCGACCCCTCGAAGCCGGAATCTGATACCG 577
Qy 58 ngIn-----AlaValGluVal---TrrpGln-GlyLeuAlaLeuLeuSerGluAlaVal 75
Db 578 CCAATGTAGAGCATGATGCTGGCTGAGGCTGAGGCTGCGCGCATGATGAGGG--C 634
Qy 75 euArgGlyGlnAlaLeuLeuValaAsnSerSerGlnProTrrpGluProLeuGlnLeuHis 95
Db 635 TTTTGGCGCGCTTCTCAACCTTCATGACTTGAATGTTCTTGACAAACCACTGGAGCAT 694
Qy 95 alaLysAlaValaSerGlyLeuArgSerLeuThrThrLeuLeuArgAlaLeuGlyAlaG 115
Db 695 TGCCATCTGATTCATCAAGCGCTGCGCTGACACGCCCTGGCGGCTGCGCAACACCC 754
Qy 115 IuLysgluAlaIleSerProProAspAlaAlaSerAlaAlaProLeuArgThrIle 133
Db 755 GTATTGCCAGATAGCGCCCGAGGACCTGCTGTGACTGCTGACCTTACAGGAATTG 810

RESULT 10

US-09-782-980-67
; Sequence 67, Application US/09782980
; Patent No. US20020072089A1
; GENERAL INFORMATION:
; APPLICANT: Khodadoust, Mehran M.
; APPLICANT: Macbeth, Kyle J.
; APPLICANT: Busfield, Samantha J.
; APPLICANT: McCarthy, Sean A.
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: Gu, Wei
; APPLICANT: White, David
; TITLE OF INVENTION: NOVEL ITALY, LOR-2, STRIFE, TRASH, BDSF, LRSG, AND
; TITLE OF INVENTION: STIMST PROTEIN AND NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: MNI-121CP
; CURRENT APPLICATION NUMBER: US/09/782,980
; CURRENT FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: PCT/US00/02125
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: 09/448,076
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: 09/276,400
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: 60/117,580
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 09/014,195

PRIOR FILING DATE: 1998-01-27
PRIOR APPLICATION NUMBER: 09/014,348
PRIOR FILING DATE: 1998-01-27
PRIOR APPLICATION NUMBER: 09/086,892
PRIOR FILING DATE: 1998-05-29
PRIOR APPLICATION NUMBER: 09/296,208
PRIOR FILING DATE: 1999-04-21
PRIOR APPLICATION NUMBER: 09/063,950
PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 09/561,381
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 09/561,810
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 09/087,121
PRIOR FILING DATE: 1998-05-29
PRIOR APPLICATION NUMBER: 09/672,721
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: 09/049,799
PRIOR FILING DATE: 1998-03-27
NUMBER OF SEQ ID NOS: 176
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 67
LENGTH: 2815
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: CDS
LOCATION: (197)..(2215)
US-09-782-980-67

Alignment Scores:
Pred. No.: 2.59 Length: 2815
Score: 79.00 Matches: 32
Percent Similarity: 40.83% Conservative: 17
Best Local Similarity: 26.67% Mismatches: 65
Query Match: 9.37% Indels: 6
DB: 10 Gaps: 3

US-09-813-775C-18 (1-166) x US-09-782-980-67 (1-2815)

OY 19 AlAluysgluAlaGluAsnIleThrGlyCysAlaGluHisCysSerLeuAsnGlu 38
DB 654 AGCTAGACGTGCGACACATGAGCTTGGGTTCGCCCATGACACTGCCCCGCTGC 713
OY 39 IleThrValProAspThrLysValAsnPhetYrAlaTrpLys-ArgAsn***Ser**G1 58
DB 714 TGCTCTTGACCTGACGCACACACACATCCAGCCCTGGAACCGGAATACGATACCG 773
OY 58 nGln-----AlaValGluVal---TrpGln-GlyLeuAlaLeuLeuSerGluAlaValL 75
DB 774 CCAATGTAGAGGCAATGAGCTGGCTGGCTGCGCTGCGGCACTGATGAGGGG---C 830
OY 75 euArgGlyGluAlaLeuValAsnSerSerGlnProTrpGluProLeuGlnLeuHisV 95
DB 831 TTTTGGCGCGCTTCAACCTCCATGACTTGATGTTTTCACAAACAGTTGGAGCAT 890
OY 95 aAlAspLysAlaValSerGlyLeuArgSerLeuThrThrLeuLeuValAlaLeuGlyAlaG 115
DB 891 TGCCATCTGTGATTCAGGCGCTGCGCTGACACAGCGCTGCGGCTGGTGGCAACACCC 950
OY 115 InLysGluAlaLeuSerProAspAlaAlaSerAlaAlaProLeuArgThrIle 133
DB 951 GTATTGCCAGATACGCGCCGAGACCTGCTGTGACTGCTTACAGGAATTC 1006

RESULT 11

US-09-815-242-4009
Sequence 4009, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyckind, Judith W.
APPLICANT: Wall, Daniel

APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 4009
LENGTH: 7419
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-815-242-4009

Alignment Scores:
Pred. No.: 22.6 Length: 7419
Score: 76.50 Matches: 38
Percent Similarity: 42.00% Conservative: 25
Best Local Similarity: 25.33% Mismatches: 60
Query Match: 9.07% Indels: 27
DB: 10 Gaps: 7

US-09-813-775C-18 (1-166) x US-09-815-242-4009 (1-7419)

OY 8 AspSerArgValLeuGluArgTrpLeuGluAlaLys-----GluAlaGlu 23
DB 3547 GATCCGTGCTGATGACGCGCTTCTCGTGAAGCATGACATCTGCTGACGCCGAG 3606
OY 24 AsnIleThrThrGlyCysAlaGluHis-----CysSerLeuAsn 36
DB 3607 GACCTGCTGAGCGCTGCGACGATCCGCGAGCGCCAGAACTGATGCTGCTGCC 3666
OY 37 GluAsnIleThrValProAspThrLysValAsnPhetYrAlaTrpLysArgAsn***Ser 56
DB 3667 GAGGAGCTCAGACACTGTCGACCGCGCGCC-----CGCATCCGAG 3708
OY 57 ***GlnGlnAlaValGluValTrpGlnGlyLeuAlaLeuLeuSerGluAlaValLeuArg 76
DB 3709 CTGCCACAGGTGGAAGAACTGCGCAGCGCTTGTAGATGCCCTGAGGAA 3768
OY 77 GlyGln-----AlaLeuLeuValAsnSerSerGlnProTrpGluProLeu 91
DB 3769 GCGCGCGTGGCGGTACGCCGCGCTTTCAGAGAAACCGCCAGGCGCGCGCTG 3828
OY 92 GlnLeuHisValAspLysAlaValSerGlyLeuArgSerLeuThrThrLeuLeuArgAla 111
DB 3829 ATCGGATGATGACGACAGGTGCGCGCGCTGCGAG---GTACGCCCGCGTGGAGCGG 3885
OY 112 LeuGlyAlaGlnLysGluAlaLeuSerProAspAlaAlaSerAlaAlaProLeu--- 130
DB 3886 GTCCGCGCGCTGCGACAGCTGTTGGAAGCGCC---GCCGCGAGGCGCTTCCCTTCA 3942
OY 131 -----ArgThrIleThrAlaAspThrPhe 138
DB 3943 GACCCGAGAGCTCTGCGCGCGACGATTC 3972

RESULT 12
 US-09-967-768A-314/c
 ; Sequence 314, Application US/09967768A
 ; Patent No. US20020150877A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Augustus, Meena
 ; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
 ; FILE REFERENCE: 689290-72
 ; CURRENT APPLICATION NUMBER: US/09/967,768A
 ; CURRENT FILING DATE: 2001-09-28
 ; PRIOR APPLICATION NUMBER: US/60/236,109
 ; PRIOR FILING DATE: 2000-09-28
 ; PRIOR APPLICATION NUMBER: US/60/236,034
 ; PRIOR FILING DATE: 2000-09-28
 ; PRIOR APPLICATION NUMBER: US/60/236,111
 ; PRIOR FILING DATE: 2000-09-28
 ; NUMBER OF SEQ ID NOS: 325
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 314
 ; LENGTH: 174424
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-967-768A-314

Alignment Scores:
 Pred. No.: 6.59e+03 Length: 174424
 Score: 73.00 Matches: 39
 Percent Similarity: 34.56% Conservative: 8
 Best Local Similarity: 28.68% Mismatches: 33
 Query Match: 8.66% Indels: 56
 DB: 10 Gaps: 9
 US-09-813-775C-18 (1-166) x US-09-967-768A-314 (1-174424)

QY 3 ProArgLeuIleCysAspSerArgValLeuGluArgTyrLeuGlnAlaLysGluAla 22
 |||||
 Db 139850 CCAGGCTGAGTGCAGTATGCCATCTATTACCACTG----- 139812
 QY 23 GluAsnIleThrThrGlyCysAlaGluHisCysSerLeuAsn----- 36
 |||||
 Db 139811 -----TGT-----CACTGCAGCCTGGATGTCCTGGGTTCAGTGAT 139776
 QY 37 -----GluAsnIleThrValProAspThrLysVal 46
 |||||
 Db 139775 CCTCCCACTCAGCCTCCTGAGTACCTGAGCTACCAATACACACCATCAACCCAGCT 139716
 QY 47 Asn-----PheTyrAlaTrpLysArgAsn***Ser**GlnGlnAlaValGluValTrpGln 65
 |||||
 Db 139715 AATTTTATTATTGTTGTAAGAA-----TGG--- 139689
 QY 66 GlyLeuAlaIleLeuSerGluAlaValLeuArg-----GlyGlnAlaLeuLeuValAsn 83
 |||||
 Db 139688 GGTCTCCTACGTTGTCCAGGGGTGCTTAACCTCCTGAGGTCAAGCAATCTT----- 139635
 QY 84 SerSerGlnProTrpGluProLeuGlnLeuHisValAspLysAlaValSerGlyLeuArg 103
 |||||
 Db 139634 CTTTCACACCTCCCAAGTGTGGATTGGCAGCATCAACCCAGCTGCCCTGACCTAAAA 139575
 QY 104 -----SerLeuThrThrLeuLeuArg 110
 |||||
 Db 139574 CTAATTTTGTGTTGTTTGGATGAGATGAGTCTACTCTGTGGCCAGG 139527

RESULT 13
 US-09-764-847-1605
 ; Sequence 1605, Application US/09764847
 ; Patent No. US20020132767A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 ; FILE REFERENCE: PC009
 ; CURRENT APPLICATION NUMBER: US/09/764,847
 ; CURRENT FILING DATE: 2001-01-17

; Prior application data removed - consult PALM or file wrapper
 ; NUMBER OF SEQ ID NOS: 2003
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 1605
 ; LENGTH: 1290
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-764-847-1605

Alignment Scores:
 Pred. No.: 6.67 Length: 1290
 Score: 72.00 Matches: 47
 Percent Similarity: 35.35% Conservative: 23
 Best Local Similarity: 23.74% Mismatches: 66
 Query Match: 8.54% Indels: 62
 DB: 10 Gaps: 5
 US-09-813-775C-18 (1-166) x US-09-764-847-1605 (1-1290)

QY 14 ArgTyrLeuGlnAlaLysGluAlaGluAsnIleThrThrGlyCysAlaGluHisCys 33
 |||||
 Db 560 CGGTATATCCACAAGCCGTGTAGCAGCGCACATTAAAGCTGTGTCACGCCATTGTGCTC 619
 QY 34 SerLeu----- 35
 |||||
 Db 620 AGTCTCTGCGCCTTCTCAACGCTCAACCCCTCCGCGACCGAGCTCCGACGCCCAT 679
 QY 36 -----AsnGluAsnIleThrValProAspThrLysValAsnPheTyr 49
 |||||
 Db 680 GCCTCTGACAGCCCTCTCTCGGAGCGCTCCAAAGCCCTGCAGCGCTCTCTCTCTCG 739
 QY 50 AlaTrp-LysArgAsn***Ser**GlnGlnAlaValGluValTrpGlnLysLeuAla 69
 |||||
 Db 740 TCTTGAAAGGTACAGAGTGTCCAGGCTATGCTGACAGTGTGGGGCCCTGGAAGTCT 799
 QY 69 uLeuSerGlu-AlaValLeu-----ArgG 77
 |||||
 Db 800 TTGTAGTACAGCGGGCTCTCTCTGACCTGAGCTGAGCTAGAGAGTGGGAGCGGGTGGCGG 859
 QY 77 GlnAlaLeuLeuValAsnSerSerGlnProTrpGluProLeuGlnLeuHisValAsp 97
 |||||
 Db 860 GTCATGACAGGCTCCACAGCCACCTGCGGCGGCTCCAGCAGCAGCAGCAGCAGCAGC 919
 QY 97 ysaAlaValSerGlyLeu-----ArgSerLeuThr 107
 |||||
 Db 920 GCCGAGGCGCTGGGCTGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 979
 QY 107 hTrpLeuArgAlaLeuGlyAlaGlnLysGluAlaIleSerProProAspAlaLys 127
 |||||
 Db 980 CCTGCTCTGCTGCTGCGGCTCCAGAGAGCGGTAAGTCTCCGCGCCGCGGCGGCGG 1039
 QY 127 IaAlaProLeuArgThrIleThrAlaAspThrPheArgLysLeuPhe----- 142
 |||||
 Db 1040 AACCTCTTCTTACATTATTAAGT-----TGTCTTTCATTATTTATTT 1084
 QY 143 -----ArgValTyrSerAsnPheLeuArgGlyLysLeuLys 154
 |||||
 Db 1085 CTTAGACATTTGATTAATCAATCACTTTCGATTTTTCAGATTAAATAATTAA 1134

RESULT 14
 US-09-901-884-15/c
 ; Sequence 15, Application US/09901884
 ; Patent No. US20020037573A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KYOMA HAKKO KOGYO CO., LTD.
 ; TITLE OF INVENTION: ForI-ATPase polypeptides and their genes
 ; FILE REFERENCE: 113290S1
 ; CURRENT APPLICATION NUMBER: US/09/901,884
 ; CURRENT FILING DATE: 2001-07-09
 ; PRIOR APPLICATION NUMBER: JP 2000-234317
 ; PRIOR FILING DATE: 2000-08-02
 ; NUMBER OF SEQ ID NOS: 21
 ; SOFTWARE: PatentIn version 2.1

```

: SEQ ID NO 15
: LENGTH: 1443
: TYPE: DNA
: ORGANISM: Corynebacterium ammoniagenes
US-09-901-884-15

Alignment Scores:
Pred. No.: 10.6 Length: 1443
Score: 71.00 Matches: 30
Percent Similarity: 34.62% Conservative: 15
Best Local Similarity: 23.08% Mismatches: 41
Query Match: 8.42% Indels: 44
DB: 10 Gaps: 5

US-09-813-775c-18 (1-166) x US-09-901-884-15 (1-1443)

QY 5 LeuileCysAspSerArgValIleuGIuArgYrIleuLeuGIuAlaIysGIuAlaGluAsn 24
DB 1284 CTTCTCTGGAGAGAAAGTTCTG-----GCCAAGAAAGCGCTCAAT 1243

QY 25 IleThrThrGIysAla----- 30
DB 1242 GCGAGC-----TGGCGCGTGAAGGTGATCTTGTCTCTTCAGACAGCTGTCATACC 1189

QY 31 -----GluHisCysSer 34
DB 1188 CAGAAATCCGATTAATATCTCGACTTCTTCTTCTGCAAAATGTATGATCAGCGCTG 1129

QY 35 LeuAsnGIuAsnIleThrValProAspThrIysValAsnPhenylAlaTrpIysArgAsn 54
DB 1128 AGCAACACGCGTAGTACCGCTCAGCAGAT-----GCTTGGCTCAGAAAT 1084

QY 55 *****Ser***GlnGlnAlaValGIuValTrpGlnGlyLeuAlaLeuLeuSerGIuAla 73
DB 1083 ACGAGACGTGCGACGACGTGGTTCACGTGCTGAGATACCTTGGAAGCAATGCGCAG 1024

QY 74 ValIleArgGIuGIuAlaIleuLeuValAsnSerGIuProTrpGIuProLeuIleu 93
DB 1023 GTCAAGCTCGGGTGTTCATCAAGTGAAGCAAGGTGCTGCTGGAAGTGGGTGAGTGA 964

QY 94 HisValAspIysAlaValSerGIuLeuArg 103
DB 963 GTCATCGGACGAGACGTAAACGCGCTGCAG 934

RESULT 15
US-09-887-576-853
: Sequence 853, Application US/09887576
: Patent No. US20020144047A1
: GENERAL INFORMATION:
: APPLICANT: Budworth, P.
: APPLICANT: Brown, D.
: APPLICANT: Chang, H.
: APPLICANT: Zhu, T.
: APPLICANT: Han, B.
: APPLICANT: Wang, X.
: APPLICANT: Cooper, Bret
: TITLE OF INVENTION: Promoters for regulation of plant expression
: FILE REFERENCE: 1360.001US1
: CURRENT APPLICATION NUMBER: US/09/887,576
: PRIOR APPLICATION NUMBER: US 60/213,848
: PRIOR FILING DATE: 2000-06-23
: PRIOR APPLICATION NUMBER: US 60/214,087
: PRIOR FILING DATE: 2000-06-23
: PRIOR APPLICATION NUMBER: US 60/258,692
: PRIOR FILING DATE: 2000-12-29
: NUMBER OF SEQ ID NOS: 875
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 853
: LENGTH: 2000
: TYPE: DNA
: ORGANISM: Oryza sativa
US-09-887-576-853

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Alignment Scores:
Pred. No.: 17.1 Length: 2000
Score: 71.00 Matches: 32
Percent Similarity: 47.41% Conservative: 23
Best Local Similarity: 27.59% Mismatches: 41
Query Match: 8.42% Indels: 20
DB: 10 Gaps: 7

US-09-813-775c-18 (1-166) x US-09-887-576-853 (1-2000)

QY 32 HisCys-----SerLeuAsnGIuAsnIleThrValProAspThrIysVal 46
DB 408 CATTCTATTTCATTATCATAGCATTCACCAACATTCCTCATTTCACTCCAAAGCTA 467

QY 47 AsnPhenylAlaTrpIysArgAsn***Ser***GlnGlnAlaValGIuValTrpGlnGly 66
DB 468 AATTTTAGCCATTATAGTAAATAATGTCTCCCAACACATTTCCAACTGGCCAAAC 527

QY 67 LeuAlaLeuLeuSerGIuAlaValIleuArgGIuAlaIleuValAsnSerGIu 86
DB 528 CTTCTCCACTAGCCAAATTT-----GGTACGCCAAAGTC-----ACTAGGCAA 572

QY 87 ProTrpGIuProLeuGIuLeuHisValAspIysAlaValSerGIuLeuArgSerIleuThr 106
DB 573 CCGTGG-----GCCCTACACACATTCCTCCCATCTCCTCCG----- 614

QY 107 ThrLeuArgAlaIleuGIuAla-----GlnIysGIuAlaIleSerProProAsp 123
DB 615 ---CTCCTCTCCGATGGCTCGACACACAGCTCTCCAAAGCTCTGCGCGCGCTT 671

QY 124 AlaIleSerAlaIleProLeuArgThrIleThrAlaAspThrPheArg 139
DB 672 GCCGCGACCTCCACCGCTCCACACCGTAGCCACAGCCGCCGC 719

Search completed: January 8, 2003, 07:53:24
Job time : 91.5404 secs

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TITLE Direct Submission
JOURNAL Submitted (12-APR-2000)

COMMENT This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at <http://www.genoscope.cns.fr/Tetraodon>.

FEATURES Location/Qualifiers

source
1..1035
/organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="224N04"
/clone_lib="G"
/note="Genoscope sequence ID : C0AG224DG02SP1-end : PUC-ori"

BASE COUNT 164 a 306 c 302 g 252 t 11 others
ORIGIN

Alignment Scores:

Pred. No.:	11.9	Length:	1035
Score:	82.50	Matches:	34
Percent Similarity:	46.79%	Conservative:	17
Best Local Similarity:	31.19%	Mismatches:	43
Query Match:	9.79%	Indels:	15
DB:	17	Gaps:	5

US-09-813-775C-18 (1-166) x CNS02175 (1-1035)

```
QY 60 AlAValGluValTrpGlnGlyLeuAlaLeuSerGluAlaValLeuArgGlyGlnAla 79
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 227 GCTGCTCCGCGATGATACGAGAGGTGTGCACCTCTCTCTCTCCACAGTGTACC 286
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 80 -----LeuLeuValAsnSerSerGlnProTrpGluProLeuGlnLeuHisValAspLys 97
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 287 ACCTTCTTATCTGCTCCCTACGATGTCCTG-----GTGGAGATC 328
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 98 AlAValSerGlyLeuArgSerLeuThrThrLeuLeuArgAlaLeuGlyAlaGlnLysGlu 117
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 329 GCAGGACAGGAGCTCGCCACGCGCTACAGTACGCCGCTGTCGCCGACCCCGGGG 388
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 118 AlaIleSerProProAspAlaIleSerAlaAlaProLeuArgThrIleThrAlaAspThr 137
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 389 GCCCGCAGCGCGCCCGACAGCTCTCTCTCGCTCTCTCCACGATGACGCGGACAGC 448
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 138 PheArgLysLeuPheArgValTyrSerAsnPheLeuArgGlyLys---LeuLysLeuTyr 156
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 449 -----CTGGCGATGGCGGCGCTCCCTTCAGGGTCGAGTGTGGCGGTGTAC 499
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 157 ThrGly-----GluAlaCysArg 162
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 500 GACGAGACAGCAGCAGCGGTGTGCG 526
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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Search completed: January 8, 2003, 07:51:02
Job time : 1407.74 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: January 8, 2003, 05:16:34 ; Search time 1392.74 Seconds
(without alignments)
1930.339 Million cell updates/sec

Title: US-09-813-775c-18

Perfect score: 843

Sequence: 1 APPRLICDSRVLEERYLEAK.....NFLRGKLYGTGACRTGDR 166

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlh
-O=/cgn2.1/USPTO.spool/US09813775/runal.07012003.153122.23837/app.query.fasta_1.718
-DB=EST -OPMT=fasta -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdt -LIST=45
-DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pco -NOR=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09813775.@CN1.1.821.@runal.07012003.153122.23837 -NCPU=6 -ICPU=3
-NO_XLPHY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMECUT=120
-MARN_TIMECUT=30 -THRFADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELPE=6 -DELEXT=7

Database :
EST :
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_estl:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estcom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inu:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_tod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	441.5	52.4	567	9	AA662379	AA662379 nu93601.s
2	179	21.2	686	13	BM438685	BM438685 IPLVr0146
3	141	16.7	444	10	BE663803	BE663803 147806 MA
4	120	14.2	968	17	CNS02P50	AL194613 Tetraodon
5	106	12.6	365	13	BM279790	BM279790 zah5505 Z
6	105.5	12.5	611	13	BM315886	BM315886 fw66c09.Y
7	92	10.9	593	14	BM931504	BM931504 UI-E-EJ1-
8	92	10.9	657	14	BM185758	BM185758 UI-E-EJ1-
9	87.5	10.4	598	17	AZ413715	AZ413715 1M0197C23
C 10	86.5	10.3	721	17	AZ981594	AZ981594 2M0262N06
11	84.5	10.0	759	13	BM072805	BM072805 MEST53-HO
12	84	10.0	2793	11	AK012169	AK012169 Mus muscu
13	83.5	9.9	619	14	BM931641	BM931641 UI-E-EJ1-
14	82.5	9.8	656	17	AZ572463	AZ572463 306PVC10
15	82.5	9.8	1035	17	CNS02175	AL176522 Tetraodon
C 16	81.5	9.7	800	13	B1909650	B1909650 60306680
17	81.5	9.7	899	12	BG173674	BG173674 602336813
C 18	81.5	9.7	908	17	CNS076E5	AL431283 T7 end of
19	81	9.6	867	12	BF184120	BF184120 601843157
20	80.5	9.5	662	13	BM103178	BM103178 fV41h09.Y
C 21	80.5	9.5	1142	14	BM906657	BM906657 AGENCOURT
22	79.5	9.4	524	13	BM437324	BM437324 VVA017G09
23	79.5	9.4	533	14	BQ462002	BQ462002 HD02J17-
24	79.5	9.4	655	10	AV914315	AV914315 AV914315
25	79.5	9.4	675	17	BM466321	BM466321 BOGHX18TF
26	79	9.4	520	13	B1490151	B1490151 BJA90151
27	79	9.4	770	14	BO751539	BO751539 EST632102
28	79	9.4	809	14	BO750964	BO750964 EST631527
29	79	9.4	938	14	BO919901	BO919901 AGENCOURT
C 30	78.5	9.3	895	12	BE914444	BE914444 601668826
C 31	78	9.3	395	10	AV696100	AV696100 AV696100
C 32	78	9.3	584	9	AA198958	AA198958 mU16406.r
C 33	78	9.3	612	10	AV734270	AV734270 AV734270
34	78	9.3	753	12	BF234939	BF234939 602027383
35	78	9.3	832	12	BF310420	BF310420 601895074
36	78	9.3	1002	12	BE963020	BE963020 601566203
37	77.5	9.2	525	14	B0617331	B0617331 fab03a08.
38	77.5	9.2	700	12	BG908975	BG908975 Talr117XG
39	77.5	9.2	804	13	B1088996	B1088996 602833543
40	77.5	9.2	895	10	BE559607	BE559607 601347245
41	77.5	9.2	1375	13	BM542459	BM542459 AGENCOURT
C 42	77	9.1	559	12	BE754300	BE754300 207777 MA
C 43	77	9.1	632	10	AW757556	AW757556 874002A10
C 44	77	9.1	657	14	BP017930	BP017930 BP017930
C 45	77	9.1	663	12	BG859057	BG859057 1024061B0

ALIGNMENTS

RESULT 1
AA662379/c
LOCUS nu93601.s1 NCI_CGAP_Pr22 Homo sapiens CDNA clone IMAGE:1218288 3'
DEFINITION similar to gb:s65458 ERYTHROPOIETIN PRECURSOR (HUMAN);. mRNA
sequence.
ACCESSION AA662379
VERSION AA662379.1 GI:2616470
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 567)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.


```

Oy 56 -----Ser***GinginalaValGluValr 64
Db 603 TTCGCATTCACCTCTTTACTCTTTGGCAAGCATCAGGAGGAGGAGGAGTGA 662
Oy 64 polnGlyLeuAlaLeuLeuSerGluAlaValLeuArgGlyGlnAlaLeuValAsnse 84
Db 663 GTCTGGCTTGTGCTCTACACAGGCTTCACGACTTCGTCCACCAAGCC 722
Oy 84 rserGlnProTPrGluProLeuGlnLeuHisValAspLysAlaValSerGlyLeuArgse 104
Db 723 ACC-----CTGCACAGCCACATAGACAGCCGCTCCGAACTGCTCAG 767
Oy 104 rleuThrThrLeuLeuArgAlaLeuGlyAlaGln 115
Db 768 CCTCAAGCTGTGCTGCGACCTCAAAACATCCAG 801

RESULT 5
LOCUS BM279790 365 bp mRNA linear EST 30-DEC-2001
DEFINITION zahn505 Zebrafish Adult hearts cDNA library Danio rerio cDNA clone
zahn505 5', mRNA sequence.
ACCESSION BM279790.1 GI:17999056
VERSION BM279790.1
KEYWORDS EST.
SOURCE zebrafish.
ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes
; Cyprinidae; Danio.
1 (bases 1 to 365)
AUTHORS Ton, C., Dempsey, A.A., Hwang, D.M. and Liew, C.C.
TITLE Identification and Characterization of Expressed Sequence Tags from
zebrafish Adult Hearts cDNA Library
JOURNAL Unpublished (2001)
COMMENT Contact: Liew CC
Brigham and Women's Hospital
Harvard Medical School
75 Francis St. Boston, MA 02115, USA
Tel: 6177328915
Fax: 6179750995
Email: cliw@rics.bwh.harvard.edu
PCR Primers
FORWARD: 5' GCCAAGCTCGAATTACCCCTCAGTAAAGG 3'
BACKWARD: 5' CCACTGAATGTATACGACTCAGTATAGGCG 3'
Insert Length: 365 Std Error: 0.00
Seq primer: T3.
FEATURES
Source 1. Location/Qualifiers
1..365
/organism="Danio rerio"
/db_xref="taxon:7955"
/clone="zahn505"
/clone_lib="zebrafish Adult hearts cDNA library"
/dev_stage="adult"
/note="Organ: heart; Vector: Lambda ZAP Express; Site_1:
EcoRI; Site_2: XhoI; mRNA was purified from zebrafish
adult hearts. cDNA was synthesized using a XhoI-Oligo dT
adaptor primer. EcoRI adaptors were ligated, followed by
digestion with XhoI, for directional cloning into
pre-digested lambda ZAP Express vector."
BASE COUNT 69 a 89 c 95 g 112 t
ORIGIN
Alignment Scores:
Pred. No.: 0.00262 length: 365
Score: 106.00 Matches: 21
Percent Similarity: 65.96% Conservative: 10
Best Local Similarity: 44.68% Mismatches: 16
Query Match: 12.57% Indels: 0
Gaps: 0
US-09-813-775c-18 (1-166) x BM279790 (1-365)

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Oy 1 AlaProProArgLeuLeuLysAspSerArgValLeuGluArgTyrLeuLeuAlaLys 20
Db 222 TCCCATATACGCCCATCTGACCTGCCTCTGACCATTTATTAAGAGGACATGG 281
Oy 21 GluAlaGluAsnIleThrThrGlyCysAlaGluHisCysSerLeuAsnGluAsnIleThr 40
Db 282 GATGACAGAGGCTGCTATGAGAACTTGTAAGACGATTCGACATTGCAACGACGTACT 341
Oy 41 ValProAspThrLysValAsn 47
Db 342 GTTCTTTGACCAAGATGCAT 362

RESULT 6
LOCUS BM315886 611 bp mRNA linear EST 03-JAN-2002
DEFINITION f666c09.y1 sugano STD adult male Danio rerio cDNA clone 5612560 5'
similar to SW:ERP_MOUSE P07321 EXTHROPOLEITIN PRECURSOR. [1] ;,
mRNA sequence.
ACCESSION BM315886
VERSION BM315886.1 GI:18050231
KEYWORDS EST.
SOURCE zebrafish.
ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes
; Cyprinidae; Danio.
1 (bases 1 to 611)
AUTHORS Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy
, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood
, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B.,
Swaller, T., Gibbons, M., Page, D., Harvey, N., Schurk, R., Ritter, E.,
Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R.
and Wilson, R.
TITLE WashU Zebrafish EST Project 1998
JOURNAL Unpublished (1998)
COMMENT Other_ESTs: f666c09.x1
Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: zbratfish@wustl.edu
Library constructed by Dr. Sumio Sugano and Dr. Koichi Kawakami DNA
Sequencing by: Washington University Genome Sequencing Center Clone
distribution information can be found through the I.M.A.G.E.
Consortium/BLNI, send email to: info@image.llnl.gov
Seq primer: T3 ET from Amersham
High quality sequence stop: 526.
FEATURES
Source 1. Location/Qualifiers
1..611
/organism="Danio rerio"
/db_xref="taxon:7955"
/clone="5612560"
/clone_lib="Sugano STD adult male"
/dev_stage="adult"
/note="Tissue_type="whole body"
/lab_host="DH10B (phage resistant)"
/note="Vector: pME18S-FL3; Site_1: DraIII (CACCATGG);
Site_2: DraIII (CACTGTGG); 1st strand cDNA was primed
with an oligo(dT) primer [ATGTGGCTTTTCTTTTCTTTTCTTTT];
double-stranded cDNA was ligated to a DraIII adaptor
[TTGTGGCTTCTAGG], digested and cloned into distinct DraIII
sites of the pME18S-FL3 vector (5' site CACTGTGG, 3' site
CACCATGG). XhoI should be used to isolate the cDNA
insert. Size selection was performed to exclude fragments
<1.5kb. Library constructed and donated by Dr. Sumio
Sugano (University of Tokyo Institute of Medical Science).
Custom primers for sequencing: 5' end primer
CTTCTGCTTAAAGCTGGC and 3' end primer
CGACCTGCAGCTCGACGACA."
BASE COUNT 156 a 172 c 144 g 139 t
ORIGIN

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="UI-E-EJ1-ajp-f-03-0-UI"
/tissue_type="fetal eyes, lens, eye anterior segment,
optic nerve, retina, Retina Foveal and Macular, RPE and
Choroid"
/dev_stage="fetal and adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/note="Organ: eye; Vector: pT73-Pac (Pharmacia) with a
modified polylinker; Site:1: Ecor I; Site:2: Not I;
UI-E-EJ1 is a subtracted cDNA library constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an Ecor I adaptor, digested
with Not I, and cloned directionally into pT73-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dt)18 tail. The
sequence tags for this library are: fetal eyes, AGATCAGACA
; lens, CGATTAGCGA; eye anterior segment, AATGCCGAT;
optic nerve, CCATTAGTG; retina, CCGCG; Retina Foveal and
Macular, GTCC; RPE and Choroid, ACCCA. This library was
created for the program, Gene Discovery in the Visual
System, supported by National Eye Institute (NEI)."
BASE COUNT      166 a      189 c      176 g      123 t
ORIGIN

```

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Alignment Scores:
Pred. No.:      0.376      Length:      657
Score:          92.00      Matches:      21
Percent Similarity: 95.45%  Conservative: 0
Best Local Similarity: 95.45%  Mismatches: 1
Query Match:    10.91%      Indels:      1
DB:             14         Gaps:        0

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US-09-813-775c-18 (1-166) x BQ185758 (1-657)

QY 145 TTTSeranpheleuarglylsleuylsleutyrrhglglualacysartrhgly 164
 LOCUS |||||||
 DEFINITION 3 TACTCCATTTCCTCGGGGAAAGTG-AGCTGTACACAGGGAGGCTCGACGACAGG 61
 Db

QY 165 Asparg 166
 ||||||
 Db 62 GACAGA 67

RESULT 9

AZ413715 598 bp DNA linear GSS 03-OCT-2000
 LOCUS AZ413715
 DEFINITION 1M0197C23R Mouse 10kb plasmid UDCG1M library Mus musculus genomic
 clone UDCG1M0197C23 R, DNA sequence.

ACCESSION AZ413715
 VERSION AZ413715.1 GI:10537728
 KEYWORDS GSS.

SOURCE house mouse.

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 598)

REFERENCE

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,
 M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
 and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT
 84112 USA
 Tel: 801 585 5606

```

FEATURES
source
1..598
Location/Qualifiers
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UDCG1M0197C23"
/clone_lib="Mouse 10kb plasmid UDCG1M library"
/sex="Male"
/note="Vector: PMD42rv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with r4 DNA polymerase and r4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (911473211419b/AP129072.1) a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

```

```

BASE COUNT      151 a      129 c      144 g      174 t
ORIGIN

```

```

Alignment Scores:
Pred. No.:      1.21      Length:      598
Score:          87.50      Matches:      39
Percent Similarity: 37.76%  Conservative: 15
Best Local Similarity: 27.27%  Mismatches: 44
Query Match:    10.38%      Indels:      45
DB:             17         Gaps:        7

```

US-09-813-775c-18 (1-166) x AZ413715 (1-598)

QY 9 SerArgValLeuGluArgTyrLeuGluAlaLysGluAlaGlnIleThrThrgly 28
 ||| |||
 Db 185 AGCAATTCGCTTGACACAACTTACTTTGTATTTTGAAGTTTGAAATTTGACGACATCA 244

QY 29 CysAlaGlu---HisCysSerLeuAsnGlnIleThrValProAspThrLysAlasn 47
 ||| |||
 Db 245 GCTCTCCAGAGGACATTC-----ATTGCG 268

QY 48 PheTyrAlaTrp-----LysArgAsn**Ser**GlnGlnAla 60
 ||| |||
 Db 269 TTTCTTCAGTGGGATGTCATTCACAGTTCGAAACCTTAGTGGATATAGTGGGCT 328

QY 61 ValGluValTTPGln-----GlyLeuAlaLeuLeuSerGlu 72
 ||| |||
 Db 329 GTCCAGCTGCTGCTTGTGAAAGTGGCCCGACATGCTGATACAGTCTGCTCCCAAT 388

QY 73 AlaValLeuArgGlyGlnAlaLeuValAsnSer-----SerGlnProTrp----- 88
 ||| |||
 Db 389 TCAAAGTATTAATGGTGAAGCTCTTTGTACGACACATCCGACACTGGGTGTC 448

QY 89 -----GluProLeu-----GlnLeuHisVal 95
 ||| |||
 Db 449 TGTGAGACTGACAGCGGCTGAAAGCCTAATGATTACCAAGAGAAATGCTGACACA 508

QY 96 AspLysAlaValSerGlyLeuArgSerLeuThrThrLeuLeuArgAlaLeuGlyAlaGln 115

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Db      509 GTTACAGCCTCAGCCGGGTGGTGGCTCAGACCTTATCCAGCCCTTGGAGGACAG 568
Qy      116 LysGluAla 118
        |||||
Db      569 AAGGAGCA 577

RESULT 10
A2981594      721 bp      DNA      linear      GSS 27-APR-2001
LOCUS      2M0262N06F Mouse 10kb plasmid UUGC2M library Mus musculus genomic
DEFINITION      clone UUGC2M0262N06 F, DNA sequence.
ACCESSION      A2981594
VERSION      A2981594
KEYWORDS      GSS.
SOURCE      house mouse.
ORGANISM      Mus musculus.
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
              1 (bases 1 to 721)
              Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
              Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
              M., Rose,M., Rose,R., Stokes,R., Tinney,A., von Niederhasern,A.
              and Wright,D., Weils,R.
              Mouse whole genome scaffolding with paired end reads from 10kb
              plasmid inserts
              Unpublished (2000)
              Contact: Robert B. Weiss
              University of Utah Genome Center
              Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
              84112, USA
              Tel: 801 585 5606
              Fax: 801 585 7177
              Email: ddunn@genetics.utah.edu
              Insert length: 10000 Std error: 0.00
              Plates: 0262 row: N column: 06
              Seq primer: CGTGTAAACGACGCGCGGT
              Class: plasmid ends
              High quality sequence stop: 721.
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                /strain="C57BL/6J"
                /db_xref="taxon:10090"
                /clone="UUGC2M0262N06"
                /clone_lib="Mouse 10kb plasmid UUGC2M library"
                /sex="Female"
                /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
                /note="Vector: PMD42nv; Purified genomic DNA from M.
                musculus C57BL/6J (female) was obtained from the Jackson
                Laboratory Mouse DNA Resource
                (http://www.jax.org/resources/documents/dnares/). The DNA
                was hydrodynamically sheared by repeated passage through a
                0.005 inch orifice at constant velocity. The sheared DNA
                was blunt end-repaired with T4 DNA polymerase and T4
                polynucleotide kinase. Adaptor oligonucleotides were
                ligated to the blunt ends in high molar excess. The
                adaptor DNA was purified and size-selected for a 9.5 to
                10.5 kb range using preparative agarose gel
                electrophoresis. Vector DNA was prepared from a derivative
                of PMD42 (g11473211419b|AF129072.1), a copy-number
                inducible derivative of plasmid R1. The vector was ligated
                with adaptors complementary to the insert adaptors and
                purified. The sheared, adaptor mouse DNA was annealed to
                adaptor vector DNA, and transformed into
                chemically-competent E. coli XL10-Gold (Stratagene) cells
                and selected for ampicillin resistance."
BASE COUNT      193 a      172 c      160 g      196 t
ORIGIN
Alignment Scores:      2.15      Length:      721
Pred. No.:

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Score:      86.50      Matches:      31
Percent Similarity:      45.74%      Conservative:      12
Best Local Similarity:      32.98%      Mismatches:      41
Query Match:      10.26%      Indels:      10
DB:      17      Gaps:      3

US-09-813-775c-18 (1-166) x A2981594 (1-721)
Qy      48 PheTYAlATrPrYsArGAsn**Ser**GlnGlnAlaValGluValTrpGlnGlyLeu 67
        |||      |||      |||      |||      |||      |||      |||
Db      721 TTGACCGGATGGGAAATGTGAGATGCGTCATGCCAAGAAAGTCTATTTGGCACTTTCTG 662
Qy      68 Ala-----LeuLeuSerGlnAlaValLeuArgGlyGlnAlaLeuValAsn 83
        ::      ::      ::      ::      ::      ::      ::
Db      661 TCACGATTCCTTGACATGACATACAGCGGTACACACTGAACCTCTGTAGTGA 602
Qy      84 SerSerGlnProTrpGluProLeuGlnLeuHisValAspLysAlaValSerGlyLeuArg 103
        |||||      |||||      |||
Db      601 CTCAGCCAGAGCTGGGAACCTTCATCTCTC-----CTCTGTGGGGGTACCTTA 554
Qy      104 SerLeuThrThrLeuLeuArgAlaLeu-GlyAlaGlnLysGluAlaLeuSerProProAs 123
        |||      |||      |||      |||      |||      |||      |||
Db      553 GAAACATGCACGCCCTTGGAATGCCATACAGCTCTGAGAGAAAGA---AGCCCTCGG 497
Qy      123 palAAlaSerAlaAlaProLeuArgTrpThrAlaAsp 136
        |||      |||      |||      |||      |||      |||
Db      496 TACCTGTTCTGGAAGCGCTCTCAGAACATACACTGAGAC 457

RESULT 11
BM072805      759 bp      mRNA      linear      EST 13-NOV-2001
LOCUS      MEST53-H09.T3 ISDN4-TN Zea mays cDNA clone MEST53-H09 3', mRNA
DEFINITION      MEST53-H09.T3 ISDN4-TN Zea mays cDNA clone MEST53-H09 3', mRNA
sequence.
ACCESSION      BM072805
VERSION      BM072805.1 GI:16916346
KEYWORDS      EST.
SOURCE      Zea mays.
ORGANISM      Zea mays.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 759)
Glu,F., Cui,F., Guo,L., Ashlock,D.A., Wen,T.J. and Schnable,P.S.
Expressed Sequence Tags from B73 Maize Seedlings and Silks
Unpublished (2001)
Contact: Patrick S. Schnable
Schnable Laboratory
Iowa State University
6405 Agronomy, Iowa State University, Ames, IA 50011-1010, USA
Tel: 515-294-0975
Fax: 515-294-2299
Email: schnable@iastate.edu
Individual basecall and confidence value were assigned using the
Phred software,
(<http://depts.washington.edu/ventures/collabtr/direct/index.htm>#
rt). Overall sequence quality assessment and vector trimming were
conducted using the Lucy software (<http://www.tigr.org/softlab/>).
Lucy parameters were set to ensure an overall trimmed quality of
97.5% or better without any vector fragments in the chosen
high-quality region of each sequence. Low-quality bases between the
poly-T and the high-quality region were replaced with N's to serve
as spacers.
PCR Primers
FORWARD: Forward PCR primer sequence, primer T7-1 (AA TAC GAC TCA
CTA TAG)
BACKWARD: Backward PCR primer sequence, primer T3 (ATT AAC CCT CAC
TAA AG)
Seq primer: primer T3 (ATT AAC CCT CAC TAA AG).
Location/Qualifiers
        1..759
        /organism="Zea mays"
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        /db_xref="taxon:4577"
FEATURES
source

```

```

/clone="MEST53-H09"
/clone_lib="ISDMA-TN"
/tissue_type="Seedling and silk"
/lab_host="DH10B"
/notes="vector: pT7T3PAC; Site_1: EcoRI; Site_2: NotI;
ds-cDNA molecules were generated as follows. First-strand
cDNA was prepared from oligo-dT selected mRNA by priming
with a NotI oligo-dT primer (5',
AATCGAGAGAAATTTCGGCGCCACAGAAATTTTATTTTATTTT). The
resulting DNA:RNA hybrid was treated with RNase H and used
as a template for DNA PolI-catalyzed second strand
synthesis. After the addition of EcoRI adaptors, the
ds-cDNAs were digested with NotI and size-selected. The
resulting molecules were directionally cloned into the
EcoRI and NotI sites of the pT7T3PAC vector. The library
then went through one round of normalization to C0t value
of 5 based on the methods of Marcelo Bento Soares (Genome
Research 6: 791-806, 1996)."
```

Alignment Scores:	
Pred. No.:	4.17
Score:	84.50
Percent Similarity:	43.56%
Best Local Similarity:	26.38%
Query Match:	10.02%
DB:	13
Gaps:	7

[illegible]

```

Oy 40 -----ThrValProAspHisLysValAsn-----Phe 48
Db 347 CTCCTCAGCAGGCGATTATTTGACTTGAAGGTTCCTGACTCTGACAGTCCAGAGTT 406
Oy 49 TyrAla-TrypIysArg-----Asn**Ser**GlnGlnAlaValGluValTr 64
Db 407 TACACTCTTTGTCACAGGACGACAGATTAATACTTCTCATCCACAAACACAGATGTT-- 466
Oy 64 pGlnIysLeuAlaLeuLeuSerGluAla-----ValLeuArgIysI 78
Db 465 ----ACACACAGTTTATGCTCAGAGAGGTGTTGGACACACACTGCGGAGTGTGAAGTCCCA 526

```

```

Oy      78  nAlaIeuValuIaInserSerGInProTPoluProIeuInIeuInuValaLysAl  98
      ||||| ||||| ||||| ||||| |||||
Db      521  TgCTTGAATGGCTTGTGTCCAGTGAACCGAGTAAAGTTCTTTGCGGAGATGACAGTGA  580

Oy      98  aValSerIly-----LeuArgSerLeuThr---ThrIeuValaGlyAlaLeuGl  112
      ||||| ||||| ||||| ||||| |||||
Db      581  AATCACTGCGCGTTGATGCGCCACTGAGGATGAACACTGCTTCAAGTGTACTTCTTGAAC  640

Oy      113  yAlaGInLysGluAlaIleSerProTioAspAlaIleSerAlaIaProIeuArgTruIl  133
      ::|||:: ||||| ||||| |||||
Db      641  AGGAATTCCTCCAGGCGATGATGCAGCATTCTCCAGTACACGCAACAGCAATCATCTCGT  700

```

Oy	133	ethrAla	135	
	:			
Db	701	GATAGCC	707	
RESULT 12				
LOCUS	AK012169			
DEFINITION	AK012169 2793 bp mRNA linear HTC 19-JAN-2003 Mus musculus 10 days embryo whole body cDNA, RIKEN full-length enriched library, clone:2610528605:leucine rich repeat C-terminal domain containing protein,full insert sequence.			

ACCESSION	AK012169
VERSION	AK012169.1
KEYWORDS	HTC; CAP trapper.
SOURCE	Mus musculus (strain:C57BL/6J) 10 days embryo cDNA to mRNA, clone_11b:RIKEN full-length enriched mouse cDNA library
ORGANISM	Mus musculus
REFERENCE	Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE	1
AUTHORS	Carninci, P. and Hayashizaki, Y.
TITLE	High-efficiency full-length cDNA cloning
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)
MEDLINE	99279253
PUBMED	10349636
REFERENCE	2
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE	20499374
PUBMED	11042159
REFERENCE	3
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,

TITLE RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multipipillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
PMID 20530913
PUBMED 11076861
REFERENCE
AUTHORS Kawai,J., Shlnagawa,A., Shnbata,K., Yoshino,M., Itoh,M., Ishii,Y.,
4

Alizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamapka, I., Saito, T., Okazaki, Y., Gotohori, T., Bono, H., Kasukawa, T., Saito, R., Katoh, K., Matsuda, Y., Ashburner, M., Batalov, S., Casavan, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochwa, H., Knehl, P., Lewis, S., Matsuno, Y., Nikaido, I., Pesole, G., Quackenbush, J., Schiraldi, L. M., Staubli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Balderacchi, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carancici, P., de Bonaldo, M. F., Brownstein, M. J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustlinchik, S., Hill, D., Hotemann, M., Hume, D. A., Kamliya, M., Lee, N. H., Lyons, P. F., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K. F., Suzuki, H., Toyok-oka, K., Wang, K. H., Weitz, C., Whitteker, C., Wilming, L., Wyshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohsaki, S. and Hayashizaki, Y.

Functional annotation of a full-length mouse cDNA collection
Nature 409 (6821), 685-690 (2001)

JOURNAL MEDLINE
PUBMED
11217851

Caninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hasegaki, T., Hara, A., Hayashi, N., Hill, D., Hiramoto, K., Hiraoka, T., Horii, F., Hume, D., Imotoani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Quackenbush, J., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Schirral, L., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, S., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yamashita, I.,

Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
 Direct Submission
 Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gs.c.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

COMMENT
 Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.

FEATURES

source

Location/Qualifiers
 1. 2793
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 /strain="C57BL/6J"
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 /db_xref="MGI:1907345"
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 /clone="2610528605"
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 /note="Leucine rich repeat C-terminal domain containing protein
 data source: Pfam, source key: PF01463, evidence: ISS
 putative"

CDS

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 LEVPIRHLPRLLLDLSHNSIPALEAGLITRNPVALRAGLGLQDDEGLRLN
 LHDVYDNLQLEHMPVSVDGKRLTRLAGNRIQITPEDIAGLITLQEDLVMS
 LQALPDSLSLEPRLRLAARNPENCILPLSWEGVRENHVLASPEPTCHPEPK
 NAGRLDLDDADFGCPVTITATVPTIIRSTIAREPLTSSQAPVWVSLTEPTQAST
 VLSAPTMRPAPQPODPCASICLNGSCRLGRHMECLCPGFGICLCESEVEQGM
 KRSISDTPRRPPLPLSLIEPVSPTSLRVKLORYLOGNTVOLRSLLTYLNSGPNR
 LVTLRLPASLAETVTLQRLNPATYSICVPLAGRTPEGEFEGEANTSOAVSNAP
 VYQARGNIPILIALPALAVLAVLAAGAATCYRRARATSTADKGOVGPGTPELE
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 2773..2778
 /note="putative"
 2793
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 2793
 BASE COUNT 576 a 840 c 769 g 608 t
 ORIGIN

Alignment Scores:

Pred. No.: 34.1 Length: 2793
 Score: 84.00 Matches: 32
 Percent Similarity: 41.67% Conservative: 18
 Best Local Similarity: 26.67% Mismatches: 64
 Query Match: 9.96% Indels: 6
 DB: 11 Gaps: 3

US-09-813-775c-18 (1-166) x AK012169 (1-2793)

QY 19 AlAlAGSLuAlaGluAnIleThhGlyCysAlaGluHisCysSerLeuAsnGluAsn 38
 DB 644 AGCTCAGCTGCAGCAAGATGAGCTGGGTGGTGGCCCATGCTGCCCCGCTGC 703
 QY 39 IleThValProAspThrLysValAsnPhetYalaIlePlys-Argasn***Ser***G1 58
 DB 704 TGTCTCTTGACCTCAGCCACACAGATCCAGCCCTGGAAAGCCGGAATCTGATACCG 763
 QY 58 ngl-----AlaValGluVal---TrpGln-GlyLeuAlaLeuLeuSerGluAlaVal 75
 DB 764 CCAATGTAGAGGAGCTTGAAGTTGGCTGAGGCTGCGGACGACGTGATGAGGG---C 820
 QY 75 euArGlglyAlaLeuLeuValAsnSerSerGlnProTrpGluProLeuGlnLeuHisV 95

DB 821 TTTTGGCCGCTTCTCAACCTCATGCTTCGATGTTATGACACCACTGGACGATA 880

QY 95 alAspLysAlaValSerGlyLeuArgSerLeuThrTrhTrhLeuArgAlaLeuGlyAla 115

DB 881 TGCCATGCTGATTCAGAGCTGGCTGGCTGACACCCCTGCGCTGGCCGACACACC 940

QY 115 InLysGluAlaIleSerProProAspAlaIleSerAlaIleProLeuArgThrIle 133
 DB 941 GTATTGCCAGATTCAGGCGCCGAGAGACCTCGCTGCTGACTGCCCTACAGAAATG 996

RESULT 13

LOCUS

BM931641 619 bp mRNA linear EST 13-MAR-2002

DEFINITION
 UI-E-EJ1-aj9-g-14-0-UI-rl UI-E-EJ1 Homo sapiens cDNA clone

ACCSSION
 BM931641

VERSION
 BM931641.1 GI:19390814

KEYWORDS

SOURCE

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

COMMENT

Genome Res. 6 (9), 791-806 (1996)
 97044477
 Contact: Soares, MB
 Program for Rat Gene Discovery and Mapping
 University of Iowa
 451 Eckstein Medical Research Building Iowa City, IA 52242, USA
 Tel: 319 335 8250
 Fax: 319 335 9565
 Email: msoares@blue.weeg.uiowa.edu
 Tissue Procurement: Dr. Gregg Hageman
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Researchers may obtain clones from Research
 Genetics (www.resgen.com).
 Seq primer: M13 REVERSE.

FEATURES

source

Location/Qualifiers
 1. 619
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="UI-E-EJ1-aj9-g-14-0-UI"
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 /tissue_type="fetal eyes, lens, eye anterior segment,
 optic nerve, retina, Retina Foveal and Macular, RPE and
 Choroid"

/dev_stage="fetal and adult"
 /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
 /note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
 modified polylinker; Site_1: EcoR I; Site_2: Not I;
 UI-E-EJ1 is a subcloned cDNA library constructed
 according to Bonaldo, Lennon and Soares, Genome Research,
 6:791-806, 1996. First strand cDNA synthesis was primed
 with an oligo-dT primer containing a Not I site. Double
 stranded cDNA was ligated to an EcoR I adaptor, digested
 with Not I, and cloned directionally into pT7T3-Pac
 vector. The oligonucleotide used to prime the synthesis of
 first-strand cDNA contains a library tag sequence that is
 located between the Not I site and the (dT)18 tail. The
 sequence tags for this library are: fetal eyes, AGAATCAAGA
 ; lens, CCAATGAGCA; eye anterior segment, AATCCCAAT;
 optic nerve, CCAATGAGCA; retina, CCGCG; Retina Foveal and
 Macular, GTCC; RPE and Choroid, ACCCA. This library was
 created for the program, Gene Discovery in the Visual
 System, supported by National Eye Institute (NEI)."

BASE COUNT

140 a 182 c 172 g 123 t 2 others

ORIGIN

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: January 8, 2003, 03:43:33 ; Search time 180.334 Seconds
(without alignments)
2072.993 Million cell updates/sec

Title: US-09-813-775c-18

Perfect score: 843
Sequence: 1 APRRLICDSRVLEKLYLEAK.....NFLRGLKLYTGECAGRTGDR 166

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODE=frame+pn.model -DEV=xlh
-Q=/cgn2.1/USPTO.spool/US09813775/runat.07012003.153120.23784/app.query.fasta_1.718
-DB=N.Geneseq.101002 -OPMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -DOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=bloms62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pio -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09813775@cgn.1.1.0@runat.07012003.153120.23784 -NCPU=6 -ICPU=3
-NO_XMAP -NO_MAP -LARGEOUTER -NEG_SCORES=0 -WAIT -LONGLOG -DEV.TIMEOUT=120
-NARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6 -Fgapext=7
-YCAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :
N.Geneseq.101002.*
1: /SID52/gcgcdata/geneseq/geneseqn-emb1/NA1980.DAT:*
2: /SID52/gcgcdata/geneseq/geneseqn-emb1/NA1981.DAT:*
3: /SID52/gcgcdata/geneseq/geneseqn-emb1/NA1982.DAT:*
4: /SID52/gcgcdata/geneseq/geneseqn-emb1/NA1983.DAT:*
5: /SID52/gcgcdata/geneseq/geneseqn-emb1/NA1984.DAT:*
6: /SID52/gcgcdata/geneseq/geneseqn-emb1/NA1985.DAT:*
7: /SID52/gcgcdata/geneseq/geneseqn-emb1/NA1986.DAT:*
8: /SID52/gcgcdata/geneseq/geneseqn-emb1/NA1987.DAT:*
9: /SID52/gcgcdata/geneseq/geneseqn-emb1/NA1988.DAT:*
10: /SID52/gcgcdata/geneseq/geneseqn-emb1/NA1989.DAT:*
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12: /SID52/gcgcdata/geneseq/geneseqn-emb1/NA1991.DAT:*
13: /SID52/gcgcdata/geneseq/geneseqn-emb1/NA1992.DAT:*
14: /SID52/gcgcdata/geneseq/geneseqn-emb1/NA1993.DAT:*
15: /SID52/gcgcdata/geneseq/geneseqn-emb1/NA1994.DAT:*
16: /SID52/gcgcdata/geneseq/geneseqn-emb1/NA1995.DAT:*
17: /SID52/gcgcdata/geneseq/geneseqn-emb1/NA1996.DAT:*
18: /SID52/gcgcdata/geneseq/geneseqn-emb1/NA1997.DAT:*
19: /SID52/gcgcdata/geneseq/geneseqn-emb1/NA1998.DAT:*
20: /SID52/gcgcdata/geneseq/geneseqn-emb1/NA1999.DAT:*
21: /SID52/gcgcdata/geneseq/geneseqn-emb1/NA2000.DAT:*
22: /SID52/gcgcdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
23: /SID52/gcgcdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
24: /SID52/gcgcdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	825	97.9	498	21 ABL50878	Modified erythropo
2	825	97.9	501	19 AAV31031	Human erythropoiet
3	825	97.9	514	22 AAD06893	Human erythropoiet
4	825	97.9	533	6 AAN50346	Human recombinant
5	825	97.9	533	19 AAV30963	ECPEPO gene used in
6	825	97.9	551	16 AAN50345	Human recombinant
7	825	97.9	551	19 AAV30970	SCPEPO gene based o
8	825	97.9	582	21 AAA46697	DNA encoding a hum
9	825	97.9	582	22 AAA46697	Human erythropoiet
10	825	97.9	585	22 AAC66882	Chimpanzee erythro
11	825	97.9	614	24 ABL59290	Nucleotide sequenc
12	825	97.9	616	20 AAX77361	Polynucleotide seq
13	825	97.9	616	21 AAQ90393	DN encoding synthe
14	825	97.9	625	15 AAQ74760	Human prepro-eryth
15	825	97.9	629	24 ABL59289	Nucleotide sequenc
16	825	97.9	629	24 ABL59291	Nucleotide sequenc
17	825	97.9	724	9 AAN81554	EPO 140B encoding
18	825	97.9	788	17 AAT31529	Human erythropoiet
19	825	97.9	788	21 AAZ31999	Human EPO long cDN
20	825	97.9	823	18 AAT64847	Human erythropoiet
21	825	97.9	994	13 AAQ24281	IL-3:Epo short, re
22	825	97.9	1015	13 AAQ24281	Epo:IL-3 short, re
23	825	97.9	1051	13 AAQ24284	IL-3:Epo Flex, rec
24	825	97.9	1072	13 AAQ24285	Epo:IL-3 Flex, rec
25	825	97.9	1158	20 AAX25701	Human erythropoiet
26	825	97.9	1245	8 AAN70360	Sequence encoding
27	825	97.9	1255	7 AAN60519	CDNA of clone lamb
28	825	97.9	1342	7 AAN60513	CDNA of clone lamb
29	825	97.9	1789	16 AAQ92296	Erythropoietin cDN
30	825	97.9	3100	24 ABR86161	Nucleotide sequenc
31	825	97.9	10524	20 AAX77355	Polynucleotide seq
32	825	97.9	10524	21 AAA90387	Plasmid pSINrep5 E
33	822	97.5	1239	18 AAT93979	DNA for oligopepti
34	821	97.4	606	21 AAA07253	Human EPO cDNA seq
35	820	97.3	498	21 AAA48373	Non-glycosylated e
36	820	97.3	501	21 ABL50863	Modified erythropo
37	820	97.3	570	21 ABL50864	Modified erythropo
38	820	97.3	582	21 ABL50865	Modified erythropo
39	817	96.9	975	19 AAV70368	Human flt3 ligand
40	817	96.9	1020	19 AAV70367	Human flt3 ligand
41	816	96.8	498	21 ABL50862	Modified erythropo
42	812	96.3	500	21 AAA29493	Erythropoietin cod
43	812	96.3	500	21 AAA29494	Erythropoietin wob
44	812	96.3	521	11 AAQ06473	Human erythropoiet
45	811	96.2	579	22 AAT71883	Erythropoietin gen

ALIGNMENTS

RESULT 1
ABL50878
ID ABL50878 standard: DNA; 498 BP.

AC ABL50878;
XX
XX 21-JUN-2002 (first entry)

DE Modified erythropoietin related gene sequence #5.

XX Modified erythropoietin; EPO; gene; ds.

XX Unidentified.

FT Key Location/Qualifiers

FT CDS 1..498
FT /tag a
FT /partial


```

Db 121 GTCCAGACCAACCAAGTAAATTTCTATGCCCTGGAGACGATGAGGTCCGGCAGCAGGCC 180
Qy 61 valGluValTTPQInGlyLeuAlaLeuSerGluAlaValLeuArgGlyGlnAlaLeu 80
Db 181 GTAGAAAGTCTGGAGAGCGCCCTGCTGTGGAAAGCTGCTGTGGGGCCAGGCCCTG 240
Qy 81 LeuValAsnSerSerGlnProTTPGluProLeuGlnLeuHisValAspLysAlaValSer 100
Db 241 TTGGTCACACTTCCCGACGCCGTGGAGCCCTGCACCTCATGTGATTAAGCCGTCAGT 300
Qy 101 GtyleuArSerleuThrleuArGluAlaLeuGlnAlaGlnLysGlnAlaIleSer 120
Db 301 GGCTTCGAGCCTCACCTCTGCTTGGGCTTGGAGCCCGAAGAGGACCATCTCC 360
Qy 121 ProProAspAlaAlaSerAlaAlaProLeuArgThrIleThrAlaAspThrPheArgLys 140
Db 361 CCTCCAGATGGCGCCCTCAGCTGCTCCACATCCGACAAATCATCTACACTTTCCCGCAA 420
Qy 141 LeuPheArgValTyrSerAsnPheLeuArgGlyLysLeuLysLeuTyrThrGlyGlnAla 160
Db 421 CTCCTCCGAGCTACTACCAATTTCCCTCCGGGAAAGCTGAAGCTGTAACACAGGAGGCC 480
Qy 161 CysArgThrGlyAspArg 166
Db 481 TCGAGGACAGGGGACAGA 498

RESULT 3
AAD06893
ID AAD06893 standard: cDNA; 514 BP.
XX
AC AAD06893:
XX
DT 06-AUG-2001 (first entry)
XX
DE Human erythropoietin (EPO) cDNA.
XX
KW Human; erythropoietin; EPO; antianaemic; nephrotrophic; anti-HIV;
KW vaccine; haemostatic; Immunoglobulin; Ig; EPO deficient disease;
KW anaemia; renal failure; Human Immunodeficiency Virus; HIV;
KW haematopoietic growth factor; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 8..508
FT FT /*tag= a
FT FT /product= "Human erythropoietin"
FT FT /note= "CDS does not include start codon"
FT FT /partial
FT FT 7
FT FT /*tag= b
FT FT /note= "Original base is changed to "r" which
FT FT results in increased expression"
FT FT 40
FT FT /*tag= c
FT FT /note= "Original base is changed to "g" which
FT FT results in increased expression"
FT FT 88
FT FT /*tag= d
FT FT /note= "Original base is changed to "c" which
FT FT results in increased expression"
FT FT 121
FT FT /*tag= e
FT FT /note= "Original base is changed to "c" which
FT FT results in increased expression"
FT FT 127
FT FT /*tag= f
FT FT /note= "Original base is changed to "c" which
FT FT results in increased expression"
FT FT 130
FT FT /*tag= g
FT FT /note= "Original base is changed to "g" which
FT FT results in increased expression"

```

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FT misc-feature 133
FT /*tag= h
FT /note= "Original base is changed to "r" which
FT results in increased expression"
FT misc-feature 145
FT /*tag= i
FT /note= "Original base is changed to "g" which
FT results in increased expression"
FT misc-feature 175
FT /*tag= j
FT /note= "Original base is changed to "r" which
FT results in increased expression"
FT misc-feature 178
FT /*tag= k
FT /note= "Original base is changed to "c" which
FT results in increased expression"
FT misc-feature 196
FT /*tag= l
FT /note= "Original base is changed to "g" which
FT results in increased expression"
FT misc-feature 283
FT /*tag= m
FT /note= "Original base is changed to "a" which
FT results in increased expression"
FT misc-feature 304
FT /*tag= n
FT /note= "Original base is changed to "g" which
FT results in increased expression"
FT misc-feature 344
FT /*tag= o
FT /note= "Original base is changed to "g" which
FT results in increased expression"
FT misc-feature 400
FT /*tag= p
FT /note= "Original base is changed to "c" which
FT results in increased expression"
FT misc-feature 489..490
FT /*tag= q
FT /note= "Original bases are changed to "g" and "c" which
FT results in increased expression"
FT misc-feature 509..514
FT /*tag= r
FT /note= "Original base are changed to "CTCGAG" which
FT results in increased expression"

WO200136489-A2.
XX
XX 25-MAY-2001.
XX
XX 03-NOV-2000; 2000WO-EP10843.
XX
XX 12-NOV-1999; 99US-0164855.
XX
XX (MERE ) MERCK PATENT GMBH.
XX
XX Hartmann A, Brandt S, Rieke E, Sobel C, Lo K, Way JC, Gillies S;
XX WPI: 2001-367563/38.
XX DR P-PSDB; AA02641.
XX
XX Novel modified erythropoietin forms such as fusion proteins, comprising
XX FC portion of an immunoglobulin molecule and a target molecule having
XX the biological activity of erythropoietin forms
XX
XX Example 1; Page 22; 58pp; English.
XX
XX The present sequence is a cDNA encoding human erythropoietin (EPO)
XX mature protein. The coding sequence for mature EPO contains modified
XX codons to optimise translation. EPO has improved biological activity and
XX an extended serum half life greater than 20 hours. The present invention
XX relates to modified EPO forms such as fusion proteins comprising a FC
XX portion of an immunoglobulin (Ig) molecule and an EPO molecule (Fc-EPO).
XX The FC portion is fused covalently through its C-terminus directly or

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CC indirectly to the EPO molecule, and where the Fc portion as well as EPO
 CC portion may be modified or mutated. The invention also relates to non-
 CC fused EPO molecules which have a pattern of cysteines or disulphide
 CC bonding which is distinct from human or animal EPO. Pharmaceutical
 CC compositions containing EPO are useful in the treatment of EPO deficient
 CC diseases such as anaemia, renal failure, HIV infection, blood loss and
 CC chronic disease that can be treated with haematopoietic growth factor.

XX
 SO Sequence 514 BP; 106 A; 159 C; 152 G; 97 T; 0 other;

Alignment Scores:

Pred. No.:	8.96e-84	Length:	514
Score:	825.00	Matches:	162
Percent Similarity:	97.59%	Conservative:	0
Best Local Similarity:	97.59%	Mismatches:	4
Query Match:	97.86%	Indels:	0
DB:	22	Gaps:	0

US-09-813-775C-18 (1-166) x AAD06893 (1-514)

QY 1 AlaProAArgLeuIleCysAspSerArgValLeuGluArgTyrLeuGluAlaLys 20
 DB 8 GCCCACCACCGGCTCATGTGTACAGCCGAGTGTGAGAGGTACTCTTGAGGCCAAG 67
 QY 21 GluAlaGluAsnIleThrThrGlyCysAlaGluHisCysSerLeuAsnGluAsnIleThr 40
 DB 68 GAGCCCGAATATCACCACCGGCTGTCTGTGACACTGTGACCTGAAAGACATCACC 127
 QY 41 ValProAspThrLysValAsnPhetYrAlaTrpLysArgAsn***Ser**GlnGlnAla 60
 DB 128 GTGCTGCACCAAGTGAATTTCTATGTGCTGGAAGAGATGAGAGTGGCCACAGGCC 187
 QY 61 ValGluValITrpgInglyLeuAlaLeuLeuSerGluAlaValLeuArgGlyGlnAlaLeu 80
 DB 188 GTAGAGATGTGGACAGGCGCTGGCTGTGTGGAAGCTGTCTGCGGGCCAGGCCCTG 247
 QY 81 LeuValAsnSerSerGlnProTrpGluProLeuGlnLeuHisValAspLysAlaValSer 100
 DB 248 TTGTCAACTCTTCCACCGGCTGAGGCCCTGCAACTGCAATGAGATGAACCCGTGAGT 307
 QY 101 GlyLeuArgSerLeuThrThrLeuLeuArgAlaLeuGlyAlaGlyLysGlnAlaLeu 120
 DB 308 GGCCTTCCAGCCTCACCACCTCTGCTGGGCTGTGGAGCCCAAGAGACCATCTCC 367
 QY 121 ProProAspAlaAlaSerAlaAlaProLeuArgThrIleThrAlaAspThrPheArgLys 140
 DB 368 CCTCCAGATGGGCTCAGCTGCTCCCTCCGACAAATCAGCTGACACTTCCGCAAA 427
 QY 141 LeuPheArgValIYrSerAsnPhetLeuArgGlyLysLeuLysLeuTyrThrGlyAla 160
 DB 428 CTCTTCGAGTCTACTCAATTTCTCTCGGGGAAAGTGAAGCTGTACACAGGAGGCC 487
 QY 161 CysArgThrGlyAspArg 166
 DB 488 TGCCGGACAGGGGACAGA 505

RESULT 4

AANS0346 ID AANS0346 standard; DNA: 533 BP.

XX AC AANS0346;

XX DT 01-JAN-1980 (first entry)

DE Human recombinant erythropoietin expressed in *Escherichia coli*.

XX Erythropoietin; red blood cell; erythrocyte; anaemia; blood;

XX disorder; ds; *Escherichia coli*.

OS Homo sapiens.

XX Key Location/Qualifiers
 FH mat_peptide 27..528
 FT

FT /*tag- a

XX MO8502610-A.

XX 20-JUN-1985.

XX 11-DEC-1984; 84WO-US02021.

XX 30-NOV-1984; 84US-0675298.

XX 13-DEC-1983; 83US-0561024.

XX 21-FEB-1984; 84US-0582185.

XX 28-SEP-1984; 84US-0655841.

XX (KIRI-) KIRIN-AMGEN INC.

XX WPI: 1985-159229/26.

XX P-PSDB: AAP50299.

XX New polypeptide having properties of erythropoietin - is prepd.

XX by cultivation of transformed eucaryotic or procaryotic host

XX Disclosure: Page 72; 113pp: English.

XX Human erythropoietin encoded by this sequence is essential for red

XX blood cell formation and is used for the diagnosis and treatment of

XX blood disorders such as anaemia. Large amounts of EPO may be obtained

XX using recombinant DNA techniques in contrast to small amounts

XX obtained from plasma and urine. This sequence is expressed in E

XX coll. See also AANS0345, AANS0347-50 and AAP50298, AAP50300-PS0301.

SO Sequence 533 BP; 131 A; 134 C; 138 G; 130 T; 0 other;

Alignment Scores:

Pred. No.:	9.4e-84	Length:	533
Score:	825.00	Matches:	162
Percent Similarity:	97.59%	Conservative:	0
Best Local Similarity:	97.59%	Mismatches:	4
Query Match:	97.86%	Indels:	0
DB:	6	Gaps:	0

US-09-813-775C-18 (1-166) x AANS0346 (1-533)

QY 1 AlaProAArgLeuIleCysAspSerArgValLeuGluArgTyrLeuGluAlaLys 20
 DB 30 GCTCCGCGCGCTGATCTGCAGCTCGAGAGTTCGAACTTACTCTGGAAGCTTAA 89
 QY 21 GluAlaGluAsnIleThrThrGlyCysAlaGluHisCysSerLeuAsnGluAsnIleThr 40
 DB 90 GAGCTGAAACATCACCACCTGCTGTGCTGACACTGTCTTGAACGAAACATTAAG 149
 QY 41 ValProAspThrLysValAsnPhetYrAlaTrpLysArgAsn***Ser**GlnGlnAla 60
 DB 150 GTACCAGACACCAAGTGAATCTTACGCTTGGAAAGCTGTAAGTGGTCAACAAACA 209
 QY 61 ValGluValITrpgInglyLeuAlaLeuLeuSerGluAlaValLeuArgGlyGlnAlaLeu 80
 DB 210 GTGAAGTTGGACAGGCTGTGCACTGTGAGCGGCTGTACTGCGGCGAGGCACTG 269
 QY 81 LeuValAsnSerSerGlnProTrpGluProLeuGlnLeuHisValAspLysAlaValSer 100
 DB 270 CTGTGTAACCTCTCTCACCCTGTGGACCCGCTGCAGCTGTGTTGACAAAGCATATCT 329
 QY 101 GlyLeuArgSerLeuThrThrLeuLeuArgAlaLeuGlyAlaGlyLysGlnAlaLeu 120
 DB 330 GGCCTGAGATCTGTGACACTGTGCTGTGGTGTGACAGAAAGAGCATATCTCT 389
 QY 121 ProProAspAlaAlaSerAlaAlaProLeuArgThrIleThrAlaAspThrPheArgLys 140
 DB 390 CCGCGGATGTGCTGATGTGACCCGCTGCTGACATCACTGCTGATACCTTCGCAAA 449
 QY 141 LeuPheArgValIYrSerAsnPhetLeuArgGlyLysLeuLysLeuTyrThrGlyAla 160
 DB 450 CTGTTCTGTATACTCTTAACCTCTGTGCTGTAAACGTGAACCTGTATATCGGGAACA 509

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OY 161 CysArgThrGlyAspArg 166
    |||
DB 510 TGCCGTAAGTGTGACCCG 527

RESULT 5
AAV30963
ID AAV30963 standard; DNA; 533 BP.
XX
AC AAV30963;
XX
DT 11-SEP-1998 (first entry)
XX
DE ECEPO gene used in the construction for human EPO.
XX
KW Human; erythropoietin; EPO; bone marrow; reticulocyte; red blood cell;
KM expression; CHO; chinese hamster ovary cell; diagnosis; blood disorder;
KK ds.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN AU688723-B.
PD 19-FEB-1998.
XX
PF 02-DEC-1997; 97AU-0046867.
XX
PR 02-DEC-1997; 97AU-0046867.
XX
PA (KIRI ) KIRIN AMGEN INC.
XX
PI Lin F;
XX
DR WPI: 1998-261957/24.
XX
PT Recombinant human erythropoietin - potentially useful for diagnosis
PT and treatment of blood disorders
XX
PS Example 11; Page 68; 100pp; English.
XX
CC The present sequence represents the ECEPO gene which resembles the
CC amino terminus of human erythropoietin (EPO). The present invention
CC describes recombinant human EPO which causes bone marrow cells to
CC increase production of reticulocytes or red blood cells, where the
CC polypeptide is the product of expression in CHO (Chinese hamster ovary)
CC cells of an exogenous DNA sequence encoding human EPO. EPO is
CC potentially useful in the diagnosis and treatment of blood disorders
CC characterised by low or defective red blood cell production.
XX
SQ Sequence 533 BP; 131 A; 134 C; 138 G; 130 T; 0 other;

Alignment Scores:
Pred. No.: 9.4e-84 Length: 533
Percent Similarity: 825.00 Matches: 162
Best Local Similarity: 97.59% Conservative: 0
Query Match: 97.86% Mismatches: 4
DB: 19 Indels: 0 Gaps: 0

US-09-813-775C-18 (1-166) x AAV30963 (1-533)
OY 1 AlaProPArgLeuIleCysAspSerArgValLeuGluArgTyrLeuGluAlaLys 20
    |||
DB 30 GCTCCGCCGCTGTGATGCGACTCGAGAGTCTGGAACGTTACTGCTGAAGCTAA 89
    |||
OY 21 GluAlaGluAsnIleThrThrGlyCysAlaGluHisCysSerLeuAsnGluAsnIleThr 40
    |||
DB 90 GAAGCGAAACATCAACCACTGCTGTGCTGAACACTGTTCTTGAACGAAACATTACG 149
    |||
OY 41 ValProAspThrIleValAsnPhetYrAlaTrpIleAsn***Ser***GlnGlnAla 60
    |||
DB 150 GTACCAAGACCAAGGTTAACTTCTACGCTTGGAACGTAATGCAAGTTGCTCAACAGCA 209

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OY 61 ValGluValTrpGlnGlyLeuAlaLeuLeuSerGluAlaValLeuArgGlyGlnAlaLeu 80
    |||
DB 210 GTTGAAGTTGGCAGGGGTGTGGCAGCTGCTAGCAGAGGCTGTACTGCTGGCCAGGCACG 269
    |||
OY 81 LeuValAsnSerSerGlnProTrpGluProLeuGlnLeuHisValAspLysAlaValSer 100
    |||
DB 270 CTGCTAAACTCTCTCAGCCGCTGGAAACCGCTCCAGCTGCTATGTGACAAACAGCATATCT 329
    |||
OY 101 GlyLeuArgSerLeuThrThrLeuLeuArgAlaLeuGlnValAlaGlnIleGlyAlaIleSer 120
    |||
DB 330 GGCTTGAGATCTCTGACTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 389
    |||
OY 121 ProProAspAlaAlaSerAlaAlaProLeuArgThrIleThrAlaAspThrPheArgLys 140
    |||
DB 390 CCGCCGGATCTCTCATCTGCTGTGACCGCTGCTGACATCATCTCTATACCTTCCGCAAA 449
    |||
OY 141 LeuPheArgValIleTyrSerAsnPhetLeuArgGlyLysLeuLysLeuTyrThrGlyGluAla 160
    |||
DB 450 CTGTTTCGTGTATACCTTCTGCGGTAAACTGAACCTGATATCTGCGGAACGA 509
    |||
OY 161 CysArgThrGlyAspArg 166
    |||
DB 510 TGCCGTAAGTGTGACCCG 527

RESULT 6
AAN50345
ID AAN50345 standard; DNA; 551 BP.
XX
AC AAN50345;
XX
DT 01-JAN-1980 (first entry)
XX
DE Human recombinant erythropoietin expressed in Saccharomyces
DE cerevisiae.
XX
KW Erythropoietin; red blood cell; erythrocyte; anaemia; blood;
KM disorder; ds; Saccharomyces cerevisiae.
XX
OS Homo sapiens.
XX
FH Key location/Qualifiers
FT mat_peptide complement (13..547)
FT /tag= a
XX
PN MO8502610-A.
XX
PD 20-JUN-1985.
XX
PF 11-DEC-1984; 84MO-US02021.
XX
PR 30-NOV-1984; 84US-0675298.
PR 13-DEC-1983; 83US-0561024.
PR 21-FEB-1984; 84US-0582185.
PR 28-SEP-1984; 84US-0655841.
XX
PA (KIRI-) KIRIN-AMGEN INC.
XX
DR WPI: 1985-159229/26.
DR P-PSDB; AAP50298.
XX
PT New polypeptide having properties of erythropoietin - is prepd.
PT by cultivation of transformed eucaryotic or procaryotic host
XX
PS Disclosure: Page 82; 113pp; English.
XX
CC Human erythropoietin encoded by this sequence is essential for red
CC blood cell formation and is used for the diagnosis and treatment of
CC blood disorders such as anaemia. Large amounts of EPO may be obtained
CC using recombinant DNA techniques in contrast to small amounts
CC obtained from plasma and urine. This sequence is expressed in S.
CC cerevisiae. See also AAN50346-50 and AAP50299-P50301.
XX

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SO Sequence 551 BP, 157 A; 112 C; 129 G; 153 T; 0 other;

Alignment Scores:

Pred. No.: 9.82e-84 Length: 551
Score: 825.00 Matches: 162
Percent Similarity: 97.59% Conservative: 0
Best Local Similarity: 97.59% Mismatches: 4
Query Match: 97.86% Indels: 0
Gaps: 0

US-09-813-775c-18 (1-166) x AAN50345 (1-551)

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OY 1 AAlaProArgLeuIleCysAspSerArgValLeuGluArgTyrLeuGluAlaLys 20
    |||||
DB 16 GCTCCACCAAGATTGATGTGACTCGAGAGCTTTGGAAAGATTAAGTCTTGAACCTAAA 75
OY 21 GluAlaGluAsnIleThrThrGlyCysAlaGluHisCysSerLeuAsnGluAsnIleThr 40
    |||||
DB 76 GAAGCTGAAACATCACCACCTGGTGTGCTGACACTGTTCTTGAACGAAACATTTACG 135
OY 41 ValProAspThrLysValAsnPhetYrAlaTyrPlysArgAsn***Ser***GlnGlnAla 60
    |||||
DB 136 GTACCAAGACACCAAGATTACTTCTACGCTTGGAAACGATATGGAAGTGTGTCACACAGCT 195
OY 61 ValGluValTTPGlnGlyLeuAlaLeuLeuSerGluAlaValLeuArgGlyGlnAlaLeu 80
    |||||
DB 196 GTTGAAGTTTGGCAAGTTTGGCTTGTATCTGAAGCTGTTTGAAGAGCTCAAGCCCTTG 255
OY 81 LeuValAsnSerSerGlnProTfPgluProLeuGlnLeuHisValAspLysAlaValSer 100
    |||||
DB 256 TTGGTTAACTCTTCAACCATGGAGAACCATTTGACATTCAGATTAAGCCGCTCT 315
OY 101 GlyLeuArgSerLeuThrThrLeuLeuArgAlaLeuGlyAlaGlnLysGlnAlaIleSer 120
    |||||
DB 316 GGTTCAGATCTTGTACATCTTGTGAGAGCTTTGGGCTCAAAAGAGCAATTC 375
OY 121 ProProAspAlaIleSerAlaIleProLeuArgThrIleThrAlaAspThrPheArgLys 140
    |||||
DB 376 CCACGAGACGCTGCTGCGCTCCATTTGAGAACCATTCAGATTAAGCTTTCAGAAAG 435
OY 141 LeuPheArgValTyrSerAsnPhetLeuArgGlyLysLeuLysLeuTyrThrGlyGlnAla 160
    |||||
DB 436 TTATTCAGAGTTTACTTCCAACTTCTTGAGAGGTAAATTGAAGTTGTACACCGGTGAAGCC 495
OY 161 CysArgThrGlyAspArg 166
    |||||
DB 496 TGTAGAACTGGTGACAGA 513

```

RESULT 7

AAV30970 AAV30970 standard; DNA; 551 BP.

AAV30970;

11-SEP-1998 (first entry)

SCERO gene based on the human EPO gene with preferred yeast codons.

Human; erythropoietin; EPO; bone marrow; reticulocyte; red blood cell;

expression; CHO; chinese hamster ovary cell; diagnosis; blood disorder;

OS Synthetic.

OS Homo sapiens.

PN AU688723-B.

19-FEB-1998.

02-DEC-1997; 97AU-0046867.

02-DEC-1997; 97AU-0046867.

PA (KIRI) KIRIN AMGEN INC.

XX Lin F;

DR WPI; 1998-261957/24.

PT Recombinant human erythropoietin - potentially useful for diagnosis

PS and treatment of blood disorders

XX Example 11; Page 78; 100pp; English.

The present sequence represents the SCERO gene which was constructed as part of the assembly of human erythropoietin (EPO) with yeast preferred codons. The present invention describes recombinant human EPO which causes bone marrow cells to increase production of reticulocytes or red blood cells, where the polypeptide is the product of expression in CHO (chinese hamster ovary) cells of an exogenous DNA sequence encoding human EPO. EPO is potentially useful in the diagnosis and treatment of blood disorders characterised by low or defective red blood cell production.

SO Sequence 551 BP, 157 A; 112 C; 129 G; 153 T; 0 other;

Alignment Scores:

Pred. No.: 9.82e-84 Length: 551
Score: 825.00 Matches: 162
Percent Similarity: 97.59% Conservative: 0
Best Local Similarity: 97.59% Mismatches: 4
Query Match: 97.86% Indels: 0
Gaps: 0

US-09-813-775c-18 (1-166) x AAV30970 (1-551)

```

OY 1 AAlaProArgLeuIleCysAspSerArgValLeuGluArgTyrLeuGluAlaLys 20
    |||||
DB 16 GCTCCACCAAGATTGATGTGACTCGAGAGCTTTGGAAAGATTAAGTCTTGAACCTAAA 75
OY 21 GluAlaGluAsnIleThrThrGlyCysAlaGluHisCysSerLeuAsnGluAsnIleThr 40
    |||||
DB 76 GAAGCTGAAACATCACCACCTGGTGTGCTGACACTGTTCTTGAACGAAACATTTACG 135
OY 41 ValProAspThrLysValAsnPhetYrAlaTyrPlysArgAsn***Ser***GlnGlnAla 60
    |||||
DB 136 GTACCAAGACACCAAGATTACTTCTACGCTTGGAAACGATATGGAAGTGTGTCACACAGCT 195
OY 61 ValGluValTTPGlnGlyLeuAlaLeuLeuSerGluAlaValLeuArgGlyGlnAlaLeu 80
    |||||
DB 196 GTTGAAGTTTGGCAAGTTTGGCTTGTATCTGAAGCTGTTTGAAGAGCTCAAGCCCTTG 255
OY 81 LeuValAsnSerSerGlnProTfPgluProLeuGlnLeuHisValAspLysAlaValSer 100
    |||||
DB 256 TTGGTTAACTCTTCAACCATGGAGAACCATTTGACATTCAGATTAAGCCGCTCT 315
OY 101 GlyLeuArgSerLeuThrThrLeuLeuArgAlaLeuGlyAlaGlnLysGlnAlaIleSer 120
    |||||
DB 316 GGTTCAGATCTTGTACATCTTGTGAGAGCTTTGGGCTCAAAAGAGCAATTC 375
OY 121 ProProAspAlaIleSerAlaIleProLeuArgThrIleThrAlaAspThrPheArgLys 140
    |||||
DB 376 CCACGAGACGCTGCTGCGCTCCATTTGAGAACCATTCAGATTAAGCTTTCAGAAAG 435
OY 141 LeuPheArgValTyrSerAsnPhetLeuArgGlyLysLeuLysLeuTyrThrGlyGlnAla 160
    |||||
DB 436 TTATTCAGAGTTTACTTCCAACTTCTTGAGAGGTAAATTGAAGTTGTACACCGGTGAAGCC 495
OY 161 CysArgThrGlyAspArg 166
    |||||
DB 496 TGTAGAACTGGTGACAGA 513

```

RESULT 8

AAA46697 AAA46697 standard; DNA; 582 BP.

AC AAA6697;
 XX
 DT 25-SEP-2000 (first entry)
 XX
 DE DNA encoding a human erythropoietin polypeptide.
 XX
 KW Human; erythropoietin; EPO; inhibitor; nuclear factor-kappaB; NF-kappaB;
 XX multi-drug resistance gene; malignant hemopathy; solid tumour;
 XX malignant blood disease; leukaemia; lymphoma; solid cancer; ds.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..582
 FT /*tag= a
 FT /product= "erythropoietin"
 XX
 PN MO200030587-A2.
 XX
 PD 02-JUN-2000.
 XX
 PF 24-NOV-1999: 99WO-FR02897.
 XX
 PR 25-NOV-1998: 98FR-0014858.
 XX
 PA (CNRS) CENT NAT RECH SCI.
 XX
 PI Hirsch F, Haeflner A;
 XX
 DR WPI: 2000-399901/34.
 XX P-PSDB; AA93638.
 XX
 PT Treatment of haematological or solid tumours using an inhibitor of the
 XX activation of nuclear factor-kappaB, particularly to prevent
 XX development of resistance to chemotherapeutics
 XX
 PS Claim 5; Page 28-29; 30pp; French.
 XX
 CC The present sequence encodes a human erythropoietin (EPO) polypeptide.
 XX The human growth hormone protein is used as an inhibitor of the
 XX activation of nuclear factor-kappaB (NF-kappaB). The inhibitor inhibits
 XX activation of NF-kappaB, and thus transcription of the multi-drug
 XX resistance gene (which contains binding sites for NF-kappaB within its
 XX regulatory regions). The inhibitors are used to produce pharmaceuticals
 XX which may be used in the treatment of malignant hemopathy or solid
 XX tumours. The inhibitors are especially used to treat malignant blood
 XX diseases (leukaemia, lymphoma) and solid cancers (of breast or ovary).
 XX
 SQ Sequence 582 BP; 113 A; 181 C; 170 G; 118 T; 0 other;
 Alignment Scores:
 Pred. No.: 1,06e-83 Length: 582
 Score: 825.00 Matches: 162
 Percent Similarity: 97.59% Conservative: 0
 Best Local Similarity: 97.59% Mismatches: 4
 Query Match: 97.86% Indels: 0
 DB: 21 Gaps: 0
 US-09-813-775c-18 (1-166) x AAA46697 (1-582)
 QY 1 A1APROPRARGLEULECYASPSERARGVALLEUCLUARGTYRLEUENGLUALALYS 20
 DB 82 GGGCCACGAGGCTCATGTGTGACACCGAGCTCTGAGAGGTAACCTCTTGAGGCCAAG 141
 QY 21 GLUALAGLUALSNLIERHTHRTGLCYSAAGLUALHISCYSERLEUANGLUASNLIERH 40
 DB 142 GAGCGGAGAAATATCATCAGACGGGCTGTCTGAACTGCACTTGGAATGGAATATCACT 201
 QY 41 VALPROASPTHLVYSVALSNPHERYRAIATRPLYSARGASN**SER**G1ING1NALA 60
 DB 202 GTGCCAGACACCAAGTAAATTCTCTATGCTTGAGAGAGATGAGGTGGGCGACGAGCC 261
 QY 61 VALG1VALTRPOLNCLYEUALALAEUUSERG1UALAVALLEUARGGLYGINALAEU 80

DB 262 GTAGAAAGTCGCGAGGGCCCTGCTCTCGGAACCTCTCCGCGGGCCAGGCCCTG 321
 QY 81 LEUVALANSERSERGINPOTRPG1UProLeuGlnLeuHisValAspLysAlaValSer 100
 DB 322 TTGGTCAACTCTTCCACGGCCGTGGAGCCCTTCAGCTGATGTGCAFTAAAGCCGTCAGT 381
 QY 101 G1YLeuArgSerLeuThrTrhLeuLeuArgAlaLeuG1YAlaGlnLysG1UALA1LeSer 120
 DB 382 GGCCTTGCAAGCCTCACACACTGTGCTTGCGGCTGTGGAGCCAGAAAGAGCATCTCC 441
 QY 121 PROPROASPA1A1ASER1A1A1APROLeuArgThr1LeThr1A1AspThrPheArgLys 140
 DB 442 CCTTCAGATGCGGCTCAGCTGCTCCAGCAACATCACTGCTGACACTTTCGCGAAA 501
 QY 141 LEUPHEARGVALTYRSERASNPHELEUARG1LYSLEULYSLEUTYRTHRTGLYGLUALA 160
 DB 502 CTCTCCGAGTCTACTCAATTTTCTCTCCGGGGAAGCTGAAGCTGTACACAGGGAGGCC 561
 QY 161 CysArgThrGlyAspArg 166
 DB 562 TGCAGACAGGAGGACAGA 579
 RESULT 9
 AAH46972
 ID AAH46972 standard; cDNA; 582 BP.
 XX
 AC AAH46972;
 XX
 XX 29-OCT-2001 (first entry)
 XX
 DE Human erythropoietin (EPO) cDNA sequence.
 XX
 XX Transgenic pig; human: erythropoietin; EPO; milk; PMSG; hCG;
 XX chorionic gonadotrophic hormone; WAP promoter; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..582
 FT /*tag= a
 FT /product= "EPO"
 FT sig_peptide 1..81
 FT /*tag= b
 FT mat_peptide 82..579
 FT /*tag= c
 PN MO200159074-A1.
 XX
 PD 16-AUG-2001.
 XX
 PF 28-JUN-2000: 2000WO-KR00675.
 XX
 PR 14-FEB-2000: 2000KR-0006888.
 XX
 PA (KORE-) REPUBLIC KOREA.
 XX
 PI Chang W, Park J, Seong H, Min K, Yang B, Im G, Lee Y, Lee C;
 XX Kim J;
 XX
 DR WPI: 2001-514656/56.
 XX P-PSDB; AAB85573.
 XX
 PT Producing transgenic porcine that secretes human erythropoietin (hEPO)
 XX in milk, by introducing vector comprising hEPO genome into fertilized
 XX eggs of porcine to which PMSG and hCG were administered, and developing
 XX progeny
 XX
 PS Claim 4; Fig 3; 21pp; English.
 XX
 CC The invention relates to producing transgenic pigs (P) that secrete
 XX human erythropoietin (hEPO) in milk. The method involves administering
 XX PMSG and human chorionic gonadotrophic hormone (hCG) into (P), collecting

CC fertilized eggs after mating, injecting expression vector containing a
 CC 2.6 kb WAP promoter, hsp90 genome and SV40 poly A DNA into male pronuclei,
 CC transplanting them in surrogate mother pig and allowing it to give birth.
 CC The method provides transgenic porcine capable of secreting hsp90 in their
 CC milk, thus producing the expensive useful medicine at a low cost with
 CC stability on a large scale, giving a contribution to the improvement of
 CC human health. The present sequence represents a base sequence for a human
 CC EPO cDNA incorporated into the genome of porcine.

XX Sequence 582 BP; 113 A; 181 C; 170 G; 118 T; 0 other;

Alignment Scores:

Pred. No.:	1.06e-83	Length:	582
Score:	825.00	Matches:	162
Percent Similarity:	97.59%	Conservative:	0
Best Local Similarity:	97.59%	Mismatches:	4
Query Match:	97.86%	Indels:	0
DB:	22	Gaps:	0

US-09-813-775c-18 (1-166) x AAA46972 (1-582)

OY 1 AAlaProArgLeuIleCysAspSerArgValLeuGluArgTyrLeuGluAlaLys 20
 DB 82 GCCCACCACGCGCTATCTGTACAGCCGAGTCTCGAGAGGTACTCTTGAGGCCAAG 141
 OY 21 GluAlaGluAsnIleThrThrGlyCysAlaGluHisCysSerLeuAsnGluAsnIleThr 40
 DB 142 GAGGCCGAGAAATATCAGCAGCGGGCTGTGCTGAACTGCGAGCTTGAATGAAATATCACT 201
 OY 41 ValProAspThrIleValAsnPhenylAlaTyrPlyAspAsn***Ser***GlnGlnAla 60
 DB 202 GTCCCGAGACACCAAGATTATTTCTATGCTGGAAGAGATGAGCTCGGGCAGCAGGCC 261
 OY 61 ValGluValTPGInGlyLeuAlaLeuLeuSerGluAlaValLeuArgGlyGlnAlaLeu 80
 DB 262 GTAGAAGTCTGGCAGCGGCTGCTGCTGCTGGAAGCTGTCTGCGGGCCAGGCCCTG 321
 OY 81 LeuValAsnSerSerGlnProTyrPlyProLeuGlnLeuHisValAspLysAlaValSer 100
 DB 322 TTGGTCAACTCTTCCAGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 381
 OY 101 GylLeuArgSerLeuThrThrLeuLeuArgAlaLeuGlyAlaGlnLysGlnAlaLeuSer 120
 DB 382 GGCCTTCGAGCTCTACCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 441
 OY 121 ProProAspAlaAlaSerAlaAlaProLeuArgThrIleThrAlaAspThrPheArgLys 140
 DB 442 CCTCCAGATGGCGCTCAGCTGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAG 501
 OY 141 LeuPheArgValTyrSerAsnPhenylAlaGlyLysLeuLysLeuTyrThrGlyGlnAla 160
 DB 502 CTCCTCCAGTCTACTCCAAATTTCTCCGGGGAAGCTGAAAGCTGTACACAGGGAGGCC 561
 OY 161 CysArgThrGlyAspArg 166
 DB 562 TGCAGGACAGGGACAGA 579

Db 562 TGCAGGACAGGGACAGA 579

RESULT 10 AAC66882 standard; cDNA: 585 BP.

XX AAC66882;

XX 27-MAR-2001 (first entry)

DE Chimpanzee erythropoietin coding sequence SEQ ID NO: 3.

KW Chimpanzee erythropoietin; EPO; hybridisation probe; gene therapy;

KW mapping; therapeutic agent; ss.

XX Pan sp.

PN WO200068376-A1.

XX 16-NOV-2000.

XX 05-MAY-2000; 2000WO-US12370.

XX 07-MAY-1999; 99US-0307307.

XX 28-MAR-2000; 2000US-0307307.

XX (GETH) GENENTECH INC.

XX Desauvage F, Henner DJ;

XX WPI: 2001-007393/01.

XX Nucleic acids encoding chimpanzee erythropoietin, useful for treatment

XX of e.g. anemia, also derived proteins, antibodies and modulators -

XX Claim 2; Fig 2; 109pp; English.

XX The present invention provides the coding and protein sequences of

XX chimpanzee erythropoietin (EPO). These sequences can be used in gene

XX therapy, to block the activity of EPO, as hybridisation probes, in

XX genetic and chromosome mapping and as therapeutic agents.

XX Sequence 585 BP; 115 A; 185 C; 168 G; 117 T; 0 other;

Alignment Scores:

Pred. No.:	1.06e-83	Length:	585
Score:	825.00	Matches:	162
Percent Similarity:	97.59%	Conservative:	0
Best Local Similarity:	97.59%	Mismatches:	4
Query Match:	97.86%	Indels:	0
DB:	22	Gaps:	0

US-09-813-775c-18 (1-166) x AAC66882 (1-585)

OY 1 AAlaProArgLeuIleCysAspSerArgValLeuGluArgTyrLeuGluAlaLys 20
 DB 82 GCCCACCACGCGCTATCTGTACAGCCGAGTCTCGAGAGGTACTCTTGAGGCCAAG 141
 OY 21 GluAlaGluAsnIleThrThrGlyCysAlaGluHisCysSerLeuAsnGluAsnIleThr 40
 DB 142 GAGGCCGAGAAATATCAGCAGCGGGCTGTGCTGAACTGCGAGAGGTACTCTTGAGGCCAAG 201
 OY 41 ValProAspThrIleValAsnPhenylAlaTyrPlyAspAsn***Ser***GlnGlnAla 60
 DB 202 GTCCCGAGACACCAAGATTATTTCTATGCTGGAAGAGATGAGCTCGGGCAGCAGGCC 261
 OY 61 ValGluValTPGInGlyLeuAlaLeuLeuSerGluAlaValLeuArgGlyGlnAlaLeu 80
 DB 262 GTAGAAGTCTGGCAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 321
 OY 81 LeuValAsnSerSerGlnProTyrPlyProLeuGlnLeuHisValAspLysAlaValSer 100
 DB 322 TTGGTCAACTCTTCCAGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 381
 OY 101 GylLeuArgSerLeuThrThrLeuLeuArgAlaLeuGlyAlaGlnLysGlnAlaLeuSer 120
 DB 382 GGCCTTCGAGCTCTACCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 441
 OY 121 ProProAspAlaAlaSerAlaAlaProLeuArgThrIleThrAlaAspThrPheArgLys 140
 DB 442 CCTCCAGATGGCGCTCAGCTGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAG 501
 OY 141 LeuPheArgValTyrSerAsnPhenylAlaGlyLysLeuLysLeuTyrThrGlyGlnAla 160
 DB 502 CTCCTCCAGTCTACTCCAAATTTCTCCGGGGAAGCTGAAAGCTGTACACAGGGAGGCC 561
 OY 161 CysArgThrGlyAspArg 166
 DB 562 TGCAGGACAGGGACAGA 579

RESULT 11

ABL59290
 ID ABL59290 standard; DNA; 614 BP.
 AC ABL59290;
 XX
 DT 07-OCT-2002 (first entry)
 XX
 DE Nucleotide sequence of a modified human erythropoietin (EPO).
 XX
 KW Human; erythropoietin; EPO; glycoprotein; reticulocyte production;
 KW red blood cell production; anaemia; chronic renal failure;
 KW acquired immunodeficiency syndrome; AIDS; cancer; bone marrow;
 KW committed erythroid progenitor; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 14..604
 FT sig_peptide /*tag= a
 FT 14..94
 FT /*tag= b
 FT /*note= "secretion signal sequence"
 XX
 PN WO200249673-A2.
 PD 27-JUN-2002.
 XX
 PF 08-DEC-2001; 2001WO-EP14434.
 XX
 PR 20-DEC-2000; 2000EP-0127891.
 XX
 PA (HOPE) HOFFMANN IA ROCHE & CO AG F.
 XX
 PI Burg J, Engel A, Franze R, Hilger B, Schurig HE, Tischer W;
 PI Wozny M;
 PI WPI: 2002-566640/60.
 DR P-PSDB; ABB7902.
 XX
 PT Novel conjugate of erythropoietin glycoprotein with polyethylene
 PT glycol, useful for treating diseases correlated with anaemia in chronic
 PT renal failure patients and acquired immunodeficiency syndrome -
 XX
 PS Disclosure; Fig 4; 40pp; English.
 XX
 CC The present sequence encodes a modified human erythropoietin (EPO)
 CC protein. The EPO was extended at the N-terminal by a proteolytic
 CC cleavage site. It was used to produce conjugates of the invention. The
 CC specification describes a conjugate comprising an EPO glycoprotein having
 CC an N-terminal alpha-amino group, chosen from human EPO (hEPO) or its
 CC analogues (where hEPO is modified by addition of 1-6 glycosylation sites
 CC or a rearrangement of a glycosylation site). The glycoprotein is
 CC covalently linked to a poly(ethylene glycol) group. The EPO glycoprotein
 CC has in vivo biological activity of causing bone marrow cells to increase
 CC production of reticulocytes and red blood cells. The conjugate increased
 CC circulating half-life and plasma residence time, decreased clearance,
 CC increased clinical activity in vivo, improved potency and stability, when
 CC compared to unmodified EPO. The EPO conjugate is useful for preparing
 CC medicaments for the treatment and prophylaxis of diseases correlated with
 CC anaemia in chronic renal failure patients (CRF), acquired
 CC immunodeficiency syndrome (AIDS) and for treating cancer patients
 CC undergoing chemotherapy. It is also useful for treating patients by
 CC stimulating the division and differentiation of committed erythroid
 CC progenitors in the bone marrow.
 XX
 SQ Sequence 614 BP; 119 A; 198 C; 176 G; 121 T; 0 other;

Alignment Scores:
 Pred. No.: 1.13e-83
 Score: 825.00
 Percent Similarity: 97.59%
 Best Local Similarity: 97.59%

Length: 614
 Matches: 162
 Conservative: 0
 Mismatches: 4

Query Match: 97.86% Indels: 0
 DB: 24 Gaps: 0
 US-09-813-775C-18 (1-166) x ABL59290 (1-614)
 QY 1 AlaProProArgLeuIleCysAspSerArgValLeuGluArgTyrLeuLeuGluAlaLys 20
 DB 104 GCCCCACACAGCCCTCTCTGTGTGCACAGCCGAGTCTGGAGAGGTACCTCTGGAGGCCAAG 163
 QY 21 GluAlaGluAsnIleThrThrGlyCysAlaGluHisCysSerLeuAsnGluAsnIleThr 40
 DB 164 GAGGCCGAGAAATATCTACGAGCGGGCTGCTGAACACTGCAGCTTGATATGAAATATCACT 223
 QY 41 ValProAspThrLysValAsnPhetYrAlaTyrPlyAspAsn**Ser**GlnGlnAla 60
 DB 224 GTCCACAGACACCAAGTATATTTCTATGCTCGAAGAGATGAGAGTCCGGCAGCGCC 283
 QY 61 ValGluValTyrGlnGlyLeuAlaLeuLeuSerGluAlaValLeuArgLysGlnAlaLeu 80
 DB 284 GTAGAGTGTGGCAGGGCCTGGCCCTGTGTGGAAGCTGTCTCGGGGCCAGGGCCCTG 343
 QY 81 LeuValAsnSerSerGlnProTyrPgluProLeuGlnLeuHisValAspLysAlaValSer 100
 DB 344 TTGGTCAACTCTTCCAGCCGTGGAGCCCTGCACTGATGTGATAAAGCCGTCACT 403
 QY 101 GlyLeuArgSerLeuThrThrLeuLeuArgAlaLeuGlyAlaGlnLysGlnAlaIleSer 120
 DB 404 GGCCCTTCGACGCTCACCACTGCTGCGGGCTGTGGAGCCAGAGCAAGACCATCTCC 463
 QY 121 ProProAspAlaAlaSerAlaAlaProLeuArgThrIleThrAlaAspThrPheArgLys 140
 DB 464 CTTCCAGATGGCGGCTCACCTGCTCCACCGCAATCATGCTGACACTTCCGCAAA 523
 QY 141 LeuPheArgValTyrSerAsnPhetLeuArgGlyLysLeuLysLeuThrThrGlyGluAla 160
 DB 524 CTCTTCGAGTCTACTCCATTTTCTCCGGGGAAGCTGATAGCTGTACACAGGGAGGCC 583
 QY 161 CysArgThrGlyAspArg 166
 DB 584 TGCAGCAGACAGGGGACAGA 601
 RESULT 12
 ID AAX77361
 AC AAX77361 standard; DNA; 616 BP.
 XX
 DT 09-AUG-1999 (first entry)
 XX
 DE Polynucleotide sequence of synthetic erythropoietin.
 XX
 KW Nucleic acid identification; exogenous protein; gene sorting;
 KW growth factor; membrane receptor; sindbis virus; erythropoietin; ss.
 XX
 OS Synthetic.
 OS W09925876-A1.
 PN W09925876-A1.
 XX
 PD 27-MAY-1999.
 XX
 PF 17-NOV-1998; 98WO-US24520.
 XX
 PR 17-NOV-1997; 97US-0972218.
 XX
 PA (CYTO-) CYTOS BIOTECHNOLOGY GMBH.
 XX
 PI Bailey JE, Koller D, Orberger GH, Renner WA;
 PI WPI: 1999-357620/30.
 DR
 XX
 PT Isolating genes encoding proteins with selected properties, useful
 PT for identifying therapeutic agents or targets
 XX

PS Disclosure: Fig 15; 136pp; English.

XX The invention relates to the identification of a recombinant nucleic acid
 CC encoding an exogenous protein having a selected property. The method
 CC comprises preparing a population of eukaryotic host cells, culturing the
 CC cells under suitable conditions and identifying cells that contain the
 CC recombinant nucleic acid. The method is used to sort genes according to
 CC the type of proteins they express, and also to identify new ligand/
 CC receptor interactions. Typical applications of the nucleic acid and the
 CC exogenous protein are in isolation of new growth factors, cytokines,
 CC membrane receptors, cytoplasmic, organelle or nuclear proteins, all of
 CC which may be useful as therapeutic agents or therapeutic targets, e.g.
 CC apoptosis-promoting or tumour suppressing proteins, regulators of cell
 CC proliferation or metabolic processes etc. The protein can also be used as
 CC screen for specific modulators. The nucleic acid can also be used as
 CC sources of therapeutic antisense or ribozyme sequences. The method allows
 CC the protein (rather than a partial DNA sequence) to be isolated and,
 CC since a wide range of cells can be used, they can be expressed with the
 CC correct glycosylation pattern.

XX
 XX Sequence 616 BP; 118 A; 191 C; 184 G; 123 T; 0 other;

Alignment Scores:

Pred. No.:	1-14e-83	Length:	616
Score:	825.00	Matches:	162
Percent Similarity:	97.59%	Conservative:	0
Best Local Similarity:	97.59%	Mismatches:	4
Query Match:	97.86%	Indels:	0
DB:	20	Gaps:	0

US-09-813-775c-18 (1-166) x AAX77361 (1-616)

QY 1 AAlAPROAATGLeuIIeCysAspSerArgValLeuGluArgTyrLeuLeuGluAlaIys 20
 Db 97 GCCCAGACAGCCGCTATCTGTGACAGCCGAGCTCGAGAGGCTACTCTTGGAGGCCAAG 156

QY 21 GUUAGUAsnIIeThrThrGlyCysAlaGluIuHsCysSerLeuAsnGluAsnIleThr 40
 Db 157 GAGGCCGAATATATACAGAGGGGCTGTGTAACACTGCAAGCTTAATGAGAAATATCACT 216

QY 41 ValProAspThrIysValAsnPhenTyraIleTyrIAspAsn**Ser**GlnGlnAla 60
 Db 217 GTCCAGACAGCCAAAGTTAATTTCTATGCTGCGAAGAGATGAGGTGGGAGAGAGCC 276

QY 61 ValGluValITrPglGlyLeuAlaLeuLeuSerGluAlaValLeuAlaGlyGlnAlaIle 80
 Db 277 GTAGAAAGTGTGGCAGAGGCTGCTGCTGTGGAAGCTGTCTGCGGGGAGAGCCCTG 336

QY 81 IeuValAsnSerSerGlnProThrGluProLeuGlnIleuHsValAspIysAlaValSer 100
 Db 337 TTGGTCAACTCTTCCACCGCGGAGCCCTGCGAGCTGATGATTAAGCCGCTCACT 396

QY 101 GlyLeuArgSerLeuThrThrLeuLeuArgAlaLeuGlyAlaGlnIleLysGlnAlaIleSer 120
 Db 397 GGCCTTGCAGCTCAGACACTCTGCTGGGGCTCTGGGAGCCCAAGAACCCATCTCC 456

QY 121 PropProAspAlaIleSerAlaIleProLeuArgThrIleThrAlaAspThrPheArgIys 140
 Db 457 CCTCAGATGCGGCTCAGCTGCTCCTCACTCCAGAACATCAGCAGACACTTCCGCAAA 516

QY 141 IeuPheArgValItyrSerAsnPhenLeuArgGlyIysLeuIysLeuTyrThrGlyGlnAla 160
 Db 517 CTCTTCGAGTCTACTCCAAATTTCTCCGGGGAAGCTGAAGCTGTACACAGGGAGGCC 576

QY 161 CysArgThrGlyAspArg 166
 Db 577 TGCAGACAGGGGACAGA 594

RESULT 13
 AAA90393
 ID AAA90393 standard; DNA; 616 BP.
 XX
 AC AAA90393;

XX 10-JAN-2001 (first entry)

DT DN encoding synthetic erythropoietin (EPO).

DE Nucleic acid identification; exogenous protein; drug screening;

KW recombinant expression; synthetic erythropoietin; EPO; ds.

XX Synthetic.

OS JP2000189173-A.

PN 11-JUL-2000.

PD 23-AUG-1999; 99JP-0236220.

PF 17-NOV-1998; 98US-0193707.

PR 17-NOV-1998; 98WO-US24520.

XX (CYTO-) CYTOS BIOTECHNOLOGY GMBH.

PA WPI; 2000-551637/51.

DR

XX Identifying a recombinant nucleic acid to identify and isolate various
 PT cellular proteins, comprises culturing a composition comprising
 PT eukaryotic host cells and identifying a cell comprising recombinant
 PT nucleic acid

PS Disclosure: Fig 15; 56pp; Japanese.

XX The invention relates to the identification of a recombinant nucleic acid
 CC encoding an exogenous protein having a selected property. The method
 CC comprises preparing populations of eukaryotic host cells, where each cell
 CC comprises an expression vector encoding a different exogenous protein.
 CC The host cells are cultured under suitable conditions and the nucleic
 CC acid which encodes the exogenous protein is identified. The method is
 CC useful for the identification and isolation of proteins with a selected
 CC property. Typical applications of the nucleic acid and the exogenous
 CC protein are in isolation of new growth factors, cytokines, membrane
 CC receptors, cytoplasmic, organelle or nuclear proteins, all of which may
 CC be useful as therapeutic agents or therapeutic targets, e.g., pro-
 CC apoptotic or tumour suppressing proteins, regulators of cell
 CC proliferation or of metabolic processes. The protein can also be used to
 CC screen for ligands and specific modulators of activity. The method of the
 CC invention allows the direct cloning of full length cDNAs in one step. It
 CC facilitates direct expression of the protein without the need to perform
 CC further procedures such as subcloning and establishment of a cell line
 CC for protein production. The method allows a protein of interest (rather
 CC than a partial DNA sequence) to be isolated and, since a wide range of
 CC cell types can be used, they can be expressed in a correctly folded and
 CC glycosylated form. The present sequence represents DNA encoding a
 CC synthetic erythropoietin (EPO) which was used in the method of the
 CC invention. This patent is related to WO9925876.

XX
 XX Sequence 616 BP; 118 A; 191 C; 184 G; 123 T; 0 other;

Alignment Scores:

Pred. No.:	1-14e-83	Length:	616
Score:	825.00	Matches:	162
Percent Similarity:	97.59%	Conservative:	0
Best Local Similarity:	97.59%	Mismatches:	4
Query Match:	97.86%	Indels:	0
DB:	21	Gaps:	0

US-09-813-775c-18 (1-166) x AAA90393 (1-616)

QY 1 AAlAPROAATGLeuIIeCysAspSerArgValLeuGluArgTyrLeuLeuGluAlaIys 20
 Db 97 GCCCAGACAGCCGCTATCTGTGACAGCCGAGTCTCGAGAGGCTACTCTTGGAGGCCAAG 156

QY 21 GUUAGUAsnIIeThrThrGlyCysAlaGluIuHsCysSerLeuAsnGluAsnIleThr 40
 Db 157 GAGGCCGAATATATACAGAGGGGCTGTGTAACACTGCAAGCTTAATGAGAAATATCACT 216


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QY 41 ValProAspThrLysValAsnPhETyRAlaTrpLysArgAsn***Ser***GInGlnAla 60
DB 217 GTCCACAGACACCAAGTTAATTCTATGCTCGAAGAGCATGAGTTCGGGACAGAGGCC 276
QY 61 ValGluValTrpGInGlyLeuAlaLeuLeuSerGlnAlaValLeuArgGlyGlnAlaLeu 80
DB 277 GTAGAAAGTCTGGACGGGCTGGCCCTGCTGTGGAACTGTCTGGGGGCGAGCCCTG 336
QY 81 LeuValAsnSerSerGlnProTrpGluProLeuGlnLeuHisValAspLysAlaValSer 100
DB 337 TTGGTCAACTCTTCCCGCCGTGGAGCCCTGACGTGATGGATTAAGCCGTAGT 396
QY 101 GlyLeuArgSerLeuThrTrpLeuLeuArgAlaLeuGlyAlaGlnLysGlnAlaLeuSer 120
DB 397 GGCCTTCGACGCTCACCACTCTGCTTCGGGCTCTGGAGCCCGAAGGAAGCCATCTCC 456
QY 121 ProProAspAlaAlaSerAlaAlaProLeuArgThrIleThrAlaAspTrpPheArgLys 140
DB 457 CCTCCAGATSCGGCTCAGCTGCTCCACCTCGAACAATCACTGCTGACACTTTCGGCAA 516
QY 141 LeuPheArgValTyrSerAsnPhLeuArgGlyLysLeuLysLeuTyrTrpGlyGlnAla 160
DB 517 CTCTTCGAGTCTACTCAATTTCCTCCGGGAAAGCTGAAGCTGTACACAGGGAGGCC 576
QY 161 CysArgThrGlyAspArg 166
DB 577 TGCAGACAGGGGACAGA 594

RESULT 14
AAQ74760 standard; DNA: 625 BP.
ID AAQ74760 standard; DNA: 625 BP.
AC AAQ74760:
XX
XX 24-JUN-1995 (first entry)
DE Human prepro-erythropoietin.
XX
XX Erythropoietin; therapeutic; ss.
OS Synthetic.
XX
XX Key Location/Qualifiers
FH 5..21
FT 5..UTR /*tag= a
FT sig-peptide 22..102
FT /*tag= b
FT CDS 103..600
FT /*tag= c
XX
XX W09425055-A.
XX
XX 10-NOV-1994.
XX
XX 29-APR-1994: 94MO-US04755.
XX
XX 29-APR-1993: 93US-0055076.
XX
XX (ABBO ) ABBOTT LAB.
XX
XX Devries PJ, Mellovitz BS, Meuth JL, Okasinski GF;
XX Schaefer VG;
XX
XX WPI: 1994-357906/44.
XX
XX P-PSDB: AAR65499.
XX
XX Erythropoietin analogues - useful for treatment of anaemia and
XX PT have enhanced erythropoietic effect.
XX
XX PS Disclosure: Page 38-39; 56pp; English.
XX
XX The synthetic DNA encoding human prepro-erythropoietin may be ligated

```

```

CC into an expression vector for erythropoietin expression in a CHO
CC cell culture. Site-directed mutagenesis may be used in the
CC construction of EPO analogues with improved activity, which may be
CC used in pharmaceutical compositions for inducing erythropoiesis and
CC treating anaemia.
XX
XX Sequence 625 BP: 123 A; 195 C; 179 G; 128 T; 0 other;
SQ

Alignment Scores:
Pred. No.: 1,16e-83 Length: 625
Score: 825.00 Matches: 162
Percent Similarity: 97.59% Conservative: 0
Best Local Similarity: 97.59% Mismatches: 4
Query Match: 97.86% Indels: 0
DB: 15 Gaps: 0

US-09-813-775c-18 (1-166) x AAQ74760 (1-625)
QY 1 AlaProAspThrLysValAsnPhETyRAlaTrpLysArgAsn***Ser***GInGlnAla 20
DB 103 GCCCACCACGCGCTCATATGTAAGTCCGAGTCCGAGAGTCACTTGGAGGCCAAG 162
QY 21 GluAlaGlnAsnIleThrTrpGlyCysAlaGlnHisCysSerLeuAsnGlnIleThr 40
DB 163 GAGCCGAGATATATTAGAGGGGCTGTGCTGAGCACTGAGCTTGAATGAAATATCACT 222
QY 41 ValProAspThrLysValAsnPhETyRAlaTrpLysArgAsn***Ser***GInGlnAla 60
DB 223 GTCCACAGACACCAAGTTAATTCTATGCTCGAAGAGCATGAGTTCGGGACAGAGGCC 282
QY 61 ValGluValTrpGInGlyLeuAlaLeuLeuSerGlnAlaValLeuArgGlyGlnAlaLeu 80
DB 283 GTAGAAAGTCTGGACGGGCTGGCCCTGCTGTGGAACTGTCTGGGGGCGAGGCCCTG 342
QY 81 LeuValAsnSerSerGlnProTrpGluProLeuGlnLeuHisValAspLysAlaValSer 100
DB 343 TTGGTCAACTCTTCCCGCCGTGGAGCCCTGCTGAGCTGATGGATTAAGCCGTAGT 402
QY 101 GlyLeuArgSerLeuThrTrpLeuLeuArgAlaLeuGlyAlaGlnLysGlnAlaLeuSer 120
DB 403 GGCCTTCGACGCTCACCACTCTGCTTCGAGCTCTGGGGGCCCGAAGGAAGCCATCTCC 462
QY 121 ProProAspAlaAlaSerAlaAlaProLeuArgThrIleThrAlaAspTrpPheArgLys 140
DB 463 CCTCCAGATSCGGCTCAGCTGCTCCACCTCGAACAATCACTGCTGACACTTTCGGCAA 522
QY 141 LeuPheArgValTyrSerAsnPhLeuArgGlyLysLeuLysLeuTyrTrpGlyGlnAla 160
DB 523 CTCTTCGAGTCTACTCAATTTCCTCCGGGAAAGCTGAAGCTTTACACAGGGAGAGCA 582
QY 161 CysArgThrGlyAspArg 166
DB 583 TGCAGACAGGGGACAGA 600

RESULT 15
ABL59289 standard; DNA: 629 BP.
ID ABL59289
AC ABL59289:
XX
XX 07-OCT-2002 (first entry)
DE Nucleotide sequence of a modified human erythropoietin (EPO).
XX
XX
XX Human: erythropoietin; EPO; glycoprotein; reticulocyte production;
XX red blood cell production; anaemia; chronic renal failure;
XX acquired immunodeficiency syndrome; AIDS; cancer; bone marrow;
XX committed erythroid progenitor; ss.
XX
XX Synthetic.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers

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GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus.p2n model

Run on: January 8, 2003, 05:15:15 ; Search time 2221.35 Seconds
(without alignments)
2174.835 Million cell updates/sec

Title: US-09-813-775C-18
Perfect score: 843
Sequence: 1 APPRLICDSRYLERYLLEAK.....NFLRGKIKLYTGACRTGDR 166

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Zgapop 6.0 , Zgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2054640 seqs, 14551402878 residues
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-DB=genEmbl -OFFT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blousum62 -TRANS=human4.0.cdi -LIST=45
-DOCFALIGN=200 -THR.SCORE=Pct -THR.MAX=100 -THR.MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
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-NO_XLPXY -NO_WMAP -LARGEQUERY -NEG.SCORES=0 -WAIT -LONGLOG -DEV.TIMEOUT=120
-WARN.TIMEOUT=10 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl :
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2: gb.htg :
3: gb.in :
4: gb.om :
5: gb.ov :
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9: gb.pr :
10: gb.ro :
11: gb.sts :
12: gb.sy :
13: gb.un :
14: gb.vl :
15: em.ba :
16: em.fun :
17: em.hum :
18: em.in :
19: em.mu :
20: em.om :
21: em.or :
22: em.ov :
23: em.pat :
24: em.ph :
25: em.pl :
26: em.ro :
27: em.sts :
28: em.un :

29: em.vl :
30: em.htg_hum :
31: em.htg_inv :
32: em.htg_other :
33: em.htg_mus :
34: em.htg_pin :
35: em.htg_rod :
36: em.htg_mam :
37: em.htg_vrt :
38: em.sy :
39: em.htgo_hum :
40: em.htgo_mus :
41: em.htgo_other :

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	825	97.9	501	6	BD007423	BD007423 Cyclicall
2	825	97.9	508	6	I49875	I49875 Sequence 69
3	825	97.9	514	6	AX150264	AX150264 Sequence
4	825	97.9	533	6	I07891	I07891 Sequence 5
5	825	97.9	551	6	I00283	I00283 Sequence 4
6	825	97.9	551	6	I07892	I07892 Sequence 6
7	825	97.9	551	6	I08350	I08350 Sequence 6
8	825	97.9	582	6	AX025442	AX025442 Sequence
9	825	97.9	582	6	I05397	I05397 Sequence 2
10	825	97.9	585	6	AX046870	AX046870 Sequence
11	825	97.9	724	6	I05399	I05399 Sequence 4
12	825	97.9	788	6	AR086679	AR086679 Sequence
13	825	97.9	823	6	AR063255	AR063255 Sequence
14	825	97.9	823	6	AR179013	AR179013 Sequence
15	825	97.9	1011	6	A47505	A47505 Sequence 12
16	825	97.9	1300	6	AX451645	AX451645 Sequence
17	817	96.9	1342	9	HSEPRP	X02157 Human mRNA
18	816	96.8	501	6	AX464420	AX464420 Sequence
19	815	96.7	501	6	AX464421	AX464421 Sequence
20	802	95.1	945	6	A47500	A47500 Sequence 7
21	802	95.1	969	6	A47497	A47497 Sequence 4
22	743.5	88.2	1344	6	I08348	I08348 Sequence 1
23	743.5	88.2	1462	9	MACEPO	M18189 Monkey (Cyn
24	743.5	88.2	5107	6	A92667	A92667 Sequence 3
25	743.5	88.2	5107	6	AR158347	AR158347 Sequence
26	741.5	88.0	691	9	MACEPTHRO	L10609 Macaca mula
27	737.5	87.5	1344	6	I07889	I07889 Sequence 1
28	733	87.0	1292	6	E00630	E00630 DNA encodin
29	709	84.1	512	6	BD007363	BD007363 Cyclicall
30	703	83.4	512	6	BD007364	BD007364 Cyclicall
31	699	82.9	512	6	BD007365	BD007365 Cyclicall
32	695	82.4	681	4	CATERYTHRO	L10606 Cat erythro
33	694	82.3	512	6	BD007366	BD007366 Cyclicall
34	692	82.1	679	10	RATEPPO	L10608 Rat erythro
35	692	82.1	1395	10	RATEPPO	D10763 Rattus norv
36	689	81.7	512	6	BD007367	BD007367 Cyclicall
37	688	81.6	725	4	FD000685	U00685 Felis domes
38	683	81.0	512	6	BD007368	BD007368 Cyclicall
39	679.5	80.6	1133	4	BTU4762	U4762 Bos taurus
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41	676	80.2	3609	6	AX249944	AX249944 Sequence
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RESULT 1

ALIGNMENTS

BD007423 501 bp DNA linear PAT 31-JAN-2002
 LOCUS Cyclically rearranged erythropoietin receptor agonist.
 DEFINITION BD007423
 ACCESSION BD007423.1 GI:18635794
 VERSION JP 2001503266-A/61.
 KEYWORDS unclassified.
 SOURCE unclassified.
 ORGANISM unclassified.
 REFERENCE 1 (bases 1 to 501)
 AUTHORS McWhorter,C.A., Feng,Y. and Somers,N.
 TITLE Cyclically rearranged erythropoietin receptor agonist
 JOURNAL Patent: JP 2001503266-A 61 13-MAR-2001;
 G.D. SEARLE & CO
 COMMENT OS Unidentified
 PN JP 2001503266-A/61
 PD 13-MAR-2001
 PF 23-OCT-1997 JP 1998520528
 PR 25-OCT-1996 US 60/034044
 PI CHARLES A MCWHORTER,YIQING FENG,NINA SOMERS
 PC C12N15/09,A61K35/18,A61K35/28,A61K38/22,A61K48/00,A61P7/06,PC
 A61P43/00,
 PC C07K14/52,C12N5/06,C12P21/02,C12N15/00,C12N5/00,A61K37/24 CC
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 CC Topology: Linear;
 FH key
 FT source
 FEATURES
 source 1..501 /organism='unclassified',
 location/Qualifiers
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 Pred. No.: 1.07e-77 Length: 501
 Score: 825.00 Matches: 162
 Percent Similarity: 97.59% Conservative: 0
 Best Local Similarity: 97.59% Mismatches: 4
 Query Match: 97.86% Indels: 0
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 QY 1 AAlaProPArgLeuIleCysAspSerArgValLeuGluArgTyrLeuGluAlaLys 20
 Db 1 GCCCACCACGCTCATCTGTGACGCGAGCTCTGAGAGGTACTCTTGAGGCCAAG 60
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 Db 61 GAGCGCGAATATCAGCAGCGGCTGCTCAACACTCAGCTTGAATGAGAAATATCACT 120
 QY 41 ValProAspThrIleValAsnPhetYrAlaTrpIlePlysArgAsn***Ser***GlnGlnAla 60
 Db 121 GTCCAGACACCAAGTTATTTCTATGCTTGGAAAGAGATGAGAGTGGGCGAGCAGGCC 180
 QY 61 ValGluValITrpgInGlyLeuAlaLeuLeuSerGlnAlaValLeuArgGlyGlnAlaLeu 80
 Db 181 GTAGAAAGTGTGGAGAGGCTGGCTGCTGCGAAAGCTGTCTCGGGGCGCAGGCCCTG 240
 QY 81 LeuValAsnSerSerGlnProITrpgIuProLeuGlnLeuHisValAspLysAlaValSer 100
 Db 241 TTGGCAACTCTTCCACCGCTGGAGGCCCTGCGAGCTGCTGGAATGGAAGCCGTCAGT 300
 QY 101 GlyLeuArgSerLeuThrThLeuLeuArgAlaLeuGlyAlaGlnIleGlnAlaIleSer 120
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 QY 121 ProProAspAlaAlaSerAlaAlaProLeuArgThrIleThrAlaAspThrPheArgLys 140
 Db 361 CCTCAGATGGGGCTCAGCTGCTCCTCACTCGGAACATCATCTGCTGACACTTTCCGCAA 420

QY 141 LeuPheArgValITyrSerAsnPhetLeuArgGlyLysLeuLysLeuTyrThrGlyGlnAla 160
 Db 421 CTTTCCACAGTCTTACTCCAAATTTCTCCGGGGAAGCTGAAGCTGTACACAGGAGGCC 480
 QY 161 CysArgThrGlyAspArg 166
 Db 481 TTCAGACAGAGGACAGA 498
 RESULT 2
 149875 508 bp DNA linear PAT 07-OCT-1997
 LOCUS Sequence 69 from patent US 5641663.
 DEFINITION 149875
 ACCESSION 149875.1 GI:2472095
 VERSION 149875.1
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 508)
 AUTHORS Garvin,R.T. and Malek,L.T.
 TITLE Expression system for the secretion of bioactive human granulocyte
 macrophage colony stimulating factor (GM-CSF) and other
 heterologous proteins from streptomyces
 JOURNAL Patent: US 5641663-A 69 24-JUN-1997;
 FEATURES
 source 1..508 /organism='unknown',
 location/Qualifiers
 BASE COUNT 82 a 193 c 161 g 72 t
 ORIGIN
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 Pred. No.: 1.09e-77 Length: 508
 Score: 825.00 Matches: 162
 Percent Similarity: 97.59% Conservative: 0
 Best Local Similarity: 97.59% Mismatches: 4
 Query Match: 97.86% Indels: 0
 DB: 6 Gaps: 0
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 QY 21 GluAlaGluAsnIleThrGlyCysAlaGluHisCysSerLeuAsnGluAsnIleThr 40
 Db 65 GAGCGGAGAATATCAGCAGCGGGGTGCCCGAGCACTGCTCCCTCAACGAGAACTACCC 124
 QY 41 ValProAspThrIleValAsnPhetYrAlaTrpIlePlysArgAsn***Ser***GlnGlnAla 60
 Db 125 GTCCCGACACCAAGTCAACTTCTACCGCTGCAAGCCACAGAGGTGGCCAGCAGCGG 184
 QY 61 ValGluValITrpgInGlyLeuAlaLeuLeuSerGlnAlaValLeuArgGlyGlnAlaLeu 80
 Db 185 GTGAGGCTGTGGAGAGGCTCGCGCTCTCTCCAGAGGCGGTCTCCGGCGAGGCCCTC 244
 QY 81 LeuValAsnSerSerGlnProITrpgIuProLeuGlnLeuHisValAspLysAlaValSer 100
 Db 245 CTGGGAACGTGTCACACCGCGGGAGCGGCTCCAGCTGCAAGTGGACAAAGCCGCTCC 304
 QY 101 GlyLeuArgSerLeuThrThLeuLeuArgAlaLeuGlyAlaGlnIleGlnAlaIleSer 120
 Db 305 GGGCTCCGCTCCAGCACCGCTGCTGCGCGCCCTCGCTGCCCAAGAGAGGCCATCTCG 364
 QY 121 ProProAspAlaAlaSerAlaAlaProLeuArgThrIleThrAlaAspThrPheArgLys 140
 Db 365 CCCCCGAGCGCGGAGCGCGCGCGCTGCGAGATCAGCGGAGACACTTCGCGAAG 424
 QY 141 LeuPheArgValITyrSerAsnPhetLeuArgGlyLysLeuLysLeuTyrThrGlyGlnAla 160
 Db 425 CTGTTCCGGGCTCTACTCGAACTTCTCTCGGGGGAAGCTGAAGCTTACACCGCGAGGCC 484
 QY 161 CysArgThrGlyAspArg 166

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DEFINITION Sequence 1 from Patent WO0136489.
ACCESSION AX150264
VERSION    AX150264.1 GI:14348284
KEYWORDS
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 514)
AUTHORS     Hartmann,A., Brandt,S., Rieke,E., Sobel,C., Lo,K.M., Way,J.C. and
            Gillies,S.
            Erythropoietin forms with improved properties
            Patent: WO 0136489-A 1 25-MAY-2001;
            MERCK PATENT GmbH (DE)
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            CRTGR"
BASE COUNT  106 a 159 c 152 g 97 t
ORIGIN
Alignment Scores:
Pred. No.:      1,11e-77      Length:      514
Score:          825.00      Matches:      162
Percent Similarity: 97.59%      Conservative: 0
Best Local Similarity: 97.59%      Mismatches: 4
Query Match:    97.86%      Indels:      0
DB:             Gaps:      0
US-09-813-775C-18 (1-166) x AX150264 (1-514)
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Db      8  GCGCCACGAGCCTCATCTGTGTGACAGCCAGTCTGAGAGTACCTTTGGAGGCCAAG 67
QY      21 GAlaAGlAsnIleThrThrGlyCysAlaGluHisCysSerLeuAsnGluAsnIleThr 40
      |||||||
Db      68 GAGCGCGAGAAATATCATCAGACCGCTGTGTAACACTGCGAGCTTGAATGAGAACATCACC 127
QY      41 ValProAspThrLysValAsnPhetYrAlaTPrLysArgAsn**Ser**GlnGlnAla 60
      |||||||
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QY      61 ValGluValTPrGlnGlyLeuAlaLeuLeuSerGluAlaValLeuArgGlyGlnAlaLeu 80
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QY      81 LeuValAsnSerSerGlnProTPrGluProLeuGlnLeuHisValAspLysAlaValSer 100
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QY      101 GlyLeuArgSerLeuThrThrLeuLeuArgAlaLeuGlyAlaGlnLysGluAlaIleSer 120
      |||||||
Db      308 GGGCTTCGAGCCTCAACACTGTGCTTGGGCTCTGGAGCCAGAAAGGACATCTCC 367
QY      121 ProProAspAlaAlaSerAlaAlaProLeuArgThrIleThrAlaAspThrPheArgLys 140
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Db      368 CATTCAAGATCCGGCTTCAGCTGCTCCCTCCGACATATCATCTTGACATTTCCGCAAA 427
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      |||||||
Db      428 CTCTTCGAGATCTACTCCAAATTTCTTCGGGGAAAGCTGAAGCTGTACACAGGGAGGCC 487
QY      161 CysArgThrGlyAspArg 166
      |||||||
Db      488 TGCCGAGACAGGGACAGAGA 505
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107891
LOCUS      107891      533 bp      DNA      linear      PAT 02-DEC-1994
DEFINITION Sequence 5 from Patent EP 0148605.
ACCESSION 107891
VERSION    107891.1 GI:589396
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 533)
AUTHORS     Lin,F.-K.
            Production of erythropoietin
            Patent: EP 0148605-A2 5 17-JUL-1985;
            Location/Qualifiers
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            /organism="unknown"
BASE COUNT  131 a 134 c 138 g 130 t
ORIGIN
Alignment Scores:
Pred. No.:      1.16e-77      Length:      533
Score:          825.00      Matches:      162
Percent Similarity: 97.59%      Conservative: 0
Best Local Similarity: 97.59%      Mismatches: 4
Query Match:    97.86%      Indels:      0
DB:             Gaps:      0
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      |||||||
Db      90 GAAGCTGAACAAATCATCAGCACTGTTGCTGTAACACTGTTTGAACGAAACATTACG 149
QY      41 ValProAspThrLysValAsnPhetYrAlaTPrLysArgAsn**Ser**GlnGlnAla 60
      |||||||
Db      150 GTACCAAGACACCAAGTTACTTCTACGCTTGGAACGTTAGTAAGTTGCTCAACAGCA 209
QY      61 ValGluValTPrGlnGlyLeuAlaLeuLeuSerGluAlaValLeuArgGlyGlnAlaLeu 80
      |||||||
Db      210 GTTGAAGTTTGGCAGAGGTGTGGCACTGCTGACGAGGCTCTACTGCGTGCAGGCACTG 269
QY      81 LeuValAsnSerSerGlnProTPrGluProLeuGlnLeuHisValAspLysAlaValSer 100
      |||||||
Db      270 CTGTGAACCTCCTCTACGCGGTGGGAACCGCTGAGCTGATGTGACAAAGCATCTCT 329
QY      101 GlyLeuArgSerLeuThrThrLeuLeuArgAlaLeuGlyAlaGlnLysGluAlaIleSer 120
      |||||||
Db      330 GGGCTGAGATCTGTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 389
QY      121 ProProAspAlaAlaSerAlaAlaProLeuArgThrIleThrAlaAspThrPheArgLys 140
      |||||||
Db      390 CCGCGGAGTCTGATCTGCTGCAACCGCTCGTAACATCACTGCTGATTCCTCCGAAA 449
QY      141 LeuPheArgValTyrSerAsnPhelLeuArgGlyLysLeuLysLeuTyrThrGlyGluAla 160
      |||||||
Db      450 CTGTTTGTGTATTAATTAATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 509
QY      161 CysArgThrGlyAspArg 166

```

DB 510 TGGCGTACTGGTACCGC 527

RESULT 5

LOCUS 100283

DEFINITION Sequence 4 from Patent US 4935350.

ACCESSION 100283

VERSION 100283.1

KEYWORDS GI:314048

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 551)

AUTHORS Patel,A.C. and Ratzkin,B.J.

TITLE Materials and methods for controlling plasmid copy number and stability

JOURNAL Patent: US 4935350-A 4 19-JUN-1990;

COMMENT On Jul 30, 1993 this sequence version replaced gi:285577.

FEATURES

source Location/Qualifiers

BASE COUNT 157 a 112 c 129 g 153 t

ORIGIN

Alignment Scores:

Pred. NO.: 1.2e-77 Length: 551

Score: 825.00 Matches: 162

Percent Similarity: 97.59% Conservative: 0

Best Local Similarity: 97.59% Mismatches: 4

Query Match: 97.86% Indels: 0

DB: Gaps: 6

US-09-813-775c-18 (1-166) x 100283 (1-551)

QY 1 AAlaProProAlaGLeuIleCysAspSerArgValLeuGluArgTyrLeuLeuGluAlaLys 20

DB 16 GCTCCACCACCAATGATGTGCTGACTCGAGAGTTTGGAAAGTACTTGTGGAAACCTTAA 75

QY 21 GluAlaGluAsnIleThrThrGlyCysAlaGluHisCysSerLeuAsnGluAsnIleThr 40

DB 76 GAAGCTGAAACATCACCACACGTGTGTGCTGACACGTCTTCTTAAGCAAAACATTACG 135

QY 41 ValProAspThrLysValAsnPhetYrAlaTrpLysArgAsn**Ser**GlnGlnAla 60

DB 136 GTACCAGACACCAGGTTAACTTACCTTGAGAAACGTATGAGAGTTGTCACAAACAGCT 195

QY 61 ValGluValITPPGInGlyLeuAlaLeuLeuSerGluAlaValLeuArgGlyGlnAlaLeu 80

DB 196 GTTGAAGTTTGGCAAGTTTGGCTTTGATCTGAAGCTGTTTGAAGGTCACAAAGCCTTG 255

QY 81 LeuValAsnSerSerGlnProTrpGluProLeuGlnLeuHisValAspLysAlaValSer 100

DB 256 TTGCTTAACCTCTTCCACACCATGGSAACCATTTGCACGTGATTAAGCCGTCTCT 315

QY 101 GlyLeuArgSerLeuThrThrLeuLeuArgAlaLeuGlyAlaGlnLysGlnAlaIleSer 120

DB 316 GGTTCAGATCTTTGACACTTGTGTTGAGACCTTGGCTGCTCAAAAGAACCCATTTC 375

QY 121 ProProAspAlaAlaSerAlaAlaProLeuArgThrIleThrAlaAspThrPheArgLys 140

DB 376 CCACCAGACGCTGCTTCGCGCTCCATTTGAGAACCATTCACGCTGATACCTTCGAAAG 435

QY 141 LeuPheArgValIYrSerAsnPhleuArgGlyLysLeuLysLeuTyrThrGlyGluAla 160

DB 436 TTATTCAAGTTTACTCCAACTTCTTGAGAGGTAATTGAAGTTTACACCGGTGAAGCC 495

QY 161 CysArgThrGlyAspArg 166

DB 496 TGTAGAACTGCTGACAGA 513

RESULT 6

107892

LOCUS 107892

DEFINITION Sequence 6 from Patent EP 0148605.

ACCESSION 107892

VERSION 107892.1

KEYWORDS GI:589397

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 551)

AUTHORS Lin,F.-K.

TITLE Production of erythropoietin

JOURNAL Patent: EP 0148605-A2 6 17-JUL-1985;

FEATURES

source Location/Qualifiers

BASE COUNT 157 a 112 c 129 g 153 t

ORIGIN

Alignment Scores:

Pred. NO.: 1.2e-77 Length: 551

Score: 825.00 Matches: 162

Percent Similarity: 97.59% Conservative: 0

Best Local Similarity: 97.59% Mismatches: 4

Query Match: 97.86% Indels: 0

DB: Gaps: 6

US-09-813-775c-18 (1-166) x 107892 (1-551)

QY 1 AAlaProProAlaGLeuIleCysAspSerArgValLeuGluArgTyrLeuLeuGluAlaLys 20

DB 16 GCTCCACCACCAATGATGTGCTGACTCGAGAGTTTGGAAAGTACTTGTGGAAACCTTAA 75

QY 21 GluAlaGluAsnIleThrThrGlyCysAlaGluHisCysSerLeuAsnGluAsnIleThr 40

DB 76 GAAGCTGAAACATCACCACACGTGTGTGCTGACACGTCTTCTTAAGCAAAACATTACG 135

QY 41 ValProAspThrLysValAsnPhetYrAlaTrpLysArgAsn**Ser**GlnGlnAla 60

DB 136 GTACCAGACACCAGGTTAACTTACCTTGAGAAACGTATGAGAGTTGTCACAAACAGCT 195

QY 61 ValGluValITPPGInGlyLeuAlaLeuLeuSerGluAlaValLeuArgGlyGlnAlaLeu 80

DB 196 GTTGAAGTTTGGCAAGTTTGGCTTTGATCTGAAGCTGTTTGAAGGTCACAAAGCCTTG 255

QY 81 LeuValAsnSerSerGlnProTrpGluProLeuGlnLeuHisValAspLysAlaValSer 100

DB 256 TTGCTTAACCTCTTCCACACCATGGSAACCATTTGCACGTGATTAAGCCGTCTCT 315

QY 101 GlyLeuArgSerLeuThrThrLeuLeuArgAlaLeuGlyAlaGlnLysGlnAlaIleSer 120

DB 316 GGTTCAGATCTTTGACACTTGTGTTGAGACCTTGGCTGCTCAAAAGAACCCATTTC 375

QY 121 ProProAspAlaAlaSerAlaAlaProLeuArgThrIleThrAlaAspThrPheArgLys 140

DB 376 CCACCAGACGCTGCTTCGCGCTCCATTTGAGAACCATTCACGCTGATACCTTCGAAAG 435

QY 141 LeuPheArgValIYrSerAsnPhleuArgGlyLysLeuLysLeuTyrThrGlyGluAla 160

DB 436 TTATTCAAGTTTACTCCAACTTCTTGAGAGGTAATTGAAGTTTACACCGGTGAAGCC 495

QY 161 CysArgThrGlyAspArg 166

DB 496 TGTAGAACTGCTGACAGA 513

RESULT 7

LOCUS 108350

DEFINITION Sequence 6 from Patent WO 8502610.

ACCESSION 108350

VERSION 108350.1

KEYWORDS GI:588940

SOURCE Unknown.

LOCUS 108350

DEFINITION Sequence 6 from Patent WO 8502610.

ACCESSION 108350

VERSION 108350.1

KEYWORDS GI:588940

SOURCE Unknown.

ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 551)
JOURNAL Lin.F.-K.
FEATURES Patent: WO 8502610-A 6 20-JUN-1985;
source Location/Qualifiers
1..551
/organism="unknown"
BASE COUNT 157 a 112 c 129 g 153 t
ORIGIN

Alignment Scores:
Pred. No.: 1,2e-77 Length: 551
Score: 825.00 Matches: 162
Percent Similarity: 97.59% Conservative: 0
Best Local Similarity: 97.59% Mismatches: 4
Query Match: 97.86% Indels: 0
DB: Gaps: 0

US-09-813-775c-18 (1-166) x 108350 (1-551)

QY 1 AlaProProArgLeuIleCysAspSerArgValLeuGluArgTyrLeuGluAlaLys 20
|||||
Db 16 GCTCCACCAAGATTGATCTGTGACTGACGAGTTTGAAAGATCTGTTGGAAGCTAAA 75
|||||
QY 21 GluAlaGluAsnIleThrThrGlyCysAlaGluHisCysSerLeuAsnGluAsnIleThr 40
|||||
Db 76 GAAGCTGAAAAACATCACACACGCTGCTGACACACTGTTCTTGAACGAAACATTTACG 135
|||||
QY 41 ValProAspThrIysValAsnPheTyrAlaTTrpLysArgAsn***Ser***GlnGlnAla 60
|||||
Db 136 GTACCGACAGCCAAAGTTAACTTCTACGCTGGAAACGTGGAAAGTTGGTCAACAAAGCT 195
|||||
QY 61 ValGluValTrpGlnGlyLeuAlaLeuLeuSerGluAlaValLeuArgGlyGlnAlaLeu 80
|||||
Db 196 GTTGAAGTTGGCAGAGTTGGCCTGTATCTGAACCTGTTTGAGAGGCTCAAGCCTTG 255
|||||
QY 81 LeuValAsnSerSerGlnProTTrpGluProLeuGlnLeuHisValAspLysAlaValSer 100
|||||
Db 256 TTGCTTAACCTCTCTCAACCATGGAGAACCAATTCACACGTCGATTAAGCCGCTCTCT 315
|||||
QY 101 GlyLeuArgSerLeuThrThrLeuLeuArgAlaLeuGlnGlyAlaGlnLysGlnAlaIleSer 120
|||||
Db 316 GGTTCGATCTTGTGACTCTTGTGTGAGAGCTTGGTCTCAAAAGGAAGCCATTTC 375
|||||
QY 121 ProProAspAlaAlaSerAlaAlaProLeuArgThrIleThrAlaAspThrPheArgLys 140
|||||
Db 376 CCACGAGAGCGCTGCTTGTGCGCTCCATGTGAGAAACATCAGTCTGATCTTACAGAAAG 435
|||||
QY 141 LeuPheArgValTyrSerAsnPheLeuArgGlyLysLeuLysLeuTyrThrGlyGluAla 160
|||||
Db 436 TTATTGAGAGTTTACTCCCAACTCTTGAGAGGTAATTAATTGAACTGACACCGGTGAAGCC 495
|||||
QY 161 CysArgThrGlyAspArg 166
|||||
Db 496 TGTAGAACTGTGTGACAGA 513
|||||

RESULT 8
AX025442 582 bp DNA linear PAT 16-SEP-2000
LOCUS AX025442
DEFINITION Sequence 3 from Patent FR2786104.
ACCESSION AX025442
VERSION AX025442.1 GI:10187118
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 582)
AUTHORS Haeflner,A. and Hirsch,F.
JOURNAL Patent: FR 2786104-A 3 26-MAY-2000;
CENTRE NAT RECH SCIENT (FR)
FEATURES Location/Qualifiers

source 1..582
/organism="Homo sapiens"
/db_xref="taxon:9606"
CDS 1..582
/feature="unnamed protein product"
/codon_start=1
/protein_id="CAC09044.1"
/db_xref="GI:10187119"
/translation="MGVHECPAMILLLSLPLSLPLVIGAPPRLICDSRYLERYLL
EAEAEVITTCGAEHCISLNEIVTPDKVAFYAKRMKREYGGQAEVWQGLALLSEAVL
RGQALLVNSQPEWPEPIQLHYDKAVSGLRSITLTLLRLAGAKKEAISPPDAASAAPLPTIT
TADTKRLFRVINSFTLKGKLTGTGEACRTGDR"

BASE COUNT 113 a 181 c 170 g 118 t
ORIGIN

Alignment Scores:
Pred. No.: 1,28e-77 Length: 582
Score: 825.00 Matches: 162
Percent Similarity: 97.59% Conservative: 0
Best Local Similarity: 97.59% Mismatches: 4
Query Match: 97.86% Indels: 0
DB: Gaps: 0

US-09-813-775c-18 (1-166) x AX025442 (1-582)

QY 1 AlaProProArgLeuIleCysAspSerArgValLeuGluArgTyrLeuGluAlaLys 20
|||||
Db 82 GCCCCACACGCGCCATCTGTGACAGCGAGCTCTGGAGAGTACCTTGGAGGCCAAG 141
|||||
QY 21 GluAlaGluAsnIleThrThrGlyCysAlaGluHisCysSerLeuAsnGluAsnIleThr 40
|||||
Db 142 GAGGCCGAGAAATACAGAGGGGCTGTGTCGACACCTGCAATGGAATATCCTACT 201
|||||
QY 41 ValProAspThrIysValAsnPheTyrAlaTTrpLysArgAsn***Ser***GlnGlnAla 60
|||||
Db 202 GTCCACAGACCCAAAGTTAACTTCTATGCTGGAGAGATGAGGTGGGACACAGCC 261
|||||
QY 61 ValGluValTrpGlnGlyLeuAlaLeuLeuSerGluAlaValLeuArgGlyGlnAlaLeu 80
|||||
Db 262 GTACAGCTGTGGCAGGGGCTGCGCCCTGCTGGAACCTGTCTCGGGGGCAGCCCTG 321
|||||
QY 81 LeuValAsnSerSerGlnProTTrpGluProLeuGlnLeuHisValAspLysAlaValSer 100
|||||
Db 322 TTGCTCAACCTCTTCCACCGGTGGAGCCCTCTGACGTGATGTGATTAAGCCGCTCAGT 381
|||||
QY 101 GlyLeuArgSerLeuThrThrLeuLeuArgAlaLeuGlnGlyAlaGlnLysGlnAlaIleSer 120
|||||
Db 382 GGCTTGGCAGCTCACACACTCTCTCGGCTTGGGAGGCCAGAAAGAACCATCTCC 441
|||||
QY 121 ProProAspAlaAlaSerAlaAlaProLeuArgThrIleThrAlaAspThrPheArgLys 140
|||||
Db 442 CCTCAGATGGGGCTCAGCGTCCAGCTCCGAAACAATCACTGCTGACACTTCCGCAAA 501
|||||
QY 141 LeuPheArgValTyrSerAsnPheLeuArgGlyLysLeuLysLeuTyrThrGlyGluAla 160
|||||
Db 502 CTCTTCGAGTCTACTCCAAATTCTCCCGGGGAAAGCTGAAGCTGTACACAGGGGAGGCC 561
|||||
QY 161 CysArgThrGlyAspArg 166
|||||
Db 562 TGCAGGACAGGGGACAGA 579
|||||

RESULT 9
105397 582 bp DNA linear PAT 02-DEC-1994
LOCUS 105397
DEFINITION Sequence 2 from Patent EP 0267678.
ACCESSION 105387
VERSION 105397.1 GI:590970
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 582)
AUTHORS Beck,A.K., Witby,R.M., Zabrecky,J.R. and Masiello,N.C.

TITLE Recombinant human erythropoietin
JOURNAL Patent: EP 0267678-A1 2 18-MAY-1988;
FEATURES Location/Qualifiers
source 1..582

BASE COUNT 113 a 181 c 170 g 118 t
ORIGIN

Alignment Scores:

Pred. No.: 1.28e-77 Length: 582
Score: 825.00 Matches: 162
Percent Similarity: 97.59% Conservative: 0
Best Local Similarity: 97.59% Mismatches: 4
Query Match: 97.86% Indels: 0
DB: Gaps: 0

US-09-813-775c-18 (1-166) x I05397 (1-582)

QY 1 AAlProProArgLeuIleCysAspSerArgValLeuGluArgTyrLeuLeuGluAlaLys 20
DB 82 GCCCACCACGCGCTCATCTGTGACAGCCGAGCTCGAGAGGATACCTCTTGAGGCGCAAG 141
QY 21 GluAlaGluAsnIleThrThrGlyCysAlaGluHisCysSerLeuAsnGluAsnIleThr 40
DB 142 GAGCGCGAATAATATCAGCAGGCGGTGTGTAACACTGCAAGCTTGATGAGATATCACT 201
QY 41 ValProAspThrLysValAsnPhetYralatPlyArgAsn***Ser**GlnGlnAla 60
DB 202 GTCCAGACACCAAGTTAATTTCTATGCTCGAAGAGATGAGAGTGGCGCAGCAGGCC 261
QY 61 ValGluValITrGlnGlyLeuAlaLeuLeuSerGluAlaValLeuArgGlyGlnAlaLeu 80
DB 262 GTAGAGAGTGTGCGAGGCGCTGCGCTGTGGAAGCTGTCTGCGGCGCAGCGCCCTG 321
QY 81 LeuValAsnSerSerGlnProITrGluProLeuGlnLeuHisValAspLysAlaValSer 100
DB 322 TTGGTCAACTCTTCCAGCGGTGGAGCCCTGCACTCATGTGATTAAGCCGTCACT 381
QY 101 GlyLeuArgSerLeuThrThrLeuLeuArgAlaLeuGlyAlaGlnLysGluAlaIleSer 120
DB 382 GGCCTTCGAGCGCTCACCACTGTGCTGCGGCTCGGAGCCAGAGGAGCAATCTCC 441
QY 121 ProProAspAlaIleSerAlaIleProLeuArgThrIleThrAlaAspThrPheArgLys 140
DB 442 CCTCCAGATGCGGCTCAGCTCTGCTGCGGCTCGGAGCCAGAGGAGCAATCTCC 501
QY 141 LeuPheArgValITyrSerAsnPhetLeuArgGlyLysLeuLysLeuTyrThrGlyGluAla 160
DB 502 CTCTCCGAGTCTACTCCAAITTTCTCCGCGGAAAGCTGAACTGATACAGAGGAGGCC 561
QY 161 CysArgThrGlyAspArg 166
DB 562 TGCAGGACAGGGGACAGA 579

RESULT 10

AX046870 AX046870 585 bp DNA linear PAT 15-DEC-2000
LOCUS Sequence 3 from Patent WO0068376.
ACCESSION AX046870
VERSION AX046870.1 GI:11876340
KEYWORDS

SOURCE

ORGANISM Chimpanzee.
Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
REFERENCE 1 (bases 1 to 585)
AUTHORS Desauvage,F. and Henner,D.J.
TITLE Chimpanzee erythropoietin (chepo) polypeptides and nucleic acids
encoding the same
JOURNAL Patent: WO 0068376-A 3 16-NOV-2000;
GENENTECH, INC. (US)
FEATURES Location/Qualifiers
source 1..585

/Organism="Pan troglodytes"
/db_xref="taxon:9598"
BASE COUNT 115 a 185 c 168 g 117 t
ORIGIN

Alignment Scores:

Pred. No.: 1.29e-77 Length: 585
Score: 825.00 Matches: 162
Percent Similarity: 97.59% Conservative: 0
Best Local Similarity: 97.59% Mismatches: 4
Query Match: 97.86% Indels: 0
DB: Gaps: 0

US-09-813-775c-18 (1-166) x AX046870 (1-585)

QY 1 AAlProProArgLeuIleCysAspSerArgValLeuGluArgTyrLeuLeuGluAlaLys 20
DB 82 GCCCACCACGCGCTCATCTGTGACAGCCGAGCTCGAGAGGATACCTCTTGAGGCGCAAG 141
QY 21 GluAlaGluAsnIleThrThrGlyCysAlaGluHisCysSerLeuAsnGluAsnIleThr 40
DB 142 GAGCGCGAATAATATCAGCAGGCGGTGTGTAACACTGCAAGCTTGATGAGATATCACT 201
QY 41 ValProAspThrLysValAsnPhetYralatPlyArgAsn***Ser**GlnGlnAla 60
DB 202 GTCCAGACACCAAGTTAATTTCTATGCTCGAAGAGATGAGAGTGGCGCAGCAGGCC 261
QY 61 ValGluValITrGlnGlyLeuAlaLeuLeuSerGluAlaValLeuArgGlyGlnAlaLeu 80
DB 262 GTAGAGAGTGTGCGAGGCGCTGCGCTGTGGAAGCTGTCTGCGGCGCAGCGCCCTG 321
QY 81 LeuValAsnSerSerGlnProITrGluProLeuGlnLeuHisValAspLysAlaValSer 100
DB 322 TTGGTCAACTCTTCCAGCGGTGGAGCCCTGCACTCATGTGATTAAGCCGTCACT 381
QY 101 GlyLeuArgSerLeuThrThrLeuLeuArgAlaLeuGlyAlaGlnLysGluAlaIleSer 120
DB 382 GGCCTTCGAGCGCTCACCACTGTGCTGCGGCTCGGAGCCAGAGGAGCAATCTCC 441
QY 121 ProProAspAlaIleSerAlaIleProLeuArgThrIleThrAlaAspThrPheArgLys 140
DB 442 CCTCCAGATGCGGCTCAGCTCTGCTGCGGCTCGGAGCCAGAGGAGCAATCTCC 501
QY 141 LeuPheArgValITyrSerAsnPhetLeuArgGlyLysLeuLysLeuTyrThrGlyGluAla 160
DB 502 CTCTCCGAGTCTACTCCAAITTTCTCCGCGGAAAGCTGAACTGATACAGAGGAGGCC 561
QY 161 CysArgThrGlyAspArg 166
DB 562 TGCAGGACAGGGGACAGA 579

RESULT 11

AX046870 AX046870 724 bp DNA linear PAT 02-DEC-1994
LOCUS Sequence 4 from Patent EP 0267678.
ACCESSION AX046870
VERSION AX046870.1 GI:590971
KEYWORDS

SOURCE

ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 724)
AUTHORS Beck,A.K., Wilthy,R.M., Zabrecky,J.R. and Mastello,N.C.
TITLE Recombinant human erythropoietin
JOURNAL Patent: EP 0267678-A1 4 18-MAY-1988;
FEATURES Location/Qualifiers
source 1..724
/Organism="unknown"

BASE COUNT

141 a 235 c 202 g 146 t
ORIGIN

Alignment Scores:

Pred. No.: 1.65e-77 Length: 724

Score: 825.00 Matches: 162
 Best Local Similarity: 97.59% Conservative: 0
 Best Local Similarity: 97.59% Mismatches: 4
 Query Match: 97.86% Indels: 0
 DB: 6 Gaps: 0

US-09-813-775C-18 (1-166) x I05399 (1-724)

QY 1 AlaProProArgLeuIleCysAspSerArgValLeuGluArgTyrLeuGluAlaLys 20
 DB 131 GCCCCACACCGCTCATCTGTGTGACAGCCGAGTCTCGAGAGTACTCTTGGAGGCCAAG 190
 QY 21 GluAlaGluAsnIleThrThrGlyCysAlaGluHisCysSerLeuAsnGluAsnIleThr 40
 DB 191 GAGCCCGAATAATATCAGCAGCGGCTGTGTAACACTGAGCTTGAATGAAATATACACT 250
 QY 41 ValProAspThrLysValAsnPhenylalanylArgAsn***Ser***GlnGlnAla 60
 DB 251 GTCCCGACACCAAAAGTTAATTTCTATGCTCGAAGAGATGAGGTCCGGCGACGAGGCC 310
 QY 61 ValGluValTrpDlnGlyLeuAlaLeuLeuSerGluAlaValLeuArgGlyGlnAlaLeu 80
 DB 311 GTAGAAGTCTGGAGAGGCGCTGGCCCTGCTGTGGAAGCTGTCTCGGGGCCAGGCCCTG 370
 QY 81 LeuValAsnSerSerGlnProTrpGluProLeuGlnLeuHisValAspLysAlaValSer 100
 DB 371 TTGGTCAACTCTTCCACGCGCTGGAGCCCTGCACCTGCATCTGATTAAGCCCTCAGT 430
 QY 101 GlyLeuArgSerLeuThrThrLeuLeuArgAlaLeuGlyAlaGlnLysGluAlaIleSer 120
 DB 431 GGCCTTCGACGCTCACCACTCTGCTTGGGCTCTGGAGCCCGAGAGGACCATCTCC 490
 QY 121 ProProAspAlaAlaSerAlaAlaProLeuArgThrIleThrAlaAspThrPheArgLys 140
 DB 491 CCTCCAGATGCGGCGCTCAGCTGCTCCACGCCAGCAATCAGTCTGACACTTCCGCAAA 550
 QY 141 LeuPheArgValTyrSerAsnPhenylalanylGlyLysLeuLysLeuTyrThrGlyAla 160
 DB 551 CTTCTCCGAGTCTACTCCAAATTTCTCCGCGGAAAGCTGAAGCTGTAAACAGGAGGCC 610
 QY 161 CysArgThrGlyAspArg 166
 DB 611 TGCAGGACAGGGGACAGA 628

RESULT 12

LOCUS AR086679 788 bp DNA linear PAT 07-SEP-2000
 DEFINITION Sequence 35 from patent US 5985607.
 ACCESSION AR086679
 VERSION AR086679.1 GI:10013445
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.

REFERENCE 1 (bases 1 to 788)
 AUTHORS DeJucue,G. and Awang,G.
 TITLE Recombinant DNA molecules and expression vectors for tissue plasminogen activator
 JOURNAL Patent: US 5985607-A 35 16-NOV-1999;
 FEATURES Location/Qualifiers
 source 1..788
 BASE COUNT 145 a 264 c 228 g 151 t
 ORIGIN

Alignment Scores:
 Pred. No.: 1,82e-77 Length: 788
 Score: 825.00 Matches: 162
 Percent Similarity: 97.59% Conservative: 0
 Best Local Similarity: 97.59% Mismatches: 4
 Query Match: 97.86% Indels: 0
 DB: 6 Gaps: 0

US-09-813-775C-18 (1-166) x AR086679 (1-788)

QY 1 AlaProProArgLeuIleCysAspSerArgValLeuGluArgTyrLeuGluAlaLys 20
 DB 161 GCCCCACACCGCTCATCTGTGTGACAGCCGAGTCTCGAGAGTACTCTTGGAGGCCAAG 220
 QY 21 GluAlaGluAsnIleThrThrGlyCysAlaGluHisCysSerLeuAsnGluAsnIleThr 40
 DB 221 GAGCCCGAATAATATCAGCAGCGGCTGTGTAACACTGAGCTTGAATGAAATATACACT 280
 QY 41 ValProAspThrLysValAsnPhenylalanylArgAsn***Ser***GlnGlnAla 60
 DB 281 GTCCCGACACCAAAAGTTAATTTCTATGCTCGAAGAGATGAGGTCCGGCGACGAGGCC 340
 QY 61 ValGluValTrpDlnGlyLeuAlaLeuLeuSerGluAlaValLeuArgGlyGlnAlaLeu 80
 DB 341 GTAGAAGTCTGGAGAGGCGCTGGCCCTGCTGTGGAAGCTGTCTCGGGGCCAGGCCCTG 400
 QY 81 LeuValAsnSerSerGlnProTrpGluProLeuGlnLeuHisValAspLysAlaValSer 100
 DB 401 TTGGTCAACTCTTCCACGCGCTGGAGCCCTGCACCTGCATGTGATTAAGCCCTCAGT 460
 QY 101 GlyLeuArgSerLeuThrThrLeuLeuArgAlaLeuGlyAlaGlnLysGluAlaIleSer 120
 DB 461 GGCCTTCGACGCTCACCACTCTGCTTGGGCTCTGGAGCCCGAGAGGACCATCTCC 520
 QY 121 ProProAspAlaAlaSerAlaAlaProLeuArgThrIleThrAlaAspThrPheArgLys 140
 DB 521 CCTCCAGATGCGGCGCTCAGCTGCTCCACGCCAGCAATCAGTCTGACACTTCCGCAAA 580
 QY 141 LeuPheArgValTyrSerAsnPhenylalanylGlyLysLeuLysLeuTyrThrGlyAla 160
 DB 581 CTTCTCCGAGTCTACTCCAAATTTCTCCGCGGAAAGCTGAAGCTGTAAACAGGAGGCC 640
 QY 161 CysArgThrGlyAspArg 166
 DB 641 TGCAGGACAGGGGACAGA 658

RESULT 13

LOCUS AR063255 823 bp DNA linear PAT 29-SEP-1999
 DEFINITION Sequence 1 from patent US 5846528.
 ACCESSION AR063255
 VERSION AR063255.1 GI:5992563
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.

REFERENCE 1 (bases 1 to 823)
 AUTHORS Podsakoff,G.M. and Kurtzman,G.J.
 TITLE Treating anemia using recombinant adeno-associated virus virions comprising an Epo DNA sequence
 JOURNAL Patent: US 5846528-A 1 08-DEC-1999;
 FEATURES Location/Qualifiers
 source 1..823
 BASE COUNT 159 a 275 c 233 g 156 t
 ORIGIN

Alignment Scores:
 Pred. No.: 1,92e-77 Length: 823
 Score: 825.00 Matches: 162
 Percent Similarity: 97.59% Conservative: 0
 Best Local Similarity: 97.59% Mismatches: 4
 Query Match: 97.86% Indels: 0
 DB: 6 Gaps: 0

US-09-813-775C-18 (1-166) x AR063255 (1-823)

QY 1 AlaProProArgLeuIleCysAspSerArgValLeuGluArgTyrLeuGluAlaLys 20
 DB 133 GCCCCACACCGCTCATCTGTGTGACAGCCGAGTCTCGAGAGTACTCTTGGAGGCCAAG 192


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Db 262 GTAGAGCTGGCAGGGCCCTGGCCCTGCTGCGAAGCTGTCCCTGGGGGCCAGGCCCTG 321
QY 81 LeuValAsnSerSerGlnProTrpGluProLeuGlnIleuHisValAspLysAlaValSer 100
Db 322 TTGGTCAACTCTTCCCGCGGTGGAGCCCTGCGAGCTGCATGGATTAAGCCGTAGT 381
QY 101 GLYLeuArgSerLeuThrLeuLeuArgAlaLeuGlyAlaGlnLysGluAlaIleSer 120
Db 382 GGCCCTTCGCGAGCCCTCACCACTGTGCTGGGGCTCTGGGAGCCCGAAGAACCATCTCC 441
QY 121 ProProAspAlaAlaSerAlaAlaProLeuArgThrIleThrAlaAspThrPheArgLys 140
Db 442 CCTCCAGATGGGCTGAGCTGCTCCACTCGAACAATCACTGCTGACACTTTCGGCAA 501
QY 141 LeuPheArgValTyrSerAsnPheLeuArgGlyLysLeuLysLeuTyrThrGlyGluAla 160
Db 502 CTCTTCGAGTCTACTCCAAATTTCCTCCGGGAAAGCTGAAGCTGTACACAGGGAGGCC 561
QY 161 CysArgThrGlyAspArg 166
Db 562 TGCAGGACAGGGGACAGA 579
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Search completed: January 8, 2003, 06:57:33
Job time : 2227.35 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 8, 2003, 03:41:38 ; Search time 28.6685 Seconds
(without alignments)
112.338 Million cell updates/sec

Title: US-09-813-775c-18
Perfect score: 843
Sequence: 1 APRRLICDSRYLERYLLEAK.....NFLRGKILTYGECACRTGDR 166

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 118974 seqs, 19401057 residues

Total number of hits satisfying chosen parameters: 118974

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications, AA.*
1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	825	97.9	166	10	US-09-853-731-2
2	825	97.9	166	12	US-10-014-363-2
3	825	97.9	169	12	US-10-014-363-4
4	825	97.9	174	12	US-10-014-363-3
5	825	97.9	174	12	US-10-014-363-5
6	820	97.3	165	10	US-09-853-731-1
7	820	97.3	165	12	US-10-014-363-1
8	284	93.7	60	10	US-09-864-761-48502
9	111	13.2	30	10	US-09-975-063-2
10	111	13.2	30	12	US-10-011-858-2
11	108	12.8	20	9	US-09-919-703-9
12	88	10.4	20	9	US-09-919-703-10
13	76.5	9.1	2472	10	US-09-815-242-5064
14	69.5	8.2	542	9	US-10-045-815-8
15	69.5	8.2	747	9	US-10-045-815-6
16	69.5	8.2	813	9	US-09-964-899-25
17	68	8.1	321	9	US-09-945-182-26
18	67.5	8.0	1564	10	US-09-801-368-244
19	66.5	7.9	119	9	US-09-738-626-6842

20	66.5	7.9	766	10	US-09-925-301-1276	Sequence 1276, Ap
21	66	7.8	210	10	US-09-731-872-387	Sequence 387, App
22	66	7.8	409	10	US-09-815-242-14050	Sequence 14050, A
23	66	7.8	7257	9	US-10-014-717-5	Sequence 5, App11
24	65.5	7.8	240	9	US-09-738-626-6760	Sequence 6760, Ap
25	65.5	7.8	711	9	US-09-738-626-3507	Sequence 3507, Ap
26	64.5	7.7	379	9	US-09-975-139-8	Sequence 8, App11
27	64.5	7.7	352	10	US-09-880-192-50	Sequence 50, App1
28	64.5	7.7	2504	9	US-09-817-514A-8	Sequence 8, App11
29	64	7.6	538	9	US-09-738-626-4165	Sequence 4165, Ap
30	64	7.6	954	9	US-09-944-413-7	Sequence 7, App11
31	64	7.6	954	9	US-09-944-403-7	Sequence 7, App11
32	64	7.6	954	9	US-09-944-896-7	Sequence 7, App11
33	64	7.6	954	9	US-09-944-944-7	Sequence 7, App11
34	64	7.6	954	9	US-09-944-907-7	Sequence 7, App11
35	64	7.6	954	9	US-09-944-929-7	Sequence 7, App11
36	64	7.6	954	10	US-09-866-028-7	Sequence 7, App11
37	64	7.6	954	10	US-09-944-449-7	Sequence 7, App11
38	64	7.6	954	10	US-09-944-457-7	Sequence 7, App11
39	64	7.6	954	10	US-09-944-862-7	Sequence 7, App11
40	64	7.6	954	10	US-09-945-587-7	Sequence 7, App11
41	64	7.6	954	10	US-09-945-015-7	Sequence 7, App11
42	64	7.6	954	10	US-09-944-396-7	Sequence 7, App11
43	64	7.6	954	10	US-09-944-097-7	Sequence 7, App11
44	64	7.6	954	10	US-09-944-432-7	Sequence 7, App11
45	64	7.6	954	10	US-09-943-762-7	Sequence 7, App11

ALIGNMENTS

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RESULT 1
US-09-853-731-2
Sequence 2, Application US/09853731
Patent No. US20020037841A1
GENERAL INFORMATION:
APPLICANT: Paradiem, Inc., Apollon
TITLE OF INVENTION: Erythropoietin Composition
FILE REFERENCE: 20619 US
CURRENT APPLICATION NUMBER: US/09/853, 731
CURRENT FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: EP/00110355.5
PRIOR FILING DATE: 2000-05-15
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 166
TYPE: PRT
ORGANISM: Homo sapiens
US-09-853-731-2

Query Match          97.9%; Score 825; DB 10; Length 166;
Best Local Similarity 97.6%; Pred. No. 1.6e-82;
Matches 162; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 APRRLICDSRYLERYLLEAKENITGCAEHCSELENITVPDTKYNFYAMKRNXXQQA 60
    |||
Db 1 APRRLICDSRYLERYLLEAKENITGCAEHCSELENITVPDTKYNFYAMKRNXXQQA 60

QY 61 VEWOGATLSEAVLRQALVNSQWPEPLQHVDAVSGLSLTLLALGAQKEAIS 120
    |||
Db 61 VEWOGATLSEAVLRQALVNSQWPEPLQHVDAVSGLSLTLLALGAQKEAIS 120

QY 121 PPDAASAPLRTITADTFKLFVYVSNFLGKILTYGECACRTGDR 166
    |||
Db 121 PPDAASAPLRTITADTFKLFVYVSNFLGKILTYGECACRTGDR 166

RESULT 2
US-10-014-363-2
Sequence 2, Application US/10014363
Patent No. US20020115833A1
GENERAL INFORMATION:

```

APPLICANT: Burg, Josef
APPLICANT: Engel, Alfred
APPLICANT: Franze, Reinhard
APPLICANT: Hilger, Bernd
APPLICANT: Schurig, Hartmut Ernst
APPLICANT: Tischer, Wilhelm
APPLICANT: Wozny, Manfred
TITLE OF INVENTION: Erythropoietin Conjugates
FILE REFERENCE: Case 20805
CURRENT APPLICATION NUMBER: US/10/014,363
CURRENT FILING DATE: 2001-12-11
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 166
TYPE: PRT
ORGANISM: Homo sapiens
US-10-014-363-2

Query Match 97.9%; Score 825; DB 12; Length 166;
Best Local Similarity 97.6%; Pred. No. 1.7e-82;
Matches 162; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 APRILICDSRVLELYLLEAKAEENITTCGAHCSINENITVPDTKVNRYAMKRNXSXQA 60
DB 1 APRILICDSRVLELYLLEAKAEENITTCGAHCSINENITVPDTKVNRYAMKRMVEGQA 60
QY 61 VEVWOGALLSEAVLRGQALLVNSQPWEPIQLHYDKAVSGIRSLTTLRALGAQKEAIS 120
DB 61 VEVWOGALLSEAVLRGQALLVNSQPWEPIQLHYDKAVSGIRSLTTLRALGAQKEAIS 120
QY 121 PPDAASAPLRTITADTFRKLFYVSNFLRGKLYTGECRTGDR 166
DB 121 PPDAASAPLRTITADTFRKLFYVSNFLRGKLYTGECRTGDR 166

RESULT 3
US-10-014-363-4
Sequence 4, Application US/10014363
Patent No. US2002011583A1
GENERAL INFORMATION:
APPLICANT: Burg, Josef
APPLICANT: Engel, Alfred
APPLICANT: Franze, Reinhard
APPLICANT: Hilger, Bernd
APPLICANT: Schurig, Hartmut Ernst
APPLICANT: Tischer, Wilhelm
APPLICANT: Wozny, Manfred
TITLE OF INVENTION: Erythropoietin Conjugates
FILE REFERENCE: Case 20805
CURRENT APPLICATION NUMBER: US/10/014,363
CURRENT FILING DATE: 2001-12-11
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin version 3.1
SEQ ID NO 4
LENGTH: 169
TYPE: PRT
ORGANISM: CHO/dhfr-
US-10-014-363-4

Query Match 97.9%; Score 825; DB 12; Length 169;
Best Local Similarity 97.6%; Pred. No. 1.7e-82;
Matches 162; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 APRILICDSRVLELYLLEAKAEENITTCGAHCSINENITVPDTKVNRYAMKRNXSXQA 60
DB 4 APRILICDSRVLELYLLEAKAEENITTCGAHCSINENITVPDTKVNRYAMKRMVEGQA 63
QY 61 VEVWOGALLSEAVLRGQALLVNSQPWEPIQLHYDKAVSGIRSLTTLRALGAQKEAIS 120
DB 64 VEVWOGALLSEAVLRGQALLVNSQPWEPIQLHYDKAVSGIRSLTTLRALGAQKEAIS 123
QY 121 PPDAASAPLRTITADTFRKLFYVSNFLRGKLYTGECRTGDR 166

DB 124 PPDAASAPLRTITADTFRKLFYVSNFLRGKLYTGECRTGDR 169

RESULT 4
US-10-014-363-3
Sequence 3, Application US/10014363
Patent No. US2002011583A1
GENERAL INFORMATION:
APPLICANT: Burg, Josef
APPLICANT: Engel, Alfred
APPLICANT: Franze, Reinhard
APPLICANT: Hilger, Bernd
APPLICANT: Schurig, Hartmut Ernst
APPLICANT: Tischer, Wilhelm
APPLICANT: Wozny, Manfred
TITLE OF INVENTION: Erythropoietin Conjugates
FILE REFERENCE: Case 20805
CURRENT APPLICATION NUMBER: US/10/014,363
CURRENT FILING DATE: 2001-12-11
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin version 3.1
SEQ ID NO 3
LENGTH: 174
TYPE: PRT
ORGANISM: CHO/dhfr-
US-10-014-363-3

Query Match 97.9%; Score 825; DB 12; Length 174;
Best Local Similarity 97.6%; Pred. No. 1.7e-82;
Matches 162; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 APRILICDSRVLELYLLEAKAEENITTCGAHCSINENITVPDTKVNRYAMKRNXSXQA 60
DB 9 APRILICDSRVLELYLLEAKAEENITTCGAHCSINENITVPDTKVNRYAMKRMVEGQA 68
QY 61 VEVWOGALLSEAVLRGQALLVNSQPWEPIQLHYDKAVSGIRSLTTLRALGAQKEAIS 120
DB 69 VEVWOGALLSEAVLRGQALLVNSQPWEPIQLHYDKAVSGIRSLTTLRALGAQKEAIS 128
QY 121 PPDAASAPLRTITADTFRKLFYVSNFLRGKLYTGECRTGDR 166
DB 129 PPDAASAPLRTITADTFRKLFYVSNFLRGKLYTGECRTGDR 174

RESULT 5
US-10-014-363-5
Sequence 5, Application US/10014363
Patent No. US2002011583A1
GENERAL INFORMATION:
APPLICANT: Burg, Josef
APPLICANT: Engel, Alfred
APPLICANT: Franze, Reinhard
APPLICANT: Hilger, Bernd
APPLICANT: Schurig, Hartmut Ernst
APPLICANT: Tischer, Wilhelm
APPLICANT: Wozny, Manfred
TITLE OF INVENTION: Erythropoietin Conjugates
FILE REFERENCE: Case 20805
CURRENT APPLICATION NUMBER: US/10/014,363
CURRENT FILING DATE: 2001-12-11
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin version 3.1
SEQ ID NO 5
LENGTH: 174
TYPE: PRT
ORGANISM: CHO/dhfr-
US-10-014-363-5

Query Match 97.9%; Score 825; DB 12; Length 174;
Best Local Similarity 97.6%; Pred. No. 1.7e-82;
Matches 162; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy 1 APPRLICDSRVLERYLLEAKAEENITTCAGHCSLNNITVPDTKYNFYAMKRNKXSQQA 60
Db 9 APPRLICDSRVLERYLLEAKAEENITTCAGHCSLNNITVPDTKYNFYAMKRNKRNVEVGOQA 68
Qy 61 VEWOGALLSEAVLRGQALLVNSQPWEPLQJHVDKAVSGLSLTLLRALGAQKEAIS 120
Db 69 VEWOGALLSEAVLRGQALLVNSQPWEPLQJHVDKAVSGLSLTLLRALGAQKEAIS 128
Qy 121 PPDASAPLRTITADTFRKLFRVYSNPLRGKLTLYTGECACRTGD 166
Db 129 PPDASAPLRTITADTFRKLFRVYSNPLRGKLTLYTGECACRTGDR 174

RESULT 6
US-09-853-731-1
; Sequence 1, Application US/09853731
; Patent No. US20020037841A1
; GENERAL INFORMATION:
; APPLICANT: Papadimitriou, Apollon
; TITLE OF INVENTION: Erythropoietin Composition
; FILE REFERENCE: 20619 US
; CURRENT APPLICATION NUMBER: US/09/853,731
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: EP/00110355.5
; PRIOR FILING DATE: 2000-05-15
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-853-731-1

Query Match 97.3%; Score 820; DB 10; Length 165;
Best Local Similarity 97.6%; Pred. No. 5,6e-82;
Matches 161; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 APPRLICDSRVLERYLLEAKAEENITTCAGHCSLNNITVPDTKYNFYAMKRNKXSQQA 60
Db 1 APPRLICDSRVLERYLLEAKAEENITTCAGHCSLNNITVPDTKYNFYAMKRNKRNVEVGOQA 60
Qy 61 VEWOGALLSEAVLRGQALLVNSQPWEPLQJHVDKAVSGLSLTLLRALGAQKEAIS 120
Db 61 VEWOGALLSEAVLRGQALLVNSQPWEPLQJHVDKAVSGLSLTLLRALGAQKEAIS 120
Qy 121 PPDASAPLRTITADTFRKLFRVYSNPLRGKLTLYTGECACRTGD 165
Db 121 PPDASAPLRTITADTFRKLFRVYSNPLRGKLTLYTGECACRTGD 165

RESULT 7
US-10-014-363-1
; Sequence 1, Application US/10014363
; Patent No. US20020115833A1
; GENERAL INFORMATION:
; APPLICANT: Burg, Josef
; APPLICANT: Engel, Alfred
; APPLICANT: Franze, Reinhard
; APPLICANT: Hilger, Bernd
; APPLICANT: Schurig, Hartmut Ernst
; APPLICANT: Tischer, Wilhelm
; APPLICANT: Wozny, Manfred
; TITLE OF INVENTION: Erythropoietin Conjugates
; FILE REFERENCE: Case 20805
; CURRENT APPLICATION NUMBER: US/10/014,363
; CURRENT FILING DATE: 2001-12-11
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-014-363-1
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Query Match 97.3%; Score 820; DB 12; Length 165;
Best Local Similarity 97.6%; Pred. No. 5,6e-82;
Matches 161; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 APPRLICDSRVLERYLLEAKAEENITTCAGHCSLNNITVPDTKYNFYAMKRNKXSQQA 60
Db 1 APPRLICDSRVLERYLLEAKAEENITTCAGHCSLNNITVPDTKYNFYAMKRNKRNVEVGOQA 60
Qy 61 VEWOGALLSEAVLRGQALLVNSQPWEPLQJHVDKAVSGLSLTLLRALGAQKEAIS 120
Db 61 VEWOGALLSEAVLRGQALLVNSQPWEPLQJHVDKAVSGLSLTLLRALGAQKEAIS 120
Qy 121 PPDASAPLRTITADTFRKLFRVYSNPLRGKLTLYTGECACRTGD 165
Db 121 PPDASAPLRTITADTFRKLFRVYSNPLRGKLTLYTGECACRTGD 165

RESULT 8
US-09-864-761-48502
; Sequence 48502, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 48502
; LENGTH: 60
; TYPE: PRT
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ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AF053356.1
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.93
OTHER INFORMATION: SWISSPROT HIT: P01588, EVALU 9.00e-28
OTHER INFORMATION: EST_HUMAN HIT: AA662379.1, EVALU 3.00e-10
US-09-864-761-48502

Query Match 33.7%; Score 284; DB 10; Length 60;
Best Local Similarity 100.0%; Pred. No. 2.8e-24;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 58 OQAVVWGLALSLFAVLRGALLVNSSQWPEPLQHLVDKAVSGRLSTLLRAAGQ 115
DB 3 OQAVVWGLALSLFAVLRGALLVNSSQWPEPLQHLVDKAVSGRLSTLLRAAGQ 60

RESULT 9
US-09-975-063-2

Sequence 2, Application US/09975063
Patent No. US20020045255A1
GENERAL INFORMATION:

APPLICANT: POWELL, Jerry S.
TITLE OF INVENTION: HUMAN ERYTHROPOIETIN GENE: HIGH LEVEL
EXPRESSION IN STABLY TRANSFECTED MAMMALIAN CELLS

NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:

ADDRESSEE: Dorsey & Whitney, LLP
STREET: Suite 3400, 1420 Fifth Avenue, U.S. Bank Centre
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98101

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.7/7/8

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/975,063
FILING DATE: 10-Oct-2001

ATTORNEY/AGENT INFORMATION:
NAME: Roberts, Mark W.

REGISTRATION NUMBER: 46,160
REFERENCE/DOCKET NUMBER: 500582.03 (112893.109)

TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-903-8728
TELEFAX: 206-903-8820

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:

LENGTH: 30 amino acids
TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-09-975-063-2

Query Match 13.2%; Score 111; DB 10; Length 30;
Best Local Similarity 83.3%; Pred. No. 7e-06;
Matches 25; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 APPRLICDSRVLERYLLLEAKENITTCGA 30
DB 1 APXRLILDSRVLERYLLLEAKENITTCGA 30

RESULT 10
US-10-011-858-2

Sequence 2, Application US/10011858
Patent No. US20020137145A1
GENERAL INFORMATION:
APPLICANT: POWELL, Jerry S.

TITLE OF INVENTION: HUMAN ERYTHROPOIETIN GENE: HIGH LEVEL
EXPRESSION IN STABLY TRANSFECTED MAMMALIAN CELLS

NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:

ADDRESSEE: Dorsey & Whitney, LLP
STREET: Suite 3400, 1420 Fifth Avenue, U.S. Bank Centre
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98101

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS-WORD

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/011,858
FILING DATE: 05-No. US20020137145A1-2001

ATTORNEY/AGENT INFORMATION:
NAME: Roberts, Mark W.

REGISTRATION NUMBER: 46,160
REFERENCE/DOCKET NUMBER: 500582.13

TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-903-8728
TELEFAX: 206-903-8820

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:

LENGTH: 30 amino acids
TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-10-011-858-2

Query Match 13.2%; Score 111; DB 12; Length 30;
Best Local Similarity 83.3%; Pred. No. 7e-06;
Matches 25; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 APPRLICDSRVLERYLLLEAKENITTCGA 30
DB 1 APXRLILDSRVLERYLLLEAKENITTCGA 30

RESULT 11
US-09-919-703-9

Sequence 9, Application US/09919703
Patent No. US20020165129A1
GENERAL INFORMATION:

APPLICANT: Krystal, Gerald
TITLE OF INVENTION: Peptides and Their Use to Ameliorate

FILE REFERENCE: 50216/003004
CURRENT APPLICATION NUMBER: US/09/919,703

PRIOR FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US 09/294,457

PRIOR FILING DATE: 1999-04-19
PRIOR APPLICATION NUMBER: US 08/759,599

PRIOR FILING DATE: 1996-12-05
PRIOR APPLICATION NUMBER: US 60/008,233

PRIOR FILING DATE: 1995-12-06
NUMBER OF SEQ ID NOS: 16

SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 9

LENGTH: 20

TYPE: PRT

ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic polypeptide

US-09-919-703-9
Query Match 12.8%; Score 108; DB 9; Length 20;

APPLICANT: Ohide, Akiko
TITLE OF INVENTION: TUMOR SUPPRESSOR GENE
FILE REFERENCE: 06501-091001
CURRENT APPLICATION NUMBER: US/10/045,815
CURRENT FILING DATE: 2001-10-26
PRIOR APPLICATION NUMBER: PCT/JP00/02731
PRIOR FILING DATE: 2000-04-26
PRIOR APPLICATION NUMBER: JP 11/118806
PRIOR FILING DATE: 1999-04-26
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 747
TYPE: PRT
ORGANISM: Mus musculus
US-10-045-815-6

Query Match 8.2%; Score 69.5; DB 9; Length 747;
Best Local Similarity 25.4%; Pred. No. 20;
Matches 30; Conservative 12; Mismatches 49; Indels 27; Gaps 6;

OY 27 TGCACGCSLNERITVPDTKVNPFYAMKRNXSXQAAVEVWGLALTSNAVLRGOALL----- 81
||| | : | | | : | | | | | : | |
Db 21 TCGCE-SEPGMDVAPDL---LYA---EGTAIYSRRDMPGVYLNMERALRSRAALRALRL 73
OY 82 -----VNSSQWEP-LQLHVDKAVS-----GLRSITTLRLALGAQKEAISPPDA 124
: | | | | : | | : | | : | | : | |
Db 74 RCRTRCATELFWAPDLIDLGPPDLSODPGAAALHDLRFFGAVLRRACLRCLGPPSA 131

Search completed: January 8, 2003, 05:17:50
Job time : 31.6685 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 8, 2003, 03:39:48 ; Search time 11.0975 Seconds
(without alignments)
440.118 Million cell updates/sec

Title: US-09-813-775C-18

Perfect score: 843
Sequence: 1 APPRLICDSRVLEERYLEAK.....NFLRGKIKLYTGECRTGDR 166

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_patents_AA.*
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCRTUS.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/Backfiles1.pep:*

Pred. NO. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	827	98.1	166	5	PCT-US94-04361-45
2	825	97.9	166	1	US-08-318-193-70
3	825	97.9	166	4	US-09-604-871-2
4	825	97.9	166	5	PCT-US94-04361-37
5	825	97.9	193	1	US-07-903-220-1
6	825	97.9	193	2	US-08-883-795A-34
7	822	97.5	412	4	US-09-366-009-34
8	820	97.3	165	4	US-09-604-871-1
9	743.5	88.2	165	5	PCT-US94-04361-38
10	741.5	88.0	165	5	PCT-US94-04361-39
11	695	82.4	166	5	PCT-US94-04361-44
12	692	82.1	166	5	PCT-US94-04361-41
13	676	80.2	167	5	PCT-US94-04361-40
14	665.5	78.9	167	5	PCT-US94-04361-42
15	665	78.9	168	5	PCT-US94-04361-43
16	182	21.6	36	5	PCT-US94-04361-50
17	128	15.2	27	5	PCT-US94-04361-51
18	114.5	13.6	34	5	PCT-US94-04361-52
19	108	12.8	20	2	US-08-759-599-9
20	108	12.8	20	4	US-09-294-457-9
21	107	12.7	21	5	PCT-US94-04361-49
22	101	12.0	20	5	PCT-US94-04361-58
23	96	11.4	332	4	US-08-875-533-67
24	95	11.3	312	4	US-08-875-533-66
25	93	11.0	153	4	US-08-875-533-65
26	93	11.0	165	1	US-08-413-803-29
27	93	11.0	174	3	US-08-471-045-56

28	93	11.0	174	3	US-08-469-712A-56	Sequence 56, Appl
29	93	11.0	174	4	US-08-446-871-56	Sequence 56, Appl
30	93	11.0	174	4	US-08-468-910-56	Sequence 56, Appl
31	93	11.0	174	4	US-08-761-907-56	Sequence 56, Appl
32	93	11.0	174	5	PCT-US95-03776-27	Sequence 27, Appl
33	93	11.0	195	1	US-08-388-779A-4	Sequence 4, Appl1
34	93	11.0	195	1	US-08-591-070A-4	Sequence 4, Appl1
35	93	11.0	195	2	US-08-927-855-4	Sequence 4, Appl1
36	93	11.0	285	4	US-08-875-533-69	Sequence 69, Appl
37	93	11.0	285	4	US-08-875-533-70	Sequence 70, Appl
38	93	11.0	288	4	US-08-875-533-71	Sequence 71, Appl
39	93	11.0	288	4	US-08-875-533-72	Sequence 73, Appl
40	93	11.0	332	4	US-08-875-533-72	Sequence 22, Appl
41	93	11.0	332	5	PCT-US95-03776-25	Sequence 25, Appl
42	93	11.0	353	1	US-08-330-517-2	Sequence 2, Appl1
43	93	11.0	353	1	US-08-347-029-4	Sequence 4, Appl1
44	93	11.0	353	1	US-08-380-779A-2	Sequence 2, Appl1
45	93	11.0	353	1	US-08-484-246-1	Sequence 1, Appl1

ALIGNMENTS

RESULT 1
PCT-US94-04361-45
Sequence 45, Application PC/TUS9404361
GENERAL INFORMATION:
APPLICANT: Brigham and Women's Hospital
APPLICANT: 75 Francis Street
APPLICANT: Boston, MA 02115
APPLICANT: Bunn, H. Franklin
APPLICANT: Wen, Danyl
TITLE OF INVENTION: Erythropoietin Mutains With Enhanced
TITLE OF INVENTION: Activity
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/04361
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/049,802
FILING DATE: 21-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Cimbala, Michele A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 0627.336PC01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 166 amino acids
TYPE: amino acid
TOPOLOGY: both
PCT-US94-04361-45

Query Match 98.1% Score 827; DB 5; Length 166;
Best Local Similarity 97.6% Pred. No. 1e-96;
Matches 162; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY	1	APPRI	CDSR	LREXYLLLEAKAE	NITTCGAC	HCSLN	INIVPDPKVFVAMKRNXS	XQOA	60
Db	1	APPRICD	SRLERYLLEAKAE	NITTCGAC	HCSLN	INIVPDPKVFVAMKRNXS	XQOA	60	
QY	61	VEVNOGLAL	LSEAVLRGOALLVN	SSOPMEPIOLHVDVA	SGLSRTLTLLRALGAOKEAIS	120			
Db	61	VEVNOGLAL	LSEAVLRGOALLVN	SSOPMEPIOLHVDVA	SGLSRTLTLLRALGAOKEAIS	120			
QY	121	PPDAASAA	PRTITADTFRKLLFRYY	SNFLRGKLKLYLGCAE	CRPGDR	166			
Db	121	PPDAASAA	PRTITADTFRKLLFRYY	SNFLRGKLKLYLGCAE	CRPGDR	166			
QY	121	PPDAASA	APPLKTITADTFRKLLFRYY	SNFLRGKLKLYLGCAE	CRPGDR	166			
Db	121	PPDAASA	APPLKTITADTFRKLLFRYY	SNFLRGKLKLYLGCAE	CRPGDR	166			

RESULT 2

US-08-318-193-70
; Sequence 70, Application US/08318193

; GENERAL INFORMATION:

;; APPLICANT: GARVIN, Robert T.
;; APPLICANT: MALE, Lawrence T

; TITLE OF INVENTION: AN EXPRESSION SYSTEM FOR THE SECRETION OF
 ; TITLE OF INVENTION: OF BIOACTIVE HUMAN GRANULOCYTE MACROPHAGE
 ;

; TITLE OF INVENTION: STIMULATING FACTOR (GM-CSF) AND OTHER HETEROLOGOUS
 ;
 ; TITLE OF INVENTION: PROTEINS FROM STREPTOMYCES
 ;

```

; NUMBER OF SEQUENCES: 91
; CORRESPONDENCE ADDRESS:

```

Query Match	97.9%	Score 825;	DB 1;	Length 166;
Best Local Similarity	97.6%	Pred. No. 1.8e-96;		
Matches 162; Conservative	0;	Mismatches 4;	Indels 0;	Gaps 0;

Qy	Db	Qy
1	1	61
APPRICDSRLREYLLLEAKFAENITTCGAHCSLNINITYPDHKNVFMAMKRXSKQA	APPRICDSRLREYLLLEAKFAENITTCGAHCSLNINITYPDHKNVFMAMKRXSKQA	VEVWQGLALISEAVLRGALLVNSQPEWPIQLHVDKAVSGLSLTLLRLALGAKQFAIS
60	60	120
1	1	61
APPRICDSRLREYLLLEAKFAENITTCGAHCSLNINITYPDHKNVFMAMKRXSKQA	APPRICDSRLREYLLLEAKFAENITTCGAHCSLNINITYPDHKNVFMAMKRXSKQA	VEVWQGLALISEAVLRGALLVNSQPEWPIQLHVDKAVSGLSLTLLRLALGAKQFAIS
60	60	120

[illegible]

RESULT 3

US-09-604-8/1-2
; Sequence 2, Application US/09604871

GENERAL INFORMATION:

APPLICANT: Hilger, Bernd
APPLICANT: Burg, Josef

```

; APPLICANT:  Josel, Haas-Peter
; TITLE OF INVENTION:  ERYTHROPOIETIN CONJUGATES

```

Query Match	97.9%	Score 825;	DB 4;	Length 166;
Best Local Similarity	97.6%	Pred. No. 1.8e-96;		
Matches 162; Conservative	0;	Mismatches 4;	Indels 0;	Gaps 0;

Qy	Db
1	1
APPLICDSRLRYEYLLLEAKAEENITTCGAHCSGLNENITTPDCKVYFAMKRXSKQA	APPLICDSRLRYEYLLLEAKAEENITTCGAHCSGLNENITTPDCKVYFAMKRXSKQA
60	60
1	1
APPLICDSRLRYEYLLLEAKAEENITTCGAHCSGLNENITTPDCKVYFAMKRXSKQA	APPLICDSRLRYEYLLLEAKAEENITTCGAHCSGLNENITTPDCKVYFAMKRXSKQA
60	60
61	61
VEVMOGALLISEAVLRQALLVYNSQWPEPQLQHVDAVSGLSRLTTLRLALGAKRAIS	VEVMOGALLISEAVLRQALLVYNSQWPEPQLQHVDAVSGLSRLTTLRLALGAKRAIS
120	120
61	61
VEVMOGALLISEAVLRQALLVYNSQWPEPQLQHVDAVSGLSRLTTLRLALGAKRAIS	VEVMOGALLISEAVLRQALLVYNSQWPEPQLQHVDAVSGLSRLTTLRLALGAKRAIS
120	120

RESULT 4
PCT-US94-04361-37

```

; Sequence 37, Application PC/TUS9404361
;
; GENERAL INFORMATION:
;
; APPLICANT: Brigham and Women's Hospital

```

APPLICANT: 75 Francis Street
APPLICANT: Boston, MA 02115

```

: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25

```

```

CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/04361
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/049, 802
FILING DATE: 21-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Cimbala, Michele A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 0627.336PC01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 166 amino acids
TYPE: amino acid
TOPOLOGY: both
PCT-US94-04361-37

Query Match
Best Local Similarity 97.9%; Score 825; DB 5; Length 166;
Matches 162; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLERYLLEAKEAENITTCGAHCSLNENITVPPTKYNFYAMKRNXSXQA 60
DB 1 APPRLICDSRVLERYLLEAKEAENITTCGAHCSLNENITVPPTKYNFYAMKRNXSXQA 60
QY 61 VEWOGIALISEAVLRGOALLVNSQWPPELOLHVDAVSGLSLTLLRALDAOKRAIS 120
DB 61 VEWOGIALISEAVLRGOALLVNSQWPPELOLHVDAVSGLSLTLLRALDAOKRAIS 120
QY 121 PPDAASAAPLRTITADTFRKLFRVYSNFLRGKILKLYTGEACRTGDR 166
DB 121 PPDAASAAPLRTITADTFRKLFRVYSNFLRGKILKLYTGEACRTGDR 166

RESULT 5
US-07-903-220-1
Sequence 1, Application US/07903220
Patent No. 5332837
GENERAL INFORMATION:
APPLICANT: Hewick, Rodney M.
TITLE OF INVENTION: METHOD FOR THE PURIFICATION OF
TITLE OF INVENTION: ERYTHROPOIETIN AND ERYTHROPOIETIN COMPOSITION
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSER: Paul H. Heller
STREET: Kenyon & Kenyon, One Broadway
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/903,220
FILING DATE: 19920731
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: 1248/27
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 429-1776
TELEFAX: (202) 429-0796
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 193 amino acids
```

```

TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-07-903-220-1

Query Match
Best Local Similarity 97.9%; Score 825; DB 1; Length 193;
Matches 162; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLERYLLEAKEAENITTCGAHCSLNENITVPPTKYNFYAMKRNXSXQA 60
DB 28 APPRLICDSRVLERYLLEAKEAENITTCGAHCSLNENITVPPTKYNFYAMKRNXSXQA 87
QY 61 VEWOGIALISEAVLRGOALLVNSQWPPELOLHVDAVSGLSLTLLRALDAOKRAIS 120
DB 88 VEWOGIALISEAVLRGOALLVNSQWPPELOLHVDAVSGLSLTLLRALDAOKRAIS 147
QY 121 PPDAASAAPLRTITADTFRKLFRVYSNFLRGKILKLYTGEACRTGDR 166
DB 148 PPDAASAAPLRTITADTFRKLFRVYSNFLRGKILKLYTGEACRTGDR 193

RESULT 6
US-08-883-795A-34
Sequence 34, Application US/08883795A
Patent No. 5985607
GENERAL INFORMATION:
APPLICANT: Delcove, Genevieve
APPLICANT: Awang, Gregor
TITLE OF INVENTION: Recombinant DNA Molecules and Expression
TITLE OF INVENTION: Vectors for Tissue Plasmidogen Activator
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSER: BERESKIN & PARR
STREET: 40 King Street West
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5H 3Y2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/883,795A
FILING DATE: 27-JUN-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gravelle, Michelle
REGISTRATION NUMBER: 40,261
REFERENCE/DOCKET NUMBER: 7841-062
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 364-7311
TELEFAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 193 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-883-795A-34

Query Match
Best Local Similarity 97.9%; Score 825; DB 2; Length 193;
Matches 162; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLERYLLEAKEAENITTCGAHCSLNENITVPPTKYNFYAMKRNXSXQA 60
DB 28 APPRLICDSRVLERYLLEAKEAENITTCGAHCSLNENITVPPTKYNFYAMKRNXSXQA 87
```

Oy	61	V E V W G I A L L S E A V L R G C A L L V N S S O P M E P I Q T H V D K A V S L R S L T T L L A L G K R A I S	120
Db	88	V E V W G I A L L S E A V L R G C A L L V N S S O P M E P I Q T H V D K A V S L R S L T T L L A L G K R A I S	147
Oy	121	P P D A S A P L R T I T A D P F R K L F R Y R Y S N F I R G K L K L Y L G E A C R G D R	166
Db	148	P P D A S A P L R T I T A D P F R K L F R Y S N F I R G K L L I T G E A C R G D R	193

RESULT 7
US-09-366-009-34

Db	293	VEVMGGLALISEAVLRGALLVNSSGQWPEPLQGLHYDKVANSLSRLSTLLRLRLGNGKRLAIS	352
Qy	121	PPDAASAPLERTITADTFKRLFRVYSNPLRGKLLKLYTGACRTGDR	166
Db	353	PPDAASAPLERTITADTFKRLFRVYSNPLRGKLLKLYTGACRTGDR	398

RESULT 8
US-09-604-871-1
Sequence 1, Application US/09604871
Patent No. 6340742
GENERAL INFORMATION

```

; SEQ ID NO 1
;
; LENGTH: 165
;
; TYPE: PRT
;
; ORGANISM: Homo sapiens
;
US-09-604-871-1

```

```

1      RESULT 9
2      PCT-US94-04361-38
3      : Sequence 38. Application PC/TUS9404361
4      :
5      : GENERAL INFORMATION:
6      :
7      : APPLICANT: Brigham and Women's Hospital
8      : APPLICANT: 75 Francis Street
9      : APPLICANT: Boston, MA 02115
10     : APPLICANT: Bunn, H. Franklin
11     : APPLICANT: Wen, Danyi
12     : APPLICANT: Showers, Mark O.
13     :
14     : TITLE OF INVENTION: Erythropoietin Mutelins With Enhanced
15     : TITLE OF INVENTION: Activity
16     :
17     : NUMBER OF SEQUENCES: 59
18     :
19     : CORRESPONDENCE ADDRESS:
20     :
21     : ADDRESSEE: Sterne, Kessler, Goldstein & Fox
22     : STREET: 1100 New York Avenue, Suite 600
23     :
24     : CITY: Washington
25     :
26     : STATE: D.C.
27     :
28     : COUNTRY: U.S.A.
29     : ZIP: 20005-3934
30     :
31     : COMPUTER READABLE FORM:
32     : MEDIUM TYPE: Floppy disk

```

```
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/04361
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/049,802
FILING DATE: 21-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Cimbala, Michele A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 0627.336PC01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 165 amino acids
TYPE: amino acid
TOPOLOGY: both
PCT-US94-04361-38

Query Match      88.2%; Score 743.5; DB 5; Length 165;
Best Local Similarity 89.2%; Pred. No. 3.8e-86;
Matches 148; Conservative 7; Mismatches 10; Indels 1; Gaps 1;

QY 1 APRRLCDSRVLEERYLLLEAKAEENITTCGAHCSLNENITVPDTKVFYAMKRNXXSQQA 60
DB 1 APRRLCDSRVLEERYLLLEAKAEENITTCGAHCSLNENITVPDTKVFYAMKRNXXSQQA 60
QY 61 VEWOGIALLEAVLRGQALLVNSQWPPELQJLHVDKAVSGLSITLLRALGQKRAIS 120
DB 61 VEWOGIALLEAVLRGQAVLANSSQPEPLQJLHMDKAIISGLRSITLLRALGQ-BAIS 119
QY 121 PPDAASAPLRTITADTFKRLFRVYSNFLRGKLYTGECACRGDR 166
DB 120 LPDAASAPLRTITADTFKRLFRVYSNFLRGKLYTGECACRGDR 165

RESULT 10
PCT-US94-04361-39
Sequence 39, Application PC/TUS9404361
GENERAL INFORMATION:
APPLICANT: Brigham and Women's Hospital
APPLICANT: 75 Francis Street
APPLICANT: Boston, MA 02115
APPLICANT: Bunn, H. Franklin
APPLICANT: Men, Danyl
APPLICANT: Showers, Mark O.
TITLE OF INVENTION: Erythropoietin Mutetins With Enhanced
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/04361
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/049,802
FILING DATE: 21-APR-1993
```

```
ATTORNEY/AGENT INFORMATION:
NAME: Cimbala, Michele A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 0627.336PC01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 165 amino acids
TYPE: amino acid
TOPOLOGY: both
PCT-US94-04361-39

Query Match      88.0%; Score 741.5; DB 5; Length 165;
Best Local Similarity 88.6%; Pred. No. 6.7e-86;
Matches 147; Conservative 8; Mismatches 10; Indels 1; Gaps 1;

QY 1 APRRLCDSRVLEERYLLLEAKAEENITTCGAHCSLNENITVPDTKVFYAMKRNXXSQQA 60
DB 1 APRRLCDSRVLEERYLLLEAKAEENITTCGAHCSLNENITVPDTKVFYAMKRNXXSQQA 60
QY 61 VEWOGIALLEAVLRGQALLVNSQWPPELQJLHVDKAVSGLSITLLRALGQKRAIS 120
DB 61 VEWOGIALLEAVLRGQAVLANSSQPEPLQJLHMDKAIISGLRSITLLRALGQ-BAIS 119
QY 121 PPDAASAPLRTITADTFKRLFRVYSNFLRGKLYTGECACRGDR 166
DB 120 LPDAASAPLRTITADTFKRLFRVYSNFLRGKLYTGECACRGDR 165

RESULT 11
PCT-US94-04361-44
Sequence 44, Application PC/TUS9404361
GENERAL INFORMATION:
APPLICANT: Brigham and Women's Hospital
APPLICANT: 75 Francis Street
APPLICANT: Boston, MA 02115
APPLICANT: Bunn, H. Franklin
APPLICANT: Men, Danyl
APPLICANT: Showers, Mark O.
TITLE OF INVENTION: Erythropoietin Mutetins With Enhanced
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/04361
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/049,802
FILING DATE: 21-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Cimbala, Michele A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 0627.336PC01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 166 amino acids
```

TYPE: amino acid
TOPOLOGY: both
PCT-US94-04361-44

Query Match
Best Local Similarity 82.4%; Score 695; DB 5; Length 166;
Matches 137; Conservative 8; Mismatches 21; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLEERYLLAKEAENITTCGAHCSENENITVDTKVNFMKRNKXSOQA 60
DB 1 APPRLICDSRVLEERYLLAKEAENITTCGAHCSENENITVDTKVNFMKRNKXSOQA 60

QY 61 VEWMOGLALISEAVLRGALLVNSSQWPEPQLHYDKAVSGLSRSLTTLRALGAQKEAIS 120
DB 61 VEWMOGLALISEAVLRGALLVNSSQWPEPQLHYDKAVSGLSRSLTTLRALGAQKEAIS 120

QY 121 PPDASAPLRTITADTFKRLFRVYSNPLRGKLTLYTGACRGRDR 166
DB 121 PPDASAPLRTITADTFKRLFRVYSNPLRGKLTLYTGACRGRDR 166

RESULT 12
PCT-US94-04361-41

Sequence 41, Application PC/TUS9404361

GENERAL INFORMATION:
APPLICANT: Brigham and Women's Hospital
APPLICANT: 75 Francis Street
APPLICANT: Boston, MA 02115
APPLICANT: Bunn, H. Franklin
APPLICANT: Men, Danyl
APPLICANT: Showers, Mark O.
TITLE OF INVENTION: Erythropoietin Mutelins With Enhanced
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3934

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/04361
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/049,802
FILING DATE: 21-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Cimbala, Michele A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 0627.336PC01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 166 amino acids
TYPE: amino acid
TOPOLOGY: both
PCT-US94-04361-41

Query Match
Best Local Similarity 82.1%; Score 692; DB 5; Length 166;
Matches 135; Conservative 12; Mismatches 19; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLEERYLLAKEAENITTCGAHCSENENITVDTKVNFMKRNKXSOQA 60
DB 1 APPRLICDSRVLEERYLLAKEAENITTCGAHCSENENITVDTKVNFMKRNKXSOQA 60

DB 1 APPRLICDSRVLEERYLLAKEAENITTCGAHCSENENITVDTKVNFMKRNKXSOQA 60
QY 61 VEWMOGLALISEAVLRGALLVNSSQWPEPQLHYDKAVSGLSRSLTTLRALGAQKEAIS 120
DB 61 VEWMOGLALISEAVLRGALLVNSSQWPEPQLHYDKAVSGLSRSLTTLRALGAQKEAIS 120

QY 121 PPDASAPLRTITADTFKRLFRVYSNPLRGKLTLYTGACRGRDR 166
DB 121 PPDASAPLRTITADTFKRLFRVYSNPLRGKLTLYTGACRGRDR 166

RESULT 13
PCT-US94-04361-40

Sequence 40, Application PC/TUS9404361

GENERAL INFORMATION:
APPLICANT: Brigham and Women's Hospital
APPLICANT: 75 Francis Street
APPLICANT: Boston, MA 02115
APPLICANT: Bunn, H. Franklin
APPLICANT: Men, Danyl
APPLICANT: Showers, Mark O.
TITLE OF INVENTION: Erythropoietin Mutelins With Enhanced
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3934

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/04361
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/049,802
FILING DATE: 21-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Cimbala, Michele A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 0627.336PC01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 166 amino acids
TYPE: amino acid
TOPOLOGY: both
PCT-US94-04361-40

Query Match
Best Local Similarity 80.2%; Score 676; DB 5; Length 166;
Matches 130; Conservative 14; Mismatches 22; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLEERYLLAKEAENITTCGAHCSENENITVDTKVNFMKRNKXSOQA 60
DB 1 APPRLICDSRVLEERYLLAKEAENITTCGAHCSENENITVDTKVNFMKRNKXSOQA 60

QY 61 VEWMOGLALISEAVLRGALLVNSSQWPEPQLHYDKAVSGLSRSLTTLRALGAQKEAIS 120
DB 61 VEWMOGLALISEAVLRGALLVNSSQWPEPQLHYDKAVSGLSRSLTTLRALGAQKEAIS 120

QY 121 PPDASAPLRTITADTFKRLFRVYSNPLRGKLTLYTGACRGRDR 166
DB 121 PPDASAPLRTITADTFKRLFRVYSNPLRGKLTLYTGACRGRDR 166

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 8, 2003, 02:01:43 ; Search time 47.6267 Seconds
(without alignments)
718.164 Million cell updates/sec

Title: US-09-813-775c-18
Perfect score: 843
Sequence: 1 APPRLICDSRVLELYLEAK.....NFLRGKIKLYTGSEACTGDR 166

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SP:archaea:*
2: SP:bacteria:*
3: SP:fungi:*
4: SP:human:*
5: SP:invertebrate:*
6: SP:mammal:*
7: SP:mhc:*
8: SP:organelle:*
9: SP:phage:*
10: SP:plant:*
11: SP:rodent:*
12: SP:virus:*
13: SP:vertebrate:*
14: SP:unclassified:*
15: SP:rvirus:*
16: SP:bacteriap:*
17: SP:archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	675.5	80.1	195	6	O9GKA3
2	675.5	80.1	195	6	O9GKA2
3	665	78.9	194	6	O9MYM8
4	188	22.3	50	11	O9QV40
5	87.5	10.4	346	16	O82K24
6	87.5	10.4	346	16	O82K25
7	84	10.0	339	16	O9HZM7
8	82.5	9.8	389	2	O9AN18
9	81	9.6	323	16	O8ZDC8
10	80.5	9.5	871	5	O9NB04
11	79	9.4	3722	2	P94873
12	78.5	9.3	383	16	O92QV7
13	78	9.3	378	17	O82K23
14	77.5	9.2	242	16	O8YV76
15	77.5	9.2	567	10	O9SVL5
16	77	9.1	348	16	O86751

17	77	9.1	451	16	P74054
18	77	9.1	480	10	O43380
19	76.5	9.1	379	2	O919F5
20	76.5	9.1	1638	2	O87001
21	76.5	9.1	2472	16	O91696
22	76	9.0	554	2	O9RPH5
23	75.5	9.0	451	16	O8XSE8
24	74.5	8.8	455	16	O8UBQ9
25	74.5	8.8	756	12	O90155
26	74.5	8.8	2556	11	O91XW2
27	74	8.8	397	8	O9TNG5
28	74	8.8	426	3	O9HCD5
29	74	8.8	815	10	O9PK91
30	74	8.8	904	5	O9VEX7
31	74	8.8	912	5	O9NHC1
32	74	8.8	912	5	O9NHB9
33	74	8.8	916	5	O9NHC2
34	74	8.8	916	5	O9NHC0
35	74	8.8	1003	10	O9FIR4
36	73	8.7	353	16	O8ZGV8
37	73	8.7	454	11	O9D7X0
38	73	8.7	1481	5	O9NEX0
39	72.5	8.6	637	16	O55413
40	72.5	8.6	762	16	O9A4Q7
41	72.5	8.6	917	2	O9F8D7
42	72.5	8.6	917	2	O51722
43	72	8.5	318	16	O8XX12
44	72	8.5	475	4	O8WU14
45	72	8.5	896	2	O9AN79

ALIGNMENTS

RESULT 1	ID	Query Match	Score	DB 6:	Length	195:
O9GKA3	O9GKA3	80.1%	675.5	DB 6:	Length	195:
AC	O9GKA3	Best Local Similarity	80.2%	Pred. No. 2,3e-60		
DT	01-MAR-2001 (TREMBLrel. 16, last sequence update)	Matches 134;	Conservative 14;	Mismatches 18;	Indels 1;	Gaps 1;
DT	01-JUN-2002 (TREMBLrel. 21, last annotation update)					
DE	Erythropoietin..					
OS	Oryctolagus cuniculus (Rabbit).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC	Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.					
OX	NCBI_TaxID=9986;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RX	MEDLINE=21290682; PubMed=11396976;					
RA	Villalta A., Wu D., Margalith M., Hobart P.;					
RT	"Rabbit Epo Gene and cDNA: Expression of Rabbit Epo after					
RT	Intramuscular Injection of pDNA."					
RL	Biochem. Biophys. Res. Commun. 284:823-827(2001).					
DR	EMBL; AF290943; AAC36961.1; -.					
DR	HSSP; P01586; ICN4.					
DR	InterPro; IPR001323; EPO_TPO.					
DR	InterPro; IPR003013; Erythropo.					
DR	Pfam; PF00758; EPO_TPO; 1.					
DR	PRINTS; PR00272; ERYTHROPTN.					
DR	PROSITE; PS00817; EPO_TPO; 1.					
SO	SEQUENCE 195 AA; 21053 MW; 0999DA7D852713F3 CRC64;					
OY	1 APPRLICDSRVLELYLEAKENITTCAGHCSLSENIIVPPTKYNFYAMKRNKXQQA 60					
DB	29 APPRLICDSRVLELYLEAKENITTCAGHCSLSENIIVPPTKYNFYAMKRNKXQQA 88					
OY	61 VEWOGIALISEAVIRGOALLVSSQPMWPELOLHVQKAVSGISLITLLRALGAKENIS 120					
DB	89 VEWOGIALISEAVIRGOALLVSSQPMWPELOLHVQKAVSGISLITLLRALGAKENIS 148					

OC Bacteria; Proteobacteria; gamma subdivision: Enterobacteriaceae;
 OC Salmonella.
 NCBI_TaxID=602;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=21534948 / SCSC1412 / ATCC 700720;
 RX MEDLINE=21534948; PubMed=11677609;
 RA McLelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
 RA Courtney L., Potwilk S., Ali J., Dante M., Du F., Hou S., Layman D.,
 RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
 RA Ryan E., Sun H., Flores L., Miller W., Stoneking T., Nhan M.,
 RA Waterston R., Wilson R.K.;
 RT "Complete genome sequence of *Salmonella enterica* serovar Typhimurium
 LT2.";
 RL Nature 413:852-856(2001).
 DR EMBL: AE008878; AL22684.1;
 DR InterPro: IPR001761; Periplabp/LacI.
 DR Pfam: PF00532; Peripla_BP_Like; 1.
 KM Complete proteome.
 SQ SEQUENCE 346 AA; 38440 MW; E37CAB58E49FD716 CRC64;

Query Match 10.4%; Score 87.5; DB 16; Length 346;
 Best Local Similarity 26.7%; Pred. No. 1.3;
 Matches 44; Conservative 22; Mismatches 48; Indels 51; Gaps 9;

OY 10 RVLERYLLAEKAEENITTG--CAEHCSLNE--NITVPDTKYNFYAMKRNKXSQQAWEYQ 65
 DB 217 RNLQEMLEHRHPDANVAGSAIAEAAMGEGRNLTPLTIVSEYL-----THQYR 267
 OY 66 GLALSEAVLRGQALLVNSO--PWEPIQLHYDKAVSGIRSLTTLRALGAO--KEAISP 122
 DB 268 GLK-----RGHILMALSDQMAO-----GELATIOSIKVIGQGPVENISPP 309
 OY 123 -----DAASAPLRTITADTFKRLFRVYSNFKLGKIKLYTGEA 160
 DB 310 VLITHNNADSARVRRLSPGFRPVY-----LYQYTSEA 344

RESULT 6

ID 0822M5 PRELIMINARY; PRT; 346 AA.
 AC 0822M5;

DT 01-MAR-2002 (TREMblrel. 20, Created)
 DT 01-MAR-2002 (TREMblrel. 20, Last sequence update)
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
 DE Solute binding receptor protein.
 GN STY3952.
 OS *Salmonella typhi*.

OC Bacteria; Proteobacteria; gamma subdivision: Enterobacteriaceae;
 OC Salmonella.
 NCBI_TaxID=601;
 RN [1]
 RP SEQUENCE FROM N.A.

RX MEDLINE=21534947; PubMed=11677608;
 RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
 RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahina M.,
 RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
 RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
 RA Feltham A., Hamlin N., Haque A., Hien T.T., Holtroyd S., Jorgels K.,
 RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
 RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
 RA Whitehead S., Barrell B.G.;
 RT "Complete genome sequence of a multiple drug resistant *Salmonella*
 RT enterica serovar Typhi CT18.";
 RL Nature 413:848-852(2001).
 DR EMBL: AL627280; CAP03169.1;
 DR InterPro: IPR001761; Periplabp/LacI.
 DR Pfam: PF00532; Peripla_BP_Like; 1.
 KM Receptor; Complete proteome.
 SQ SEQUENCE 346 AA; 38546 MW; F80FBI688BC3ABF CRC64;

Query Match 10.4%; Score 87.5; DB 16; Length 346;

Best Local Similarity 26.7%; Pred. No. 1.3;
 Matches 44; Conservative 22; Mismatches 48; Indels 51; Gaps 9;

OY 10 RVLERYLLAEKAEENITTG--CAEHCSLNE--NITVPDTKYNFYAMKRNKXSQQAWEYQ 65
 DB 217 RNLQEMLEHRHPDANVAGSAIAEAAMGEGRNLTPLTIVSEYL-----THQYR 267
 OY 66 GLALSEAVLRGQALLVNSO--PWEPIQLHYDKAVSGIRSLTTLRALGAO--KEAISP 122
 DB 268 GLK-----RGHILMALSDQMAO-----GELATIOSIKVIGQGPVENISPP 309
 OY 123 -----DAASAPLRTITADTFKRLFRVYSNFKLGKIKLYTGEA 160
 DB 310 VLITHNNADSARVRRLSPGFRPVY-----LYQYTSEA 344

RESULT 7

ID 09H2M7 PRELIMINARY; PRT; 339 AA.
 AC 09H2M7;

DT 01-MAR-2001 (TREMblrel. 16, Created)
 DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
 DE UDP-N-acetylpyruvoylglyucosamine reductase.
 GN MURB OR PA2977.
 OS *Pseudomonas aeruginosa*.

OC Bacteria; Proteobacteria; gamma subdivision: Pseudomonadaceae;
 OC Pseudomonas.
 NCBI_TaxID=287;
 RN [1]
 RP SEQUENCE FROM N.A.

RX MEDLINE=20437337; PubMed=10984043;
 RA Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warriner P.,
 RA Hickey M.J., Brinkman F.S.L., Hutnagle M.O., Kowalik D.J., Lagrou M.,
 RA Gardner R.L., Goltz L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
 RA Brody L.R., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
 RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
 RT "Complete genome sequence of *Pseudomonas aeruginosa* PAO1, an
 RT opportunistic pathogen.";
 RL Nature 406:959-964(2000).
 DR EMBL: AE004723; AAC06365.1; -
 DR HSSP: P08373; ZMBR.
 DR InterPro: IPR003170; MurB.
 DR InterPro: IPR001575; Oxid_FAD_bind.
 DR InterPro: IPR000531; TonB_boxC.
 DR Pfam: PF01565; FAD_binding_4; 1.
 DR Pfam: PF02873; MurB_C; 1.
 DR PROSITE: PS00430; TONB_DEPENDENT_REC_1; UNKNOWN_1.
 KM Complete proteome.

SQ SEQUENCE 339 AA; 37627 MW; C0C8EF9F2938FE27 CRC64;

Query Match 10.0%; Score 84; DB 16; Length 339;
 Best Local Similarity 22.4%; Pred. No. 2.9;
 Matches 41; Conservative 24; Mismatches 48; Indels 70; Gaps 8;

OY 31 EHCSLNE--NITVPDTKYNFYAMKRNKXSQQAWEYQGLALSEAVLRGQALLV 82
 DB 7 EHCSLKPYNFTGIDVRLARLAHARDEA---DVREALALARE---RGLPLVTGGGSQL 58
 OY 83 -----NSQPEP--LQLHYDKAVSGIRSLTTL 109
 DB 59 LLTRDVEALVRMASQGRRIYSDAASVLYEAGEAMDPRVQSLSEGLAGLENTLSI- 117
 OY 110 RALGAQKEAISPPDAASAPLRTITTA-----DFFKRLFRVYSNFKLGKIKLYTGEACRT 163
 DB 118 -----PQTVGAAPWONIGAYGVELKDWFDLSITLAL--DRDGTILREFDQACRF 163
 OY 164 GDR 166
 DB 164 GYR 166

```

RESULT 8
ID 09AN18 PRELIMINARY; PRT; 389 AA.
AC 09AN18:
DT 01-JUN-2001 (TREMBLREL. 17, Created)
DT 01-JUN-2001 (TREMBLREL. 17, Last sequence update)
DE ID626.
GN 1D626.
OS Bradyrhizobium japonicum.
OC Bacteria: Proteobacteria: alpha subdivision: Rhizobiaceae group:
OC Bradyrhizobium group, Bradyrhizobium.
OX NCBI_TaxID=375;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN=110SPC4;
RX MEDLINE=21101824; PubMed=11157954;
RA Gottfert M., Rothlisberger S., Kundig C., Beck C., Marty R.,
  Hennecke H.;
RT "Potential symbiosis-specific genes uncovered by sequencing a 410-kb
  DNA region of the Bradyrhizobium japonicum chromosome.";
RL J. Bacteriol. 183:1405-1412(2001).
DR EMBL: AF322013; AAG60960.1; -
SQ SEQUENCE 389 AA; 42316 MW; 6E37DC9BA9872D45 CRC64;

Query Match 9.8%; Score 82.5; DB 2; Length 389;
Best Local Similarity 24.4%; Pred. No. 4.8;
Matches 47; Conservative 15; Mismatches 74; Indels 57; Gaps 8;

QY 6 ICDSRLRYL-----LEAKAENITTCGAHCSLNERITVPTKVFYANKRXSKX 58
DB 75 LASAELRYLRKTPASRIAEDAVALVAGAAHMDSLKN-----SAS 116
QY 59 OAVEV-----MOGLA-----LTSEAVLNGQALLVNSQPMPELOLHYKAVSGLSL-- 105
DB 117 QVAEVRGKRTWGVASSDVEITRDAPVLAQAILANK-----HICVDIKTTSRTVGH 169
QY 106 -TTLRALGAOKRAIS-----PPDASAAPLRITITADTFKRLFRVSNF-----LRGKL 153
DB 170 SMTLERIEAGAVVRLSGILEFFPGARPREALRAIGLERFAPPELLIAGKIDLDGADLSGS 229
QY 154 KLTGEACRTGDR 166
DB 230 PVLGITPREADR 242

RESULT 9
ID 08ZDC8 PRELIMINARY; PRT; 323 AA.
AC 08ZDC8:
DT 01-MAR-2002 (TREMBLREL. 20, Created)
DT 01-MAR-2002 (TREMBLREL. 20, Last sequence update)
DT 01-JUN-2002 (TREMBLREL. 21, Last annotation update)
DE Ribonucleoside-diphosphate reductase 2 beta chain (EC 1.17.4.1).
GN NRDP OR YP02648.
OS Yersinia pestis.
OC Bacteria: Proteobacteria: gamma subdivision; Enterobacteriaceae;
OC Yersinia.
OX NCBI_TaxID=632;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN=CO-92 / BIOVAR ORIENTALIS;
RX MEDLINE=21470413; PubMed=11586360;
RA Parhill J., Wren B.W., Thomson N.R., Tibball R.W., Holden M.T.G.,
  Baker S., Basham D., Bentley S.D., Brooks K., Cerdano-Tarraga A.M.,
  Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
  Felwell T., Hamlin N., Holtroyd S., Jagels K., Kariyshev A.V.,
  Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
  Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
RT "Genome sequence of Yersinia pestis, the causative agent of plague.";
RL Nature 413:523-527(2001).

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DR EMBL: AJ414153; CAC92889.1; -
DR InterPro: IPR000358; RibonucL_redctse.
DR Pfam: PF00268; ribonuc_red_sm; 1.
DR PROSITE: PS00368; RIBORED_SMALL; 1.
KW OXidoreductase; Complete proteome.
SQ SEQUENCE 323 AA; 36823 MW; 87C21F7BB9B7FD2 CRC64;

Query Match 9.6%; Score 81; DB 16; Length 323;
Best Local Similarity 24.4%; Pred. No. 5.4;
Matches 33; Conservative 19; Mismatches 61; Indels 22; Gaps 5;

QY 38 NITVPPTKVNFTAKRNKXKQAVEWQGLALSEAVLNGQALLVNSQPMPELOLHYD- 96
DB 2 NVKAPTRISALIMWK-IEDDKDLEVMN--RLTSNFMLEKVPKPLSDIPSMATLTPHEQ 58
QY 97 ---KAVSGRLSTTLRLAQO---KEATSPDASAAPLRITITADTFKRLFRVSNFLR 150
DB 59 LTRVFTGLTLDLTONTIGAPALIKDALTPHEALFISNIFWEAVHANSYSIFSTL-- 116
QY 151 GKLLYTGACRTGD 165
DB 117 -----CLTSD 121

RESULT 10
ID 09NB04 PRELIMINARY; PRT; 871 AA.
AC 09NB04:
DT 01-OCT-2000 (TREMBLREL. 15, Created)
DT 01-OCT-2000 (TREMBLREL. 15, Last sequence update)
DT 01-MAR-2002 (TREMBLREL. 20, Last annotation update)
DE Discs LOST.
GN DUT OR BCDNA:LD22238 OR CG12021.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN 11
RP SEQUENCE FROM N.A.
RA Tenentzapf G., Smith C.A., Bhat M., Mogliade J., Tepass U.;
RT "Apical, lateral, and basal polarization cues contribute to the
  development of the follicular epithelium during Drosophila
  oogenesis.";
RL EMBL: AF274350; AAF81829.1; -
DR EMBL: AF274350; AAF81829.1; -
DR HSSP: 012923; 3PDZ.
DR FlyBase: FBgn0024246; dlt.
DR InterPro: IPR001478; PDZ.
DR Pfam: PF00595; PDZ; 4.
DR SMART: SM00228; PDZ; 4.
DR PROSITE: PS50106; PDZ; 4.
SQ SEQUENCE 871 AA; 92905 MW; C9A72F6DB4DB5B4D CRC64;

Query Match 9.5%; Score 80.5; DB 5; Length 871;
Best Local Similarity 26.9%; Pred. No. 21;
Matches 50; Conservative 25; Mismatches 72; Indels 39; Gaps 11;

QY 15 YLLEAKE-----AENTTTCGAHCSLNERITVPTKVFYANK-RKXSKQAVEV---W 64
DB 335 YVCEKEELSGIFVKVNSPSSA--ADLNGRIYVNDRIIEVDGSLQSYNHQAVELLKSG 392
QY 65 OGGLALSEAVLNG-----QALLVN-----SSQPMPELOLHYDKAVSGLRLSTT-----L 108
DB 393 QVAVNLRLEKLVKPKREQLQQAIAANDKLPSAPGTPSPAPMPPTPVATTSATTPSRGI 452
QY 109 LRALGAOKRAISPPDASAAP-----LRTITADTF---RKLFRVSNFLRGKILTYTGEA 160
DB 453 TRRL--EEBALPAPAEAFMTTPSVTTMTTTLSSFCAGQLVAVROS-LDGSKRIIPTEV 509
QY 161 CRGDR 166
DB 510 VPLADK 515

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RESULT 11
ID P94873 PRELIMINARY; PRT; 3722 AA.
AC P94873;
DT 01-MAY-1997 (TREMblrel. 03, Created)
DT 01-MAY-1997 (TREMblrel. 03, Last sequence update)
DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
DE Alpha-aminoadipyl-L-cysteinyl-valine synthetase.
GN PCBAB.
OS Lysobacter lactamgenus.
OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
OC Lysobacter.
OC NCBI_TaxID=39596;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VK90.
RX MEDLINE=96275949; PubMed=8737573;
RA Kimura H., Miyashita H., Sumino Y.;
RT "Organization and expression in Pseudomonas putida of the gene cluster
RT involved in cephalosporin biosynthesis from Lysobacter lactamgenus
RT VK90."
RL Appl. Microbiol. Biotechnol. 45:490-501(1996).
DR EMBL; D50308; BAA08846.1; -.
DR HSSP; P14687; IAMU.
DR InterPro: IPR002106; AALRNA_LigaseII.
DR InterPro: IPR000873; AMP-bind.
DR InterPro: IPR001242; Condensatn.
DR InterPro: IPR000977; DNA_Ligase.
DR InterPro: IPR003880; Ppantne_attach.
DR InterPro: IPR000379; Ser_estrs_site.
DR InterPro: IPR001031; Thioesterase.
DR Pfam; PF00501; AMP-binding_3.
DR Pfam; PF00668; Condensation_3.
DR Pfam; PF00550; pp-binding_3.
DR Pfam; PF00975; Thioesterase_1.
DR PROSITE; PS00179; AA_TRNA_LIGASE_II_1; UNKNOWN_1.
DR PROSITE; PS50075; ACP_DOMAIN_3.
DR PROSITE; PS00455; AMP_BINDING_1.
DR PROSITE; PS00697; DNA_LIGASE_A1; UNKNOWN_2.
DR PROSITE; PS00012; PHOSPHOPANTHETHEINE; UNKNOWN_2.
KW Phosphopantetheine.
SQ SEQUENCE 3722 AA; 411607 MW; 3597B3483463809B CRC64;

Query Match 9.4%; Score 79; DB 2; Length 3722;
Best Local Similarity 22.1%; Pred. No. 1.9e+02;
Matches 34; Conservative 16; Mismatches 52; Indels 52; Gaps 5;

QY 16 LLEAKAEENITTCGAHCSLNENITVPDTKVNFTYAMKRNKXSOQAVEV---WQGLALLS 71
DB 2138 LLEGATTAQTLP-----PLPATYADFVSMOROLSDRLDALFDYWO----- 2178
QY 72 EAVLRGALLVNSQPWEPLQLHYDKAVSGLSRLTTLRALGAQ-----KRAISPPDAAS 126
DB 2179 -----RSIAGKQPIQLPLD-----HARPAQDYILGRIEIVDVDAATT 2214
QY 127 AAPLRITTAADTFRKLFRVYSNFKGLKLYTGEA 160
DB 2215 CDQLRVLAQTTRTSFVSVALAAYLVTLKAYSCQS 2248

RESULT 12
ID Q920V7 PRELIMINARY; PRT; 383 AA.
AC Q920V7;
DT 01-DEC-2001 (TREMblrel. 19, Created)
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
DE Problemle ribonuclease D protein (EC 3.1.26.3).
GN RND OR R01191 OR SMC00622.
OS Rhizobium meliloti (Sinorhizobium meliloti).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;

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OC Rhizobiaceae; Sinorhizobium.
OX NCBI_TaxID=382;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE=2136507; PubMed=11481430;
RA Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
RA Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
RA Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Maury D.,
RA Pohl T., Portetle D., Puehler A., Purnelle B., Ramsperger U.,
RA Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.;
RT "Analysis of the chromosome sequence of the legume symbiont
RT Sinorhizobium meliloti strain 1021."
RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
DR EMBL; AL591786; CAC45770.1; -.
DR InterPro: IPR002562; 3_5_exonuclease.
DR InterPro: IPR002121; HRDC.
DR Pfam; PF01612; 3_5_exonuclease; 1.
DR Pfam; PF00570; HRDC; 1.
KW Hydrolase; Complete proteome.
SQ SEQUENCE 383 AA; 42884 MW; 49972055BE17D076 CRC64;

Query Match 9.3%; Score 78.5; DB 16; Length 383;
Best Local Similarity 25.6%; Pred. No. 12;
Matches 45; Conservative 27; Mismatches 57; Indels 47; Gaps 9;

QY 4 RLICDSRYLERYLEAKAEENITTCGAHCSLNENITVPDTKVNFTYAMKRNKXSOQAVEV 63
DB 233 RLINDDAIYELAQQPKDAE-----ALGLRTIPK-----GHERSSA----- 269
QY 64 WQGLALLSEAVLRGALLVNSQ-PWEPLQLHYDKAVSGLSRLTTLRALGAQKEAISPP 122
DB 270 --GALTI-EAV--SEALAI PRGELPRLPRQNHAEAGAAASSELKVLKLISEKGVAAK 324
QY 123 DAASAPLRITTAAD-----TRKLFRRVYSNFKGLKLYTGE-ACRTGDR 166
DB 325 IIAASDLDRIAEGADVAALKGRRELFGMTA-----LKLINGEVALRFDVK 374

RESULT 13
ID Q8Z2K3 PRELIMINARY; PRT; 378 AA.
AC Q8Z2K3;
DT 01-MAR-2002 (TREMblrel. 20, Created)
DT 01-MAR-2002 (TREMblrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Amidophosphoribosyltransferase (purf).
GN PAF0218.
OS Pyrobaculum aerophilum.
OC Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
OC Thermoproteaceae; Pyrobaculum.
OX NCBI_TaxID=13773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IM2 / ATCC 51768 / DSM 7523;
RX PubMed=11792869;
RA Fitz-Gibbon S.T., Lader H., Kim U.-J., Stetter K.O., Simon M.I.,
RA Miller J.H.;
RT "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum
RT aerophilum."
RL Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).
DR EMBL; AF009756; AAL62636.1; -.
DR InterPro: IPR000836; PRTtransferase.
DR Pfam; PF00156; Pribosyltran; 1.
KW Transferase; Glycosyltransferase; Complete proteome.
SQ SEQUENCE 378 AA; 40574 MW; 0BE840A6A621A51D CRC64;

Query Match 9.3%; Score 78; DB 17; Length 378;
Best Local Similarity 25.8%; Pred. No. 13;
Matches 42; Conservative 19; Mismatches 56; Indels 46; Gaps 10;

QY 2 PPRICDSRYLERYLEAKAEENITTC--CAE-HCSLNEN-----ITVPDTKVN 47

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DB 173 PREC---AME--LYYASRLSDVIGVEIAEYRAKLGKAGRADVIVICPDTGLY 227
QY 48 FYAMKRNKXQQAWEVWQGLALLSEAVLRQALLVNSQPEWPLQJHV----- 95
DB 228 YAAW-----AARAGAMVHAPGVFS-TIKRSLALDDEVKIRISALQKANYVRHVAAGKRV 281
QY 96 ----DKAVSG--LRSLTLRLAIGAOKEAISPPDAASAPLRT 132
DB 282 LVVDSDIISGLRLRIHAIOLIRVAKAKEVHA---ATAAPPLRS 321

RESULT 14
Q8Y76 PRELIMINARY: PRT: 242 AA.
AC Q8Y76;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Hypothetical protein A10975.
GN A10975.
OS Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_TaxID=103690;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-21595285; PubMed-11759840;
RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
RA Matsubae A., Iriuchij M., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
RA Yasuda M., Tabata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing
RT cyanobacterium Anabaena sp. strain PCC 7120.";
RL DNA Res. 8:205-213(2001).
DR EMBL; AP003584; BAB72932.1;
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 242 AA; 27163 MW; 746A46CE10CCF6FC CRC64;

Query Match 9.2%; Score 77.5; DB 16; Length 242;
Best Local Similarity 28.4%; Pred. No. 8.5;
Matches 27; Conservative 14; Mismatches 27; Indels 27; Gaps 4;

QY 66 GLALSEAVL-----RGQALLY--NSSQPEWPLQJ-----HYDKAVSGLR 103
DB 14 GLCLSSQVLAQTLTLPNLIGFNSNEGKLLTSSKREDPPLSMQVYQVNAVCVGA 73
QY 104 SLTLRLAIGAOKEAISPPDAASAPLRTTADTF 138
DB 74 SLIMVNLISG-----INAPETAQSPYRFTQDNF 103

RESULT 15
Q9SVL5 PRELIMINARY: PRT: 567 AA.
AC Q9SVL5;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Hypothetical 64.1 kDa protein.
GN F18B3.120.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Rieger M., Gabel C., Mueller-Auer S., Schaefer M., Zipp M.,
RA Mewes H.W., Mayer K.F.X., Lemcke K., Schueller C., Quetler F.,
RA Salanoubat M.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RP SEQUENCE FROM N.A.

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RA EU Arabidopsis sequencing project;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL049862; CAB42913.1;
DR InterPro: IPR000210; BTF_P02.
DR InterPro: IPR004249; NPH3.
DR Pfam: PF00651; BTF; 1.
DR Pfam: PF03000; NPH3; 1.
DR SMART; SM00225; BTF; 1.
DR PROSITE; PS50097; BTF; 1.
KW Hypothetical protein.
SQ SEQUENCE 567 AA; 64090 MW; 1A6550B03165D6F CRC64;

Query Match 9.2%; Score 77.5; DB 10; Length 567;
Best Local Similarity 22.7%; Pred. No. 25;
Matches 47; Conservative 27; Mismatches 76; Indels 57; Gaps 11;

QY 1 APRRLICDSVLERYLE-----AKEAENITTCGAHCGLNENITVPDPKV----- 46
DB 105 SPENLISKT---EKFLSERVFTNVQESIRALAKACESVSSLAESLCITEOCIDSIYFQASS 161
QY 47 ---NFYAW-----KRNKXQQAWEVW-QGLALLSEAVLRQALLVNS--QP- 87
DB 162 TDPSSPYGMPIINNGCIFTVDKRRQSKDSKTELMFEDLTSLSPFRVILSMKSSVLSPE 221
QY 88 --WEPLQLHDKAVSGL-----RSLTLRLAIGAOKEAISPPDAASAPLRTTA 135
DB 222 IVERSLTLTYAKKHIPICIRSSSSASSSSSSSTPIASENOORELLE--TITSDPL--TA 276
QY 136 DFFPKLFRVSNFLRGKLLKLYGCACR 162
DB 277 TTRSLF-----GLLRATITLNMSENCR 299

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Search completed: January 8, 2003, 05:13:54
 Job time : 56.1267 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 8, 2003, 00:55:32 ; Search time 11.5599 Seconds
(without alignments)
595.600 Million cell updates/sec

Title: US-09-813-775c-18

Perfect score: 843
Sequence: 1 APPRLICDSRVLELYLEAK.....NFLRGKLYTGECAGRTGDR 166

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	825	97.9	193	1	EPO_HUMAN
2	743.5	88.2	192	1	EPO_MACEFA
3	741.5	88.0	192	1	EPO_MACMU
4	692	82.1	192	1	EPO_RAT
5	688	81.6	192	1	EPO_FELCA
6	679.5	80.6	192	1	EPO_BOVIN
7	676	80.2	192	1	EPO_MOUSE
8	672.5	79.8	194	1	EPO_SHEEP
9	665	78.9	190	1	EPO_PIG
10	615	73.0	175	1	EPO_CANFA
11	110	13.0	352	1	TPO_CANFA
12	93	11.0	353	1	TPO_HUMAN
13	78	9.3	326	1	TPO_RAT
14	76.5	9.1	543	1	CH60_BARBA
15	76	9.0	356	1	TPO_MOUSE
16	76	9.0	552	1	CH60_COXBU
17	75	8.9	1089	1	YH25_YEAST
18	74	8.8	1063	1	YH25_YEAST
19	73.5	8.7	897	1	EP15_MOUSE
20	73	8.7	353	1	NADA_YERPE
21	71.5	8.5	220	1	Y085_MYCTU
22	71	8.4	547	1	G6P2_NEIMA
23	70.5	8.4	381	1	MODD_MYCAV
24	70.5	8.3	3033	1	POLG_HCVJ8
25	70	8.3	544	1	CH60_PRAU8
26	69.5	8.2	547	1	CH60_LEGPN
27	69.5	8.2	896	1	EP15_HUMAN
28	69	8.2	3685	1	DMD_HUMAN
29	68.5	8.1	347	1	NADA_SALIT
30	68.5	8.1	360	1	CVS2_MALZE
31	68.5	8.1	552	1	CH60_PSEST
32	68.5	8.1	907	1	GACS_PSEST
33	68	8.1	542	1	CH65_RHIME

34	68	8.1	548	1	CH60_BUCMP	051832 buchnera ap
35	67.5	8.0	239	1	GIDB_SYRGO	054571 streptomyces
36	67.5	8.0	388	1	TRA6_BURCE	P24575 burkholderia
37	67.5	8.0	778	1	RG12_MOUSE	061193 mus musculus
38	67.5	8.0	1564	1	PDRA_YEAST	P51593 saccharomyces
39	67	7.9	551	1	CH60_BUCAP	Q59177 buchnera ap
40	67	7.9	622	1	FACG_HUMAN	015287 homo sapiens
41	67	7.9	747	1	ATCS_SYNP7	P37279 synechococcus
42	67	7.9	1228	1	ATC_PLAFK	008853 plasmodium
43	66.5	7.9	309	1	YBCK_HAEIN	P44298 haemophilus
44	66.5	7.9	511	1	P60_LISGR	001835 listeria gr
45	66.5	7.9	531	1	TRPE_ARTGO	P96556 arthrobacter

ALIGNMENTS

RESULT 1
EPO_HUMAN STANDARD: PRT: 193 AA.
ID EPO_HUMAN
AC P01588; Q9UHA0; Q9UEZ5; Q9UDZ0;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Erythropoietin precursor (Epoetin).
GN EPO.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85137899; PubMed=3838366;
RA Jacobs K., Shoemaker C., Ruderstorf R., Neill S.D., Kaufman R.J.,
RA Mufson A., Seehra J., Jones S.S., Hewick R., Fritsch E.F.,
RA Kawakita M., Shimizu T., Miyake T.,
RT Isolation and characterization of genomic and cDNA clones of human
RT erythropoietin.
RL Nature 313:806-810(1985).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=86067948; PubMed=3865178;
RA Lin F.-K., Suggs S., Lin C.-H., Browne J.K., Smalling R., Egrie J.C.,
RA Chen K.K., Fox G.M., Martin F., Stabinsky Z., Badrawi S.M., Lai P.-H.,
RA Goldwasser E.,
RT Cloning and expression of the human erythropoietin gene.
RL Proc. Natl. Acad. Sci. U.S.A. 82:7580-7584(1985).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=99018118; PubMed=9799793;
RA Gloeckner G., Scherer S., Schattevoy R., Boright A., Weber J.,
RA Tsui L.-C., Rosenthal A.,
RT Large-scale sequencing of two regions in human chromosome 7q22:
RT analysis of 650 kb of genomic sequence around the EPO and CUTL1 loci
RT reveals 17 genes.
RL Genome Res. 8:1060-1073(1998).
RN [4]
RP SEQUENCE FROM N.A.
RA Rupert J.L., Hochachka P.W.,
RT Erythropoietin gene sequence in the Quechua, a high altitude native
RT population.
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE OF 58-193 FROM N.A., AND VARIANTS HEPATOCELLULAR CARCINOMA.
RX MEDLINE=93384593; PubMed=8396923;
RA Funakoshi A., Muta H., Baba T., Shimizu S.,
RT Gene expression of mutant erythropoietin in hepatocellular
RT carcinoma.
RL Biochem. Biophys. Res. Commun. 195:717-722(1993).
RN [6]
RP SEQUENCE OF 28-193, AND DISULFIDE BONDS.
RX TISSUE-Urine; PubMed=3949763;
RX MEDLINE=86140080; PubMed=3949763;

16-OCT-2001 (Rel. 40, last annotation update)
 Erythropoietin precursor.
 GN EPO.
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 CC NCBI_TaxId=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Mistral; TISSUE=Kidney;
 RX MEDLINE=93042015; PubMed=1420369;
 RA Nagao M., Suga H., Okano M., Masuda S., Narita H., Ikura K.,
 RA Sasaki R.;
 RT "Nucleotide sequence of rat erythropoietin.";
 RL Blochim. Biophys. Acta 1171:99-102(1992).
 RN [2]
 RP SEQUENCE OF 4-192 FROM N.A.
 RC STRAIN-Sprague-Dawley; TISSUE=Kidney;
 RX MEDLINE=93372347; PubMed=8364201;
 RA Wen D., Boissel J.P.R., Tracy T.E., Mulcahy L.S., Czelusniak J.,
 RA Goodman M., Bunn H.F.;
 RT "Erythropoietin structure-function relationships: high degree of
 RT sequence homology among mammals.";
 RL Blood 82:1507-1516(1993).
 CC -1- FUNCTION: ERYTHROPOIETIN IS THE PRINCIPAL HORMONE INVOLVED IN THE
 CC REGULATION OF ERYTHROCYTE DIFFERENTIATION AND THE MAINTENANCE OF A
 CC PHYSIOLOGICAL LEVEL OF CIRCULATING ERYTHROCYTE MASS.
 CC -1- TISSUE SPECIFICITY: PRODUCED BY KIDNEY OR LIVER OF ADULT MAMMALS
 CC AND BY LIVER OF FETAL OR NEONATAL MAMMALS.
 CC -1- SIMILARITY: BELONGS TO THE EPO / TPO FAMILY.
 CC -----
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 CC -----
 DR EMBL: D10763; BAA01593.1; -;
 DR EMBL: L10608; AAA41126.1; -;
 DR PIR: S28148; S28148.
 DR HSSP: P01588; ICN4.
 DR InterPro: IPR001323; EPO_TPO.
 DR InterPro: IPR003013; Erythropo.
 DR Pfam: PF00758; EPO_TPO.1.
 DR PRINTS: PR00272; ERYTHROPTN.
 DR PROSITE: PS00817; EPO_TPO.1.
 DR Erythrocyte maturation; Glycoprotein; Hormone; Signal.
 KM SIGNAL
 FT CHAIN 1 26
 FT CHAIN 27 192
 FT DISULFID 33 187
 FT CARBOHYD 50 50
 FT CARBOHYD 64 64
 FT CARBOHYD 109 109
 FT SEQUENCE 192 AA; 21286 MW; 3EA632737E7D2443 CRC64;
 Query Match 81.1%; Score 692; DB 1; Length 192;
 Best Local Similarity 81.3%; Pred. No. 3,8e-63;
 Matches 135; Conservative 12; Mismatches 19; Indels 0; Gaps 0;
 QY 1 APRRLICDSRVLYRLLEKAEKENTTGCAGHCSEINENTVPTDKVNFYAMRNKNSXQA 60
 DB 27 APRRLICDSRVLYRLLEKAEKENTTGCAGHCSEINENTVPTDKVNFYAMRNKNSXQA 86
 QY 61 VEWGGLALLSAVLRGQALLVNSSQWPEPLDHYDKAVSGIRSLTTLRLAAGAKREAS 120
 DB 87 VEWGGLALLSAVLRGQALLVNSSQWPEPLDHYDKAVSGIRSLTTLRLAAGAKREAS 146
 QY 121 PPDAAASAPLRTITADTFKRLFRVYSNFKGLKLYTGACRTGR 166
 DB 147 PPDAAASAPLRTITADTFKRLFRVYSNFKGLKLYTGACRTGR 192

RESULT 5
 EPO_FELCA
 ID EPO_FELCA STANDARD: PRT: 192 AA.
 AC P33708;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-OCT-1996 (Rel. 34, last sequence update)
 DT 16-OCT-2001 (Rel. 40, last annotation update)
 DE Erythropoietin precursor.
 GN EPO.
 OS Felis silvestris catus (Cat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 CC NCBI_TaxId=9685;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RA Goodman R.E., Bell R.G.;
 RL Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 5-192 FROM N.A.
 RX MEDLINE=93372347; PubMed=8364201;
 RA Wen D., Boissel J.P.R., Tracy T.E., Gruninger R.H., Mulcahy L.S.,
 RA Czelusniak J., Goodman M., Bunn H.F.;
 RT "Erythropoietin structure-function relationships: high degree of
 RT sequence homology among mammals.";
 RL Blood 82:1507-1516(1993).
 CC -1- FUNCTION: ERYTHROPOIETIN IS THE PRINCIPAL HORMONE INVOLVED IN THE
 CC REGULATION OF ERYTHROCYTE DIFFERENTIATION AND THE MAINTENANCE OF A
 CC PHYSIOLOGICAL LEVEL OF CIRCULATING ERYTHROCYTE MASS.
 CC -1- TISSUE SPECIFICITY: PRODUCED BY KIDNEY OR LIVER OF ADULT MAMMALS
 CC AND BY LIVER OF FETAL OR NEONATAL MAMMALS.
 CC -1- SIMILARITY: BELONGS TO THE EPO / TPO FAMILY.
 CC -----
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 CC or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL: U00685; AAA18282.1; -;
 DR EMBL: L10606; AAA30807.1; -;
 DR HSSP: P01588; ICN4.
 DR InterPro: IPR001323; EPO_TPO.
 DR InterPro: IPR003013; Erythropo.
 DR Pfam: PF00758; EPO_TPO.1.
 DR PRINTS: PR00272; ERYTHROPTN.
 DR PROSITE: PS00817; EPO_TPO.1.
 DR Erythrocyte maturation; Glycoprotein; Hormone; Signal.
 KM SIGNAL
 FT CHAIN 1 26
 FT CHAIN 27 192
 FT DISULFID 33 187
 FT CARBOHYD 50 50
 FT CARBOHYD 64 64
 FT CARBOHYD 109 109
 FT CONFLICT 44 44
 FT SEQUENCE 192 AA; 20914 MW; 61C5EA0F5E937293 CRC64;
 Query Match 81.6%; Score 688; DB 1; Length 192;
 Best Local Similarity 81.9%; Pred. No. 9,6e-63;
 Matches 136; Conservative 8; Mismatches 22; Indels 0; Gaps 0;
 QY 1 APRRLICDSRVLYRLLEKAEKENTTGCAGHCSEINENTVPTDKVNFYAMRNKNSXQA 60
 DB 27 APRRLICDSRVLYRLLEKAEKENTTGCAGHCSEINENTVPTDKVNFYAMRNKNSXQA 86
 QY 61 VEWGGLALLSAVLRGQALLVNSSQWPEPLDHYDKAVSGIRSLTTLRLAAGAKREAS 120

DB 87 VEWGQIALLEALIRGQALLANSSOPSEFTQLHVDKAVSSLSLTSLLALCAQKEATS 146

QY 121 PPDAASAPLRITTTADTFERKLFVRYSNFKLTKLYTGACRTGDR 166

DB 147 LPBATSAPLRITFTVDTLCKLFRIYSNFKLTKLYTGACRGRDR 192

RESULT 6

EPO_BOVIN

ID EPO_BOVIN STANDARD; PRT; 192 AA.

AC P48617;

DT 01-FEB-1996 (Rel. 33, Created)

DT 01-FEB-1996 (Rel. 33, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Erythropoietin precursor.

GN EPO.

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Bovidae; Bovinae; Bos.

NCBI_TaxID=9913;

ON (1)

RP SEQUENCE FROM N.A.

RC STRAIN=Bozan; Tissue=Kidney;

RX MEDLINE=96257233; PubMed=8666286;

RA Sullivan H.B., Majliva P.A.O., Feldman B.F., Mertens B.,

RA Logan-Henfrey L.L.;

RT "Cloning of a cDNA encoding bovine erythropoietin and analysis of its

RT transcription in selected tissues.";

RL Gene 171:275-280(1996).

CC -1- FUNCTION: ERYTHROPOIETIN IS THE PRINCIPAL HORMONE INVOLVED IN THE

CC REGULATION OF ERYTHROCYTE DIFFERENTIATION AND THE MAINTENANCE OF A

CC PHYSIOLOGICAL LEVEL OF CIRCULATING ERYTHROCYTE MASS.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- TISSUE SPECIFICITY: PRODUCED BY KIDNEY OR LIVER OF ADULT MAMMALS

CC AND BY LIVER OF FETAL OR NEONATAL MAMMALS.

CC -1- SIMILARITY: BELONGS TO THE EPO / TPO FAMILY.

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CC or send an email to license@isb-sib.ch).

CC -----

DR EMBL: L41354; AAA841268.1; -

DR EMBL: U44762; AAA86653.1; -

DR HSSP: P01588; 1CM4.

DR InterPro: IPR001323; EPO_TPO.

DR InterPro: IPR003013; Erythropo.

DR Pfam: PF00758; EPO_TPO; 1.

DR PRINTS: PR00272; ERYTHROPTN.

DR PROSITE: PS00817; EPO_TPO; 1.

KW Erythrocyte maturation; Glycoprotein; Hormone; Signal.

FT SIGNAL 1 25

FT CHAIN 26 192

FT DISULFID 32 187

FT DISULFID 54 58

FT CARBOHYD 49 49

FT CARBOHYD 63 63

FT CARBOHYD 108 108

SEQUENCE 192 AA: 21075 MW: DBC419022F7B483A CRC64:

Query Match 80.6%; Score 679.5; DB 1; Length 192;

Best Local Similarity 81.4%; Pred. No. 7e-62;

Matches 136; Conservative 8; Mismatches 22; Indels 1; Gaps 1;

QY 1 APPRLICDSRVLERYLLLEAKENITTCGAHCSLNMENITVPDTKYNFYAMKRNXSXQA 60

DB 26 APARLICDSRVLERYLLLEAKENITTCGAHCSLNMENITVPDTKYNFYAMKRNMEVQQA 85

QY 61 VEWGQIALLEALIRGQALLANSSOPSEFTQLHVDKAVSSLSLTSLLALCAQKEATS 120

DB 86 LEWQGIALLEALIRGQALLANSSOPSEFTQLHVDKAVSSLSLTSLLALCAQKEATS 145

QY 121 PPDAASAPLRITTTADTFERKLFVRYSNFKLTKLYTGACRTGDR 166

DB 146 LPBATSAPLRITFTVDTLCKLFRIYSNFKLTKLYTGACRGRDR 192

RESULT 7

EPO_MOUSE

ID EPO_MOUSE STANDARD; PRT; 192 AA.

AC P07321;

DT 01-APR-1988 (Rel. 07, Created)

DT 01-APR-1988 (Rel. 07, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Erythropoietin precursor.

GN EPO.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI_TaxID=10090;

ON (1)

RP SEQUENCE FROM N.A.

RC STRAIN=ICFW;

RX MEDLINE=87039105; PubMed=3773894;

RA Shoemaker C.B., Miltsock L.D.;

RT "Murine erythropoietin gene: cloning, expression, and human gene

RT homology.";

RL Mol. Cell. Biol. 6:849-858(1986).

CC -1- FUNCTION: ERYTHROPOIETIN IS THE PRINCIPAL HORMONE INVOLVED IN THE

CC REGULATION OF ERYTHROCYTE DIFFERENTIATION AND THE MAINTENANCE OF A

CC PHYSIOLOGICAL LEVEL OF CIRCULATING ERYTHROCYTE MASS.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- TISSUE SPECIFICITY: PRODUCED BY KIDNEY OR LIVER OF ADULT MAMMALS

CC AND BY LIVER OF FETAL OR NEONATAL MAMMALS.

CC -1- SIMILARITY: BELONGS TO THE EPO / TPO FAMILY.

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CC -----

DR EMBL: M12482; AAA37568.1; -

DR EMBL: M12930; AAA37570.1; -

DR EMBL: AF312033; AK28825.1; -
 DR EMBL: Y11971; CA472707.1; -
 DR PIR: A24901; A24901.
 DR PIR: A24902; A24902.
 DR HSSP: P01588; ICNA.
 DR MGD: MGI:95407; EPO.
 DR InterPro: IPR001323; EPO_TPO.
 DR InterPro: IPR003013; Erythropo.
 DR Pfam: PF00758; EPO_TPO.1.
 DR PRINTS: PR00272; ERYTHROPTN.
 DR PROSITE: PS00817; EPO_TPO.1.
 KW Erythrocyte maturation; Glycoprotein; Hormone; signal.
 FT SIGNAL 1 26
 FT CHAIN 27 192
 FT DISULFID 33 187 BY SIMILARITY.
 FT CARBOHYD 50 50 N-LINKED (GLCNAC. . .) (BY SIMILARITY).
 FT CARBOHYD 64 64 N-LINKED (GLCNAC. . .) (BY SIMILARITY).
 FT CARBOHYD 109 109 N-LINKED (GLCNAC. . .) (BY SIMILARITY).
 SQ SEQUENCE 192 AA: 21365 MW: 6594E214E0DEF2E CRC64;

Query Match 80.2%; Score 676; DB 1; Length 192;
 Best Local Similarity 78.3%; Pred. No. 1.6e-61;
 Matches 130; Conservative 14; Mismatches 22; Indels 0; Gaps 0;

OY 1 APPRLICDSRVLYERLYLEAKKENTTTCAGHCISNENITVPDTKYVNYAMKRNKXQQA 60
 DB 27 APPRLICDSRVLYERLYLEAKKENTTTCAGHCISNENITVPDTKYVNYAMKRNKXQQA 86
 OY 61 VEWMOGLALISPAVLRGQALLVNSSOPWEPQLQVHDKAVSGIRSLTTLRALGAQKEAIS 120
 DB 87 LEVMOGLALISPAVLRGQALLVNSSOPWEPQLQVHDKAVSGIRSLTTLRALGAQKEAIS 146
 OY 121 PPDAASAPLRTITADTFRKLFYVSNFLRGKLLKLYTGACRTGDR 166
 DB 147 PDDTTPAPALRTITVDTFCKLFRVYANFLRGKLLKLYTGACRTGDR 192

RESULT 8

EPO_SHEEP STANDARD; PRT; 194 AA.

AC P33709; Q28572;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Erythropoietin precursor.
 GN EPO.
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 OX NCBI_TaxID:9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Kidney;
 RX MEDLINE:93372347; PubMed:8349021;
 RA Fu P., Evans B., Lim G.B., Moritz K., Wintour M.E.;
 RT "The sheep erythropoietin gene: molecular cloning and effect of
 hemorrhage on plasma erythropoietin and renal/liver messenger RNA in
 adult sheep.";
 RL Mol. Cell. Endocrinol. 93:107-116(1993).
 RL [2]
 RN SEQUENCE OF 4-194 FROM N.A.
 RC TISSUE-Kidney;
 RX MEDLINE:93372347; PubMed:8364201;
 RA Wen D., Boissel J.P.R., Tracy T.E., Gruninger R.H., Mulcahy L.S.,
 RT Czelusniak J., Goodman M., Bunn H.F.;
 RT "Erythropoietin structure-function relationships: high degree of
 sequence homology among mammals.";
 RL Blood 82:1507-1516(1993).
 CC -I- FUNCTION: ERYTHROPOIETIN IS THE PRINCIPAL HORMONE INVOLVED IN THE
 CC REGULATION OF ERYTHROCYTE DIFFERENTIATION AND THE MAINTENANCE OF A
 CC PHYSIOLOGICAL LEVEL OF CIRCULATING ERYTHROCYTE MASS.
 CC -I- SUBCELLULAR LOCATION: Secreted.

CC -I- TISSUE SPECIFICITY: PRODUCED BY KIDNEY OR LIVER OF ADULT MAMMALS
 CC AND BY LIVER OF FETAL OR NEONATAL MAMMALS.

CC -I- SIMILARITY: BELONGS TO THE EPO / TPO FAMILY.

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DR EMBL: Z24681; CA480848.1; -
 DR EMBL: L10610; AAA31518.1; -
 DR HSSP: P01588; ICNA.
 DR InterPro: IPR001323; EPO_TPO.
 DR InterPro: IPR003013; Erythropo.
 DR Pfam: PF00758; EPO_TPO.1.
 DR PRINTS: PR00272; ERYTHROPTN.
 DR PROSITE: PS00817; EPO_TPO.1.
 KW Erythrocyte maturation; Glycoprotein; Hormone; signal.
 FT SIGNAL 1 27
 FT CHAIN 28 194
 FT DISULFID 34 189 BY SIMILARITY.
 FT CARBOHYD 51 51 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 65 65 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 110 110 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 16 16 F -> L (IN REF. 2).
 FT CONFLICT 108 108 L -> P (IN REF. 2).
 SQ SEQUENCE 194 AA: 21335 MW: C025AAB0528131A9 CRC64;

Query Match 79.8%; Score 672.5; DB 1; Length 194;
 Best Local Similarity 80.2%; Pred. No. 3.7e-61;
 Matches 134; Conservative 9; Mismatches 23; Indels 1; Gaps 1;

OY 1 APPRLICDSRVLYERLYLEAKKENTTTCAGHCISNENITVPDTKYVNYAMKRNKXQQA 60
 DB 28 APPRLICDSRVLYERLYLEAKKENTTTCAGHCISNENITVPDTKYVNYAMKRNKXQQA 87
 OY 61 VEWMOGLALISPAVLRGQALLVNSSOPWEPQLQVHDKAVSGIRSLTTLRALGAQKEAIS 120
 DB 88 LEVMOGLALISPAVLRGQALLVNSSOPWEPQLQVHDKAVSGIRSLTTLRALGAQKEAIS 147
 OY 121 PPDAASAPLRTITADTFRKLFYVSNFLRGKLLKLYTGACRTGDR 166
 DB 148 LPDAPPSAPLRTITVDTFCKLFRVYANFLRGKLLKLYTGACRTGDR 194

RESULT 9

EPO_PIG STANDARD; PRT; 190 AA.

AC P49157;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Erythropoietin precursor (Fragment).
 GN EPO.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID:9623;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Kidney;
 RX MEDLINE:93372347; PubMed:8364201;
 RA Wen D., Boissel J.P.R., Tracy T.E., Gruninger R.H., Mulcahy L.S.,
 RT Czelusniak J., Goodman M., Bunn H.F.;
 RT "Erythropoietin structure-function relationships: high degree of
 sequence homology among mammals.";
 RL Blood 82:1507-1516(1993).
 CC -I- FUNCTION: ERYTHROPOIETIN IS THE PRINCIPAL HORMONE INVOLVED IN THE
 CC REGULATION OF ERYTHROCYTE DIFFERENTIATION AND THE MAINTENANCE OF A

CC	-1	TISSUE SPECIFICITY: PRODUCED BY KIDNEY OR LIVER OF ADULT MAMMALS
CC	-1	AND BY LIVER OF FETAL OR NEONATAL MAMMALS.
CC	-1	SIMILARITY: BELONGS TO THE EPO / TPO FAMILY.
CC	-1	THIS SWISS-PROT entry is copyright. It is produced through a collaboration
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CC	-1	the European Bioinformatics Institute. There are no restrictions on its
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CC	-1	entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC	-1	or send an email to license@isb-sib.ch).
CC	-1	-----
DR	EMBL: L13027; AAA30842.1; -	
DR	HSSP; P01588; ICN4.	
DR	InterPro: IPR001323; EPO_TPO.	
DR	Pfam: PF00758; EPO_TPO; 1.	
DR	PROSITE: PS00817; EPO_TPO; 1.	
KW	Erythrocyte maturation; Glycoprotein; Hormone; signal.	
FT	NON_TER	1
FT	SIGNAL	<1 22
FT	CHAIN	23 >175
FT	DISULFID	29 >175
FT	DISULFID	51 55
FT	CARBOHYD	46 46
FT	CARBOHYD	60 60
FT	CARBOHYD	105 105
FT	NON_TER	175 175
SQ	SEQUENCE	175 AA; 19193 MW; B504F8DE6676BF4 CRC64;
Qy	1	APPRICDSRYLERYLLTAKKAEENTTTCGAEHCSTLNENTVPTDPTVYNKYAMKRNKXSXQA 60
Db	23	APPRICGSRYLERYLLTAKKAEENTTTCGAEHCSTLNENTVPTDPTVYNKYAMKRNKXSXQA 82
Qy	61	VEWVGALLSEAVYLRGQALLVYNSQSPQPELQJHYDKAVSGHSLTTLRLAAGAKKAS 120
Db	83	LEWVGALLSEAVYLRGQALLVYNSQSPQPELQJHYDKAVSGHSLTTLRLAAGAKKAS 142
Qy	121	PPDASAPLRTITADTFRKLFYVSNFLRGKL 153
Db	143	LPEASAPLRTITADTFRKLFYVSNFLRGKL 175

RESULT 11

ID	TPO_CANFA	STANDARD:	PRT:	352 AA.
AC	P42705;			
DT	01-NOV-1995 (Rel. 32, Created)			
DT	01-NOV-1995 (Rel. 32, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Thrombopoietin precursor (Megakaryocyte colony stimulating factor) (C-MPL ligand) (ML) (Megakaryocyte growth and development factor) (MGDF).			
GN	THPO OR TPO.			
OS	Canis familiaris (Dog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.			
OX	NCBI_taxid=9615;			
RP	[1]			
RC	SEQUENCE FROM N.A., AND SEQUENCE OF 24-44.			
RC	TISSUE=Kidney;			
RX	MEDLINE=94291201; PubMed=8020099;			
RA	Battley T.D., Bogenberger J., Hunt P., Li Y.-S., Lu H.S., Martin F.,			
RA	Chang M.-S., Samal B.B., Nichol J.L., Swift S., Johnson M.J.,			
RA	Hsu R.-Y., Parker V.P., Suggs S., Skrine J.D., Merewether L.A.,			
RA	Clogson C., Hsu E., Horkov M.M., Horkov A., Choi E., Pangelinan M.,			
RA	Sun Y., Mar Y., McNich J., Simonet L., Jacobsen F., Xie C.,			
RA	Shutter J., Chute H., Basu R., Selander L., Trollinger D., Siew L.,			
RA	Padilla D., Trall G., Elliott G., Izumi R., Covey T., Crouse J.,			
RA	Garcia A., Xu W., del Castillo J., Biron J., Cole S., Hu M.C.-T.,			

RA Pacific R., Ponting I., Saris C., Wen D., Yung Y.P., Lin H.,
 RA Bosseman R.A.:
 RT "Identification and cloning of a megakaryocyte growth and development
 RT factor that is a ligand for the cytokine receptor Mpl.";
 RL Cell 77:1117-1117(1994).
 CC -1- FUNCTION: LINEAGE-SPECIFIC CYTOKINE AFFECTING THE PROLIFERATION
 CC AND MATURATION OF MEGAKARYOCYTES FROM THEIR COMMITTED PROGENITOR
 CC CELLS. IT ACTS AT A LATE STAGE OF MEGAKARYOCYTE DEVELOPMENT. IT
 CC MAY BE THE MAJOR PHYSIOLOGICAL REGULATOR OF CIRCULATING PLATELETS.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- DOMAIN: TWO-DOMAIN STRUCTURE WITH AN ERYTHROPOIETIN-LIKE N-
 CC -1- TERMINAL AND A SER/PRO/THR-RICH C-TERMINAL.
 CC -1- SIMILARITY: BELONGS TO THE EPO / TPO FAMILY.
 DR InterPro: IPR001323; EPO_TPO.
 DR InterPro: IPR003978; thrombopoietin.
 DR Pfam: PF00758; EPO_TPO.1.
 DR PRINTS: PR01485; THROMBOPTN.
 DR PROSITE: PS00817; EPO_TPO.1.
 KM Cytokine; Glycoprotein; Hormone; Signal.
 FT SIGNAL 1 23
 FT CHAIN 24 352 THROMBOPOIETIN.
 FT DISULFID 28 172 POTENTIAL.
 FT DISULFID 50 106 POTENTIAL.
 FT CARBOHYD 185 185 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 206 206 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 255 255 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 347 347 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SO SEQUENCE 352 AA; 73641 MW; 024F3B41B061FBDB8 CRC64;
 Query Match 13.0%; Score 110; DB 1; Length 352;
 Best Local Similarity 24.0%; Pred. NO. 0.0011;
 Matches 40; Conservative 22; Mismatches 63; Indels 42; Gaps 5;
 Oy 1 APPRLICDSRVLEKLEKKEKNTTGCAGKSLNENTVVDVTNPFAMKRNKXQQA 60
 Db 24 APP--ACDPRLNKMRLSHVLSRLSOPDIPPLSTPLVAVDFSLGEMTQREQTKA 81
 Oy 61 VFWOGLALISEAVL--RQALLVNNSQWPEPLQLHVDKAVSLSTLTLLALGAKKA 118
 Db 82 ODWCAVALLDGVLAARKQL-----GPSCLSLALQQLSGQVAL 120
 Oy 119 I-----SPDAAASAPRLRTTADTFERKLFRRVYSNFKLKLK 154
 Db 121 LLAGLGLGLGTQLPPG-----RTTHKDPNALFLSFGQLLRGKVR 161
 RESULT 12
 ID TPO_HUMAN STANDARD; PRT; 353 AA.
 AC P40225; Q13020; Q15790; Q15791; Q15792;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Thrombopoietin precursor (Megakaryocyte colony stimulating factor)
 DE (Myeloproliferative leukemia virus oncogene ligand) (C-mpl ligand)
 DE (Mpl) (Megakaryocyte growth and development factor) (MGDF).
 GN THPO.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Fetal liver;
 RX MEDLINE=94261202; PubMed=8202154;
 RA de Sauvage F.J., Haas P.E., Spencer S.D., Malloy B.E., Gurney A.L.,
 RA Spencer S.A., Darbonne W.C., Henzel W.J., Wong S.C., Kuang W.-J.,
 RA Oles K.J., Hultgren B., Solberg L.A. Jr., Goeddel D.V., Eaton D.L.:
 RT "Stimulation of megakaryocytopoiesis and thrombopoiesis by the c-Mpl
 RL ligand.";
 RL Nature 369:533-538(1994).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Fetal liver;
 RX MEDLINE=94291202; PubMed=8020099;
 RA Bartley T.D., Bogenberger J., Hunt P., Li Y.-S., Lu H.S., Martin F.,
 RA Chang M.-S., Samal B.B., Nichol J.L., Swift S., Johnson M.J.,
 RA Hsu R.-Y., Parker V.P., Sugis S., Skrine J.D., Merewether L.A.,
 RA Closson C., Hsu E., Hokom M.M., Hornkohl A., Choi E., Pangellian M.,
 RA Sun Y., Mar V., McNich J., Simonet L., Jacobsen F., Xie C.,
 RA Shutter J., Chute H., Basu R., Selander L., Trollinger D., Siu L.,
 RA Padilla D., Trail G., Elliott G., Izumi R., Covey T., Crouse J.,
 RA Garcia A., Xu W., del Castillo J., Biron J., Cole S., Hu M.C.-T.,
 RA Pacific R., Ponting I., Saris C., Wen D., Yung Y.P., Lin H.,
 RA Bosseman R.A.:
 RT "Identification and cloning of a megakaryocyte growth and development
 RT factor that is a ligand for the cytokine receptor Mpl.";
 RL Cell 77:1117-1124(1994).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=95108091; PubMed=7809166;
 RA Foster D.C., Sprecher C.A., Grant F.J., Kramer J.M., Kuipper J.L.,
 RA Holly R.D., Whitmore T.E., Heipel M.D., Bell L.A.N., Ching A.F.,
 RA McGlane V., Hart C., O'Hara P.J., Lok S.,
 RT "Human thrombopoietin: gene structure, cDNA sequence, expression, and
 RT chromosomal localization.";
 RL Proc. Natl. Acad. Sci. U.S.A. 91:13023-13027(1994).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=95010765; PubMed=7926023;
 RA Sohma Y., Akahori H., Seki N., Hori T.-A., Ogami K., Kawamura K.,
 RA Miyazaki H.:
 RT "Molecular cloning and chromosomal localization of the human
 RT thrombopoietin gene.";
 RL FEBS Lett. 353:57-61(1994).
 RN [5]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RX MEDLINE=95152076; PubMed=7849319;
 RA Gurney A.L., Kuang W.-J., Xie M.-H., Malloy B.E., Eaton D.L.,
 RA de Sauvage F.J.:
 RT "Genomic structure, chromosomal localization, and conserved
 RT alternative splice forms of thrombopoietin.";
 RL Blood 85:981-988(1995).
 RN [6]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Liver;
 RX MEDLINE=96015174; PubMed=8537317;
 RA Kato T., Ogami K., Shimada Y., Iwamatsu A., Sohma Y., Akahori H.,
 RA Hori K., Kokubo A., Kudo Y., Maeda E., Kobayashi K., Ohashi H.,
 RA Ozawa T., Inoue H., Kawamura K., Miyazaki H.:
 RT "Purification and characterization of thrombopoietin.";
 RL J. Biochem. 118:229-236(1995).
 RN [7]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Placenta;
 RX MEDLINE=95122483; PubMed=7822271;
 RA Chang M., McNinch J., Basu R., Shutter J., Hsu R., Perkins C., Mar V.,
 RA Sungs S., Welcher A., Li L., Lu H., Bartley T., Hunt P., Martin F.,
 RA Samal B., Bogenberger J.:
 RT "Cloning and characterization of the human megakaryocyte growth and
 RT development factor (MGDF) gene.";
 RL J. Biol. Chem. 270:511-514(1995).
 RN [8]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 3).
 RC TISSUE=Fetal liver;
 RX MEDLINE=95122483; PubMed=7822271;
 RA "Cloning and sequencing of human thrombopoietin.";
 RL Submitted (May-1996) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: LINEAGE-SPECIFIC CYTOKINE AFFECTING THE PROLIFERATION
 CC AND MATURATION OF MEGAKARYOCYTES FROM THEIR COMMITTED PROGENITOR
 CC CELLS. IT ACTS AT A LATE STAGE OF MEGAKARYOCYTE DEVELOPMENT. IT
 CC MAY BE THE MAJOR PHYSIOLOGICAL REGULATOR OF CIRCULATING PLATELETS.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS; 1 (SHOWN HERE), 2/TPO-2 AND


```

CC 3/TUNCATED: ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- DOMAIN: TWO-DOMAIN STRUCTURE WITH AN ERYTHROPOIETIN-LIKE N-
CC TERMINAL AND A SER/PRO/THR-RICH C-TERMINAL.
CC -1- SIMILARITY: BELONGS TO THE EPO / TPO FAMILY.
CC -1- DATABASE: NAME-RESD SYSTEMS' cytokine source book: TPO:
CC WWW="http://www.rndsystems.com/asp/g_sitbuilder.asp?bodyid=225".
CC -----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: L33410; AAA59857.1; -
DR EMBL: U11025; AAA50553.1; -
DR EMBL: L36051; AAC37568.1; -
DR EMBL: L36052; AAC37566.1; -
DR EMBL: D32046; BAA06807.1; -
DR EMBL: S76771; AAB33390.1; -
DR EMBL: D32047; BAA21930.1; -
DR EMBL: U59493; AAB03392.1; -
DR EMBL: U59494; AAB03393.1; -
DR EMBL: U59495; AAB03394.1; -
DR EMBL: U17071; AAA74083.1; -
DR PIR: S45331; S45331.
DR Gene: HGNC:11795; THPO.
DR MIM: 600044; -
DR InterPro: IPR001333; EPO_TPO.
DR InterPro: IPR003978; Thrombopoietin.
DR Pfam: PF00758; EPO_TPO; 1.
DR PRINTS: PR01485; THROMBOPTN.
DR PROSITE: PS00817; EPO_TPO; 1.
KM Cytokine; Glycoprotein; Hormone; Signal; Alternative splicing;
KW Polymorphism.
FT SIGNAL 1 21
FT CHAIN 22 353
FT DISULFID 28 172
FT CARBOHYD 50 106
FT CARBOHYD 197 197
FT CARBOHYD 206 206
FT CARBOHYD 234 234
FT CARBOHYD 235 235
FT CARBOHYD 340 340
FT CARBOHYD 348 348
FT VARSPPLIC 133 136
FT VARSPPLIC 160 198
FT VARIANT 14 14
FT VARIANT 14 14
FT VARIANT 116 116
FT CONFLICT 46 46
FT CONFLICT 76 76
FT CONFLICT 113 113
FT CONFLICT 131 131
FT CONFLICT 277 277
FT CONFLICT 346 346
SQ SEQUENCE 353 AA: 37822 MW: F0AB5449B72E5526 CRC64;

Query Match 11.0%; Score 93; DB 1; Length 353;
Best Local Similarity 26.3%; Pred. No. 0.057;
Matches 41; Conservative 20; Mismatches 75; Indels 20; Gaps 5;

```

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DB 133 -LPPQG-----RTYAKKDPAIFLSPFHLLRQKVR 161
RESULT 13
TPO_RAT ID TPO_RAT STANDARD; PRT; 326 AA.
AC P49745;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Thrombopoietin precursor.
GN THPO.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxId:10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=9531639; Pubmed=7607561;
RA Ogami K., Shimada Y., Sohma Y., Akahori H., Kato T., Kawamura K.,
RA Miyazaki H.:
RT "The sequence of a rat cDNA encoding thrombopoietin."
RL Gene 158:309-310(1995).
CC -1- FUNCTION: LINEAGE-SPECIFIC CYTOKINE AFFECTING THE PROLIFERATION
CC AND MATURATION OF MEGAKARYOCYTES FROM THEIR COMMITTED PROGENITOR
CC CELLS. IT ACTS AT A LATE STAGE OF MEGAKARYOCYTE DEVELOPMENT. IT
CC MAY BE THE MAJOR PHYSIOLOGICAL REGULATOR OF CIRCULATING PLATELETS.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DOMAIN: TWO-DOMAIN STRUCTURE WITH AN ERYTHROPOIETIN-LIKE N-
CC TERMINAL AND A SER/PRO/THR-RICH C-TERMINAL.
CC -1- SIMILARITY: BELONGS TO THE EPO / TPO FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: D32207; BAA06906.1; -
DR InterPro: IPR001323; EPO_TPO.
DR InterPro: IPR003978; Thrombopoietin.
DR Pfam: PF00758; EPO_TPO; 1.
DR PRINTS: PR01485; THROMBOPTN.
DR PROSITE: PS00817; EPO_TPO; 1.
KM Cytokine; Glycoprotein; Hormone; Signal.
KW Cytokine; Glycoprotein; Hormone; Signal.
FT SIGNAL 1 21
FT CHAIN 22 326
FT DISULFID 28 172
FT CARBOHYD 50 106
FT CARBOHYD 197 197
FT CARBOHYD 206 206
FT CARBOHYD 235 235
FT CARBOHYD 249 249
FT CARBOHYD 256 256
SQ SEQUENCE 326 AA: 34556 MW: F99D7F77F8956F2C CRC64;

Query Match 9.3%; Score 78; DB 1; Length 326;
Best Local Similarity 22.3%; Pred. No. 1.7;
Matches 37; Conservative 22; Mismatches 65; Indels 42; Gaps 6;

```

DB 122 LGALGLCTQLPPOG-----RTAHKDPSSALFLSLQOLLRKVR 161

RESULT 14

CH60_BABBA STANDARD: PRT: 543 AA.

ID CH60_BABBA

AC P3635:

DT 01-JUN-1994 (Rel. 29, Created)

DT 01-JUN-1994 (Rel. 29, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE 60 kDa chaperonin (protein Cpn60) (groEL protein) (Immunoreactive protein Bb65) (Immunoreactive protein Bb63) (Heat shock protein 60) (HSP 60).

GN GROEL OR MOGA OR GROEL OR 7b2 OR Bb65 OR Bb63.

OS Bartonella bacilliformis.

OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group; Bartonellaceae; Bartonella.

OX NCBI_Taxid:774;

RN NCBI_Taxid:774;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-B13;

RA Schreiber M.G.;

RL Submitted (SEP-1992) to the EMBL/Genbank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RA Xu Y., Lu Z., Ihler G.;

RL Submitted (XX-1993) to the EMBL/Genbank/DBJ databases.

RN [3]

RP SEQUENCE OF 1-36.

RX MEDLINE-91052092; PubMed-1700634;

RA Knobloch J., Schreiber M.G.;

RT "Bb65, a major immunoreactive protein of Bartonella bacilliformis."

RL Am. J. Trop. Med. Hyg. 43:373-379(1990).

CC -1- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS CONDITIONS (BY SIMILARITY).

CC -1- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF 7 SUBUNITS (BY SIMILARITY).

CC -1- DISEASE: THIS PROTEIN IS A MAJOR ANTIGEN IN PATIENTS WITH BARTONELLOSIS, AN INFECTIOUS DISEASE ENDEMIC IN HIGH ALTITUDE VALLEYS OF THE ANDES.

CC -1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.

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CC -----

DR EMBL: 215160; CAA78859.1; -

DR EMBL: M98257; AAA22898.1; -

DR PIR: A60146; A60146.

DR PIR: S37039; S37039.

DR HSPD: P06139; IGRU.

DR InterPro: IPR001844; Chaprinin_Cpn60.

DR InterPro: IPR002423; Cpn60_TCP1.1.

DR Pfam: PF00118; cpn60_TCP1.1.

DR PRINTS: PR00298; CHAPERONIN60.

DR PRINTS: PR00304; TCOMPLEXTCP1.

DR PROSITE: PS00296; CHAPERONINS_CPN60; 1.

DR Chaperone; ATP-binding; Antigen.

FT INIT_MET 0

FT CONFLICT 9 9 R->N (IN REF. 3).

FT CONFLICT 15 15 L->M (IN REF. 3).

FT CONFLICT 33 35 KGR->VGV (IN REF. 3).

FT CONFLICT 240 240 A->V (IN REF. 2).

FT CONFLICT 417 417 P->A (IN REF. 2).

FT CONFLICT 485 485 R->G (IN REF. 2).

SO SEQUENCE 543 AA; 57486 MM; ABB3407033A64D03 CMC64.

Query Match 9.1%; Score 76.5; DB 1; Length 543;

Best Local Similarity 27.0%; Pred. No. 4.6;

Matches 43; Conservative 24; Mismatches 59; Indels 33; Gaps 8;

DB 17 LEAKENITTCACRCSL--NEN--ITVPTKVNFRYAKRNKSXQAAVWVGCLA----- 68

DB 149 ISANGAEDIGKAIADMEKVGNEGVITVEAK-----TATLELVGGMQFDRCY 198

QY 69 LSEAVLRGQALLVNSQPEPLQLHVDKAVGSLRSLTLRALGAQKEAISPDAASA 128

DB 199 LSPYFTNKKMMVDDDDY--ILIH-EKKLSNLSLPVLEAV-----AQSGK 244

QY 129 PLRTTADT-FKLRVYSNFKLKYTGACRTGDR 166

DB 245 PLLIAEDVEGEALATLVNKLKGLKIAVAPGCDR 283

RESULT 15

TPO_MOUSE STANDARD: PRT: 356 AA.

ID TPO_MOUSE

AC P40226;

DT 01-FEB-1995 (Rel. 31, Created)

DT 01-FEB-1995 (Rel. 31, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Thrombopoietin precursor (Megakaryocyte colony stimulating factor) (Mpl) (Megakaryocyte growth and development factor) (MGDF).

GN THPO.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_Taxid:10090;

RN NCBI_Taxid:10090;

RN [1]

RP SEQUENCE FROM N.A. (ISOFORM 1).

RC TISSUE-Kidney;

RX MEDLINE-94261207; PubMed-8202158;

RA Lok S., Kaushansky K., Holly R.D., Kuiper J.L., Lofton-Day C.E., Oort P.J., Grant F.J., Hapel M.D., Burkhed S.K., Kramer J.M., Bell L.A.N., Sprecher C.A., Blumberg H., Johnson R., Prunkard D., Ching A.F.T., Mathews S.L., Bailey M.C., Forstrom J.W., Buddle M.M., Osborn S.G., Evans S.J., Sheppard P.O., Presnell S.R., O'Hara P.J., Hagen F.S., Roth G.J., Foster D.C.;

RT "Cloning and expression of murine thrombopoietin cDNA and stimulation of platelet production in vivo."

RT Nature 369:565-568(1994).

RT [2]

RP SEQUENCE FROM N.A. (ISOFORM 1).

RC TISSUE-Liver;

RX MEDLINE-94291201; PubMed-8020099;

RA Bartley T.D., Bogenberger J., Hunt P., Li Y.-S., Lu H.S., Martin F., Chang M.-S., Samal B.B., Nichol J.L., Swift S., Johnson M.J., Hsu R.-Y., Parker V.P., Suggs S., Skrine J.D., Merewether L.A., Closson C., Hsu E., Horkom M.M., Hornkohl A., Choi E., Pangelinan M., Sun Y., Mar V., McNich J., Simonet L., Jacobsen F., Xie C., Shutter J., Chute H., Basu R., Selander L., Trollinger D., Siu L., Padilla D., Trail G., Elliott G., Izumi R., Covey T., Crouse J., Garcia A., Xu W., del Castillo J., Biron J., Cole S., Hu M.C.-T., Pacifici R., Ponting I., Sarris C., Wen D., Yung Y.P., Lin H., Bosseman R.A.;

RT "Identification and cloning of a megakaryocyte growth and development factor that is a ligand for the cytokine receptor Mpl."

RT Cell 77:1117-1117(1994).

RN [3]

RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).

RX MEDLINE-95152076; PubMed-7849319;

RA Gurney A.L., Kuang W.-J., Xie M.-H., Malloy B.E., Eaton D.L., de Sauvage F.J.;

RT "Genomic structure, chromosomal localization, and conserved alternative splice forms of thrombopoietin."

RT Blood 85:981-984(1995).

CC -1- FUNCTION: LINEAGE-SPECIFIC CYTOKINE AFFECTING THE PROLIFERATION AND MATURATION OF MEGAKARYOCYTES FROM THEIR COMMITTED PROGENITOR CELLS. IT ACTS AT A LATE STAGE OF MEGAKARYOCYTE DEVELOPMENT. IT

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 8, 2003, 02:35:14 ; Search time 23.1198 Seconds
(without alignments)
690.245 Million cell updates/sec

Title: US-09-813-775c-18

Perfect score: 843
Sequence: 1 APPRLICDSRVLELYLEAK.....NFLRGKCLKLTGEACRTGDR 166

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	825	97.9	193	1 ZUHU	erythropoietin pre
2	743.5	88.2	192	1 JQ0173	erythropoietin pre
3	741.5	88.0	192	1 I84613	erythropoietin pre
4	695	82.4	188	1 I46083	erythropoietin pre
5	692	82.1	192	1 S28148	erythropoietin pre
6	675.5	80.1	195	2 JC7699	erythropoietin - r
7	672.5	79.8	194	1 I46401	erythropoietin pre
8	668	79.2	192	1 A24902	erythropoietin pre
9	665	78.9	190	1 I46578	erythropoietin - p
10	615	73.0	175	2 I46199	erythropoietin - d
11	94	11.2	353	2 G02729	thrombopoietin - h
12	93	11.0	353	2 I80105	thrombopoietin pre
13	90	10.7	286	2 A55530	megakaryocyte grow
14	87.5	10.4	346	2 AE0959	solute binding rec
15	84	10.0	339	2 A83274	UDP-N-acetylpyruvo
16	81	9.6	323	2 AB0323	ribonucleoside-dip
17	78	9.3	326	2 JC4125	thrombopoietin pre
18	77.5	9.2	242	2 AD1928	hypothetical prote
19	77.5	9.2	267	2 T08405	hypothetical prote
20	77	9.1	348	2 T35450	ABC transporter AT
21	77	9.1	451	2 S75569	hypothetical prote
22	77	9.1	480	2 S56639	ribosomal protein
23	76.5	9.1	544	2 S37039	groEL protein - Ba
24	76.5	9.1	1638	2 T30313	chemotaxis protein
25	76.5	9.1	2472	2 E83594	still frameshift p
26	76	9.0	356	2 S45330	thrombopoietin - m
27	75	8.9	552	2 S39765	chaperonin 60 - Co
28	75	8.9	263	2 B75361	WD-repeat family p
29	74.5	8.8	455	2 H97693	methylamine util12

30	74.5	8.8	455	2 AG2919	conserved hypothet
31	74	8.8	1089	2 S53978	PSEI protein - yea
32	73.5	8.7	897	2 A54696	EGF receptor subst
33	73	8.7	353	2 AG0138	guinolate synth
34	72.5	8.6	637	2 S75772	hypothetical prote
35	72.5	8.6	762	2 E87592	hypothetical prote
36	72	8.5	1846	2 T33079	hypothetical prote
37	71.5	8.5	220	2 E70749	probable hycp prot
38	71.5	8.5	296	2 A10443	probable 2-hydroxy
39	71.5	8.5	821	2 T49560	probable excision
40	71	8.4	243	2 AE1800	reductases homolog
41	71	8.4	300	2 E84310	hypothetical prote
42	71	8.4	354	2 B75355	hypothetical prote
43	70.5	8.4	547	2 G81787	glucose-6-phosphat
44	70.5	8.4	401	2 H83911	hypothetical prote
45	70.5	8.4	401	2 AF3341	precorrin-6y c5,15

ALIGNMENTS

RESULT 1

erythropoietin precursor [validated] - human
ZUHU
C:Species: Homo sapiens (man)
C:Date: 27-Nov-1985 #sequence_revision 27-Nov-1985 #text_change 08-Dec-2000
C:Accession: A01855; A24744; A25384; A23210; S56178
R:Jacobs, K.; Shoemaker, C.; Radersdorf, R.; Neill, S.D.; Kaufman, R.J.; Mulson, A.;
Nature 313, 806-810, 1985
A:title: Isolation and characterization of genomic and cDNA clones of human erythropo
A:Reference number: A01855; M01D:851378959; PMID:3838366
A:Accession: A01855
A:Molecule type: mRNA; DNA
A:Residues: 1-193 <LIN>
A:Cross-references: GB:X02157; GB:X02158
R:Lin, F.K.; Suggs, S.; Lin, C.H.; Browne, J.K.; Smalling, R.; Eyrle, J.C.; Chen, K.K
Proc. Natl. Acad. Sci. U.S.A. 82, 7580-7584, 1985
A:title: Cloning and expression of the human erythropoietin gene.
A:Reference number: A24744; M01D:86067948; PMID:3865178
A:Accession: A24744
A:Molecule type: DNA
A:Residues: 1-193 <LIN>
A:Cross-references: GB:M11319; M1D:g182197; PIDN:AA52400.1; PID:g182198
R:Li, P.H.; Everett, R.; Wang, F.F.; Arakawa, T.; Goldwasser, E.
J. Biol. Chem. 261, 3116-3121, 1986
A:title: Structural characterization of human erythropoietin.
A:Reference number: A25384; M01D:86140080; PMID:3949763
A:Accession: A25384
A:Molecule type: protein
A:Residues: 28-86, 'Q', 87-193 <LAT>
A:Experimental source: urine
A:Note: forms without the carboxyl-terminal residue and the four carboxyl-terminal re
R:Yangaw, S.; Hirade, K.; Ohnora, H.; Sasaki, R.; Chiba, H.; Ueda, M.; Goto, M.
J. Biol. Chem. 259, 2707-2710, 1984
A:title: Isolation of human erythropoietin with monoclonal antibodies.
A:Reference number: A22210; M01D:84135751; PMID:6698989
A:Accession: A22210
A:Molecule type: protein
A:Residues: 28-29, 'X', 31-33, 'L', 35-50, 'X', 52-53, 'D', 55, 'G', 57 <YAN>
R:Matsumoto, S.; Ikura, K.; Ueda, M.; Sasaki, R.
Plant Mol. Biol. 27, 1163-1172, 1995
A:title: Characterization of a human glycoprotein (erythropoietin) produced in cultur
A:Reference number: S56178; M01D:95284365; PMID:7766897
A:Accession: S56178
A:Molecule type: protein
A:Residues: 28-33, 'X', 35-37 <MTS>
C:Comment: Erythropoietin is produced by kidney or liver of adult mammals and by live
C:Genetics:
A:Gene: GDB:EPO
A:Cross-references: GDB:119110; OMIM:133170
A:Map position: 7q21.3-7q22.1
A:Introns: 5/1; 53/3; 82/3; 142/3
C:Function:

A:Description: the primary inducer of erythrocyte formation
C:Superfamily: erythropoietin
C:Keywords: erythropoiesis; glycoprotein; hormone; kidney; liver
F:1-27/Domain: signal sequence #status predicted <SIG>
F:28-193/Product: erythropoietin #status experimental <MAT>
F:34-188,56-60/Disulfide bonds: #status experimental
F:51,65,110/Binding site: carbohydrate (asn) (covalent) #status experimental
F:152/Binding site: carbohydrate (Ser) (covalent) #status experimental

Query Match 97.9%; Score 825; DB 1; Length 193;
Best Local Similarity 97.6%; Pred. No. 2,4e-75;
Matches 162; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 APPRLICDSRYLERLYLLEAKAEENITTCGAHCSINENITVPDTKVNRYAMKRNKSXQQA 60
DB 28 APPRLICDSRYLERLYLLEAKAEENITTCGAHCSINENITVPDTKVNRYAMKRNKSXQQA 87
QY 61 VEWVWGALLSEAVLRGALLVNSSQPEPQLDHYDKAVSGIRSLTTLRALGAQKEAIS 120
DB 88 VEWVWGALLSEAVLRGALLVNSSQPEPQLDHYDKAVSGIRSLTTLRALGAQKEAIS 147
QY 121 PPDAASAPLRTITADTFRKLFRVYSNFKLKGKLYTGEACRTGDR 166
DB 148 PPDAASAPLRTITADTFRKLFRVYSNFKLKGKLYTGEACRTGDR 193

RESULT 2

QY00173
erythropoietin precursor - crab-eating macaque
C:Species: Macaca fascicularis (crab-eating macaque)
C:Date: 07-Sep-1990 #sequence_revision 15-Nov-1996 #text_change 22-Jun-1999
C:Accession: J00173
R:Lin, F.K.; Lin, C.H.; Lai, P.H.; Browne, J.K.; Egrie, J.C.; Smalling, R.; Fox, G.M.; C
Gene 44, 201-209, 1986
A:Title: Monkey erythropoietin gene: cloning, expression and comparison with the human
A:Reference number: J00173; MUID:87055236; PMID:2877922
A:Accession: J00173
A:Molecule type: mRNA
A:Residues: 1-192 <LIN>
A:Cross-references: GB:M18189; GB:M15818; GB:M15819; GB:M18188; NID:g342093; PIDN:AAA368
A:Experimental source: kidney
C:Comment: This protein is the principal hormone involved in the regulation of erythrocy
C:Function: Erythropoietin is produced by kidney or liver of adult mammals and by liver
A:Description: the primary inducer of erythrocyte formation
C:Superfamily: erythropoietin
C:Keywords: erythropoiesis; glycoprotein; hormone; kidney; liver
F:1-27/Domain: signal sequence #status predicted <SIG>
F:28-193/Product: erythropoietin #status experimental <MAT>
F:34-187,56-60/Disulfide bonds: #status predicted
F:51,65,110/Binding site: carbohydrate (asn) (covalent) #status predicted
F:152/Binding site: carbohydrate (Ser) (covalent) #status predicted

Query Match 88.2%; Score 743.5; DB 1; Length 192;
Best Local Similarity 89.2%; Pred. No. 3.6e-67;
Matches 148; Conservative 7; Mismatches 10; Indels 1; Gaps 1;

QY 1 APPRLICDSRYLERLYLLEAKAEENITTCGAHCSINENITVPDTKVNRYAMKRNKSXQQA 60
DB 28 APPRLICDSRYLERLYLLEAKAEENITTCGAHCSINENITVPDTKVNRYAMKRNKSXQQA 87
QY 61 VEWVWGALLSEAVLRGALLVNSSQPEPQLDHYDKAVSGIRSLTTLRALGAQKEAIS 120
DB 88 VEWVWGALLSEAVLRGALLVNSSQPEPQLDHYDKAVSGIRSLTTLRALGAQKEAIS 146
QY 121 PPDAASAPLRTITADTFRKLFRVYSNFKLKGKLYTGEACRTGDR 166
DB 147 PPDAASAPLRTITADTFRKLFRVYSNFKLKGKLYTGEACRTGDR 192

RESULT 3
184613
erythropoietin precursor - rhesus macaque

C:Species: Macaca mulatta (rhesus macaque)
C:Date: 02-Aug-1996 #sequence_revision 15-Nov-1996 #text_change 22-Jun-1999
C:Accession: I84613
R:Men, D.; Boissel, J.
Blood 82, 1507-1516, 1993
A:Title: Erythropoietin structure-function relationships: High degree of sequence hom
A:Reference number: I46083; MUID:93372347; PMID:8364201
A:Accession: I84613
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-192 <RES>

Query Match 88.0%; Score 741.5; DB 1; Length 192;
Best Local Similarity 88.6%; Pred. No. 5.8e-67;
Matches 147; Conservative 8; Mismatches 10; Indels 1; Gaps 1;

QY 1 APPRLICDSRYLERLYLLEAKAEENITTCGAHCSINENITVPDTKVNRYAMKRNKSXQQA 60
DB 28 APPRLICDSRYLERLYLLEAKAEENITTCGAHCSINENITVPDTKVNRYAMKRNKSXQQA 87
QY 61 VEWVWGALLSEAVLRGALLVNSSQPEPQLDHYDKAVSGIRSLTTLRALGAQKEAIS 120
DB 88 VEWVWGALLSEAVLRGALLVNSSQPEPQLDHYDKAVSGIRSLTTLRALGAQKEAIS 146
QY 121 PPDAASAPLRTITADTFRKLFRVYSNFKLKGKLYTGEACRTGDR 166
DB 147 PPDAASAPLRTITADTFRKLFRVYSNFKLKGKLYTGEACRTGDR 192

RESULT 4

I46083
erythropoietin precursor - cat (fragment)
C:Species: Felis silvestris catus (domestic cat)
C:Date: 16-Aug-1996 #sequence_revision 15-Nov-1996 #text_change 22-Jun-1999
C:Accession: I46083
R:Men, D.; Boissel, J.
Blood 82, 1507-1516, 1993
A:Title: Erythropoietin structure-function relationships: High degree of sequence hom
A:Reference number: I46083; MUID:93372347; PMID:8364201
A:Accession: I46083
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-188 <MEN>
A:Cross-references: GB:L10606; NID:g163820; PIDN:AAA30807.1; PID:g163821
C:Comment: Erythropoietin is produced by kidney or liver of adult mammals and by live
C:Function: Erythropoietin is produced by kidney or liver of adult mammals and by live
A:Description: the primary inducer of erythrocyte formation
C:Superfamily: erythropoietin
C:Keywords: erythropoiesis; glycoprotein; hormone; kidney; liver
F:1-22/Domain: signal sequence (fragment) #status predicted <SIG>
F:23-186/Product: erythropoietin #status predicted <MAT>
F:29-183,51-55/Disulfide bonds: #status predicted
F:46,60,105/Binding site: carbohydrate (asn) (covalent) #status predicted
F:148/Binding site: carbohydrate (Ser) (covalent) #status predicted

Query Match 82.4%; Score 695; DB 1; Length 188;
Best Local Similarity 82.5%; Pred. No. 2.6e-62;
Matches 137; Conservative 8; Mismatches 21; Indels 0; Gaps 0;

QY 1 APPRLICDSRYLERLYLLEAKAEENITTCGAHCSINENITVPDTKVNRYAMKRNKSXQQA 60
DB 23 APPRLICDSRYLERLYLLEAKAEENITTCGAHCSINENITVPDTKVNRYAMKRNKSXQQA 82


```

Db      24 APP--ACDLRVLSKLLRDSHVLSHSKLSQCEVHPRLPPVLLPAVDFSLGEMKTOMEETKA 81
QY      61 VEWOGIALLSEAVL--RGQALLVNSSQPWEPIQLHVDKAVSGRLSTTLRALGAQKEA 118
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      82 QDILGAVTLLLEGVMAARGQLGPTCLSSLLGQLSGQVRLILGALQSL-----LGTO--- 132
QY      119 ISPPDASAAPLRTITADTFERKLEFRVYSNPLRGK 154
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      133 -LPPQG-----RTAHKDPNAIFLSPQHLLRGKVR 161

RESULT 12
180105
thrombopoietin precursor - human
N:Alternate names: c-MPL ligand; megakaryocyte growth and development factor precursor
C:Species: Homo sapiens (man)
C>Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 20-Jun-2000
C:Accession: I59281, 180105; S45331; S48740; I38672; I52610
R:Foster, D.C.; Sprecher, C.A.; Grant, F.J.; Kramer, J.M.; Kuljper, J.L.; Holly, R.D.; W
Proc. Natl. Acad. Sci. U.S.A. 91, 13023-13027, 1994
A:Title: Human thrombopoietin: gene structure, cDNA sequence, expression, and chromosomal
A:Reference number: I59281; MUID:95108091; PMID:7809166
A:Accession: I59281
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-353 <RE2>
A:Cross-references: GB:L36051; NID:9533214; PIDN:AAC37568.1; PID:9533215
A:Accession: 180105
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-353 <RE2>
A:Cross-references: GB:L36052; NID:9533216; PIDN:AAC37566.1; PID:9533217
R:de Sauvage, F.J.; Hass, P.E.; Spencer, S.D.; Malloy, B.E.; Gurney, A.L.; Spencer, S.A.
Nature 369, 533-538, 1994
A:Title: Stimulation of megakaryocytopoiesis and thrombopoiesis by the c-MPL ligand.
A:Reference number: S45331; MUID:94261202; PMID:8202154
A:Accession: S45331
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-353 <SAU>
A:Cross-references: GB:L34310; NID:9506826; PIDN:AAA59857.1; PID:9506827
R:Solima, Y.; Akahori, H.; Seki, N.; Hori, T.; Ogami, K.; Kato, T.; Shimada, Y.; Kawamura
FEBS Lett. 353, 57-61, 1994
A:Title: Molecular cloning and chromosomal localization of the human thrombopoietin gene
A:Reference number: S48740; MUID:95010765; PMID:7926023
A:Accession: S48740
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-353 <SOH>
A:Cross-references: GB:D32046; NID:9577319; PIDN:BAA06807.1; PID:9577320
R:Barclay, T.D.; Bogenberger, J.; Hunt, P.; Li, Y.S.; Lu, H.S.; Martin, F.; Chang, M.S.;
Cell 77, 1117-1124, 1994
A:Title: Identification and cloning of a megakaryocyte growth and development factor tha
A:Reference number: A54463; MUID:94291201; PMID:8020099
A:Accession: I38672
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-112, 'E', 114-353 <RE3>
A:Cross-references: EMBL:011025; NID:9511223; PIDN:AAA50553.1; PID:9558078
R:Curney, A.L.; Kuang, W.J.; Xie, M.H.; Malloy, B.E.; Eaton, D.L.; de Sauvage, F.J.
Blood 85, 981-988, 1995
A:Title: Genomic structure, chromosomal localization, and conserved alternative splice f
A:Reference number: I52610; MUID:95152076; PMID:7849319
A:Accession: I52610
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-353 <RE4>
A:Cross-references: GB:S76771; NID:914225; PIDN:AAB33390.1; PID:914226
C:Genetics:
A:Gene: GDB:THPO; MGD:
A:Cross-references: GDB:374007; OMIM:600044

```

```

A:Map position: 3q26.3-3q27
A:Insertions: 5/71; 47/3; 76/3; 132/3
C:Keywords: alternative splicing; cytokine; glycoprotein

Query Match      11.0%; Score 93; DB 2; Length 353;
Best Local Similarity 26.3%; Pred. No. 0.16;
Matches 41; Conservative 20; Mismatches 75; Indels 20; Gaps 5;

QY      1 APPRLDSDVLERYLLEAKAEENITTCGAECHECSLNNITVPDTKYVFYAMKRXSXQA 60
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      24 APP--ACDLRVLSKLLRDSHVLSHSKLSQCEVHPRLPPVLLPAVDFSLGEMKTOMEETKA 81

QY      61 VEWOGIALLSEAVL--RGQALLVNSSQPWEPIQLHVDKAVSGRLSTTLRALGAQKEA 118
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      82 QDILGAVTLLLEGVMAARGQLGPTCLSSLLGQLSGQVRLILGALQSL-----LGTO--- 132
QY      119 ISPPDASAAPLRTITADTFERKLEFRVYSNPLRGK 154
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      133 -LPPQG-----RTAHKDPNAIFLSPQHLLRGKVR 161

RESULT 13
A55530
megakaryocyte growth and development factor, long form - human
N:Alternate names: MPL ligand, long form
C:Species: Homo sapiens (man)
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 07-May-1999
C:Accession: A55530
R:Chang, M.; McNinch, J.; Basu, R.; Shutter, J.; Hsu, R.; Perkins, C.; Mar, V.; Suggs
J. Biol. Chem. 270, 511-514, 1995
A:Title: Cloning and characterization of the human megakaryocyte growth and developme
A:Reference number: A55530; MUID:95122483; PMID:7822271
A:Accession: A55530
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-286 <CHA>
A:Cross-references: GB:017071
C:Genetics:
A:Gene: MGD:
A:Map position: 3q26.3
C:Keywords: alternative splicing; cytokine

Query Match      10.7%; Score 90; DB 2; Length 286;
Best Local Similarity 26.6%; Pred. No. 0.25;
Matches 41; Conservative 18; Mismatches 75; Indels 20; Gaps 5;

QY      1 APPRLDSDVLERYLLEAKAEENITTCGAECHECSLNNITVPDTKYVFYAMKRXSXQA 60
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      24 APP--ACDLRVLSKLLRDSHVLSHSKLSQCEVHPRLPPVLLPAVDFSLGEMKTOMEETKA 81

QY      61 VEWOGIALLSEAVL--RGQALLVNSSQPWEPIQLHVDKAVSGRLSTTLRALGAQKEA 118
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      82 QDILGAVTLLLEGVMAARGQLGPTCLSSLLGQLSGQVRLILGALQSL-----LGTO--- 132
QY      119 ISPPDASAAPLRTITADTFERKLEFRVYSNPLRGK 152
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      133 -LPPQG-----RTAHKDPNAIFLSPQHLLRGK 159

RESULT 14
AE0959
Solute binding receptor protein (imported) - Salmonella enterica subsp. enterica sero
C:Species: Salmonella enterica subsp. enterica serovar Typh
A:Note: this species has also been called Salmonella typhi
C>Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
C:Accession: AE0959
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Church
th, T.; Connerton, P.; Croft, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Fair
, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens,
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica se
A:Reference number: AB0502; PMID:11677608

```


GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus.p2n model

Run on: January 8, 2003, 05:18:00 ; Search time 49.4596 Seconds
(without alignments)
1717.360 Million cell updates/sec

Title: US-09-813-775c-2

Perfect score: 998
Sequence: 1 MGVECPAMWLLSLSLP.....NFLRKKLYTGECRTGDR 193

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 389086 seqs, 220051671 residues

Total number of hits satisfying chosen parameters: 778172

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODE=frame_plus.model -DEV=xlh
-Q=/cgn2_1/USPTO.spool/US09813775/runat.07012003.153123.23862/app.query.fasta_1.718
-DB=Published Applications NA -QMT=fastlap -SUFFIX=p2n.rnpb -MINMATCH=0.1
-LOOPL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blousum62
-TRANS=human40.ccd1 -LIST=45 -DOCLIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pico -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US09813775_@CGN_1.1.25_runat.07012003.153123.23862
-NCPU=6 -ICPU=3 -NO_XLPEXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6
-Fgapext=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications_NA:

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
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9: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	709	71.0	2426	10	US-09-975-063-1 Sequence 1, Appli
2	709	71.0	2426	12	US-10-011-858-1 Sequence 1, Appli
3	377	32.8	423	10	US-09-864-761-16087 Sequence 16087, A
4	286	28.7	191	10	US-09-864-761-32584 Sequence 32584, A

5	90	9.0	3149	10	US-09-729-674-127 Sequence 127, App
6	84	8.4	2124	9	US-09-731-872-39 Sequence 39, Appl
7	84	8.4	2300	10	US-09-992-598-137 Sequence 137, App
8	84	8.4	2300	9	US-09-989-293A-137 Sequence 137, App
9	84	8.4	2300	9	US-09-989-735-137 Sequence 137, App
10	84	8.4	2300	9	US-09-990-444-137 Sequence 137, App
11	84	8.4	2300	9	US-09-989-730-137 Sequence 137, App
12	84	8.4	2300	9	US-09-990-436-137 Sequence 137, App
13	84	8.4	2300	9	US-09-991-181-137 Sequence 137, App
14	84	8.4	2300	9	US-09-993-687-137 Sequence 137, App
15	84	8.4	2300	9	US-09-989-734-137 Sequence 137, App
16	84	8.4	2300	10	US-09-989-722-137 Sequence 137, App
17	84	8.4	2300	10	US-09-989-723-137 Sequence 137, App
18	84	8.4	2300	10	US-09-989-279-137 Sequence 137, App
19	84	8.4	2300	10	US-09-989-727-137 Sequence 137, App
20	84	8.4	2300	10	US-09-989-731-137 Sequence 137, App
21	84	8.4	2300	10	US-09-989-732-137 Sequence 137, App
22	84	8.4	2300	10	US-09-991-073-137 Sequence 137, App
23	84	8.4	2300	10	US-09-990-442-137 Sequence 137, App
24	84	8.4	2300	10	US-09-991-163-137 Sequence 137, App
25	84	8.4	2300	10	US-09-993-604-137 Sequence 137, App
26	84	8.4	2300	10	US-09-990-456-137 Sequence 137, App
27	84	8.4	2300	10	US-09-989-721-137 Sequence 137, App
28	84	8.4	2300	12	US-10-052-566-115 Sequence 115, App
29	84	8.4	2357	9	US-10-098-841-62 Sequence 62, Appl
30	83.5	8.4	1786	10	US-09-969-708-492 Sequence 492, App
31	80	8.0	4308	9	US-09-978-295A-527 Sequence 527, App
32	80	8.0	4308	9	US-09-978-697-527 Sequence 527, App
33	80	8.0	4308	9	US-09-978-192A-527 Sequence 527, App
34	80	8.0	4308	9	US-09-999-832A-527 Sequence 527, App
35	80	8.0	4308	9	US-09-978-189-527 Sequence 2, Appli
36	86.3	8.0	3666	9	US-10-136-224-2 Sequence 3, Appli
37	79.5	8.0	3885	10	US-09-815-242-9626 Sequence 9626, Ap
38	79.5	8.0	3940	9	US-10-136-224-1 Sequence 1, Appli
39	79.5	8.0	1372	10	US-09-925-301-575 Sequence 575, App
40	77.5	7.8	2442	9	US-09-964-899-24 Sequence 24, Appl
41	77.5	7.8	78056	9	US-10-109-551-1 Sequence 1, Appli
42	77.5	7.7	1663	10	US-09-070-927A-277 Sequence 277, App
43	76.5	7.7	3090	10	US-09-768-436-1 Sequence 1, Appli
44	76.5	7.7	4006	10	US-09-768-436-3 Sequence 3, Appli
45	76.5	7.7	4006	10	US-09-768-436-3 Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-09-975-063-1
Sequence 1, Application US/09975063
Patent No. US20020045255A1
GENERAL INFORMATION:
APPLICANT: POWELL, Jerry S.
TITLE OF INVENTION: HUMAN ERYTHROPOIETIN GENE: HIGH LEVEL
EXPRESSION IN STABLY TRANSFECTED MAMMALIAN CELLS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dorsey & Whitney, LLP
STREET: Suite 3400, 1420 Fifth Avenue, U.S. Bank Centre
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6/7/8
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/975,063
FILING DATE: 10-Oct-2001
ATTORNEY/AGENT INFORMATION:
NAME: Roberts, Mark W.
REGISTRATION NUMBER: 46,160
REFERENCE/DOCKET NUMBER: 500582.03 (112893.109)

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 206-903-8728
 TELEFAX: 206-903-8820
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2426 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 US-09-975-063-1

Alignment Scores:
 Pred. No.: 2,93e-78 Length: 2426
 Score: 709.00 Matches: 186
 Percent Similarity: 35.80% Conservative: 3
 Best Local Similarity: 35.23% Mismatches: 4
 Query Match: 71.04% Indels: 337
 DB: 10 Gaps: 3

US-09-813-775c-2 (1-193) x US-09-975-063-1 (1-2426)

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OY 1 MetGlyValHisGluCysProAlaTrpLeuTrpLeuLeuSerLeuLeuSerLeuPro 20
    ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 625 CTATCTGTCTGAAGATGCTCTGCTGGCTTCTCTCTGCTCCCTGCTGCTCTCT
OY 21 LeuGlyLeuProValLeuGlyAlaProProAlaGlyLeuIleCysAspSerArgValLeuGlu 40
    |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 685 CTGGGCTCCAGCTCCTGGGCGCCGCCACACGCTCATCTGTGACAGCGAGCTCGCAG 744
OY 41 ArgTrpLeuLeuGluAlaIleGlyAlaGluAsnIleThr----- 53
    |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 745 AGGTACCTCTTGGAGGCCAAGAGCGGAGAAATATCATCGTAGAGACCCCTTCCACAGAC 804
OY 53 ----- 53
DB 805 ATTCCAGAACTACACGCTCAGGGCTTTCAGGAACTCTCCAGATCCAGAACTCTGCA 864
OY 53 ----- 53
DB 865 CTTCGTTGGGGTGGAGTTGGGAAGCTAGACACTGCCCTCATATGAATTAAGTCTGG 924
OY 53 ----- 53
DB 925 TGGCCCAACCATACCTGGAATACTAGGCAAGAGCAAAAGCAGATCTAAGCCTGT 984
OY 54 -----ThrG1 55
DB 985 GGGCAGGGCCAGAGCCTTTCAGGGACCTTGACTCCCGGGGCTGTGCAATTTCAGAGCGGG 1044
OY 55 yCysAlaGluHisCysSerLeuAsnGluAsnIleThrValProAspThrLysValAsnPh 75
    |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 1045 CTGTCTGAACACTGACAGCTGAATGAGAAATATCACTGTCCAGACACCAAGTTAAATT 1104
OY 75 eTrpAlaTrpLysArgMetGluValArg----- 84
    |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 1105 CTATGCTGGAGAGAGTAGAGTAGAG-TTCCTTTTTTTTTTTTTTTTCTTTTGGGA 1163
OY 84 ----- 84
DB 1164 GAATCTCATTTTCCAGCCTGATTTTGGATGAAGAAGGAGAAATGATGAGGAAAGTAAAA 1223
OY 84 ----- 84
DB 1224 TGGAGCAGCAGATGAGGCTGCTGGGCGCAGAGGCTCAGCTATATAATCCAGGCTGA 1283
OY 84 ----- 84
DB 1284 GATGCCGAGATGGAGAAATTTGCTTGTAGCCCGGAGTTTCAGACCAACCTAGCAGACATA 1343
OY 84 ----- 84

```

```

DB 1344 GTGAGATCCCACTCTCTACAAACATTTAAAAAATTAGTCAGGTGAGTGTGATGCT 1403
OY 84 ----- 84
DB 1404 GGTAGTCCAGATATTTGGAAAGGCTGAGGCGGAGAGATGCTGAGACCAGGAATTTGAG 1463
OY 84 ----- 84
DB 1464 GCTGAGTAGAGTGTGATCATCACACACTGAATCCAGCTCAGTAGACAGATGAGGCCCTG 1523
OY 84 ----- 84
DB 1524 TCTCAAAAAAGAAAAAGAAAAAATAATGAGGCGTGTATGAAATACGTTCAATTATT 1583
OY 84 ----- 84
DB 1584 CATTCACCTACCTACCTACCTACCTATTCATTTCATTTCATTTCATTTCATTTCATTTC 1643
OY 84 ----- 84
DB 1644 CTTCGTGTTGCTACAGTGTGCTGCTGGGCTGCTGAGGGGAGAGAGAGGTGACAT 1703
OY 85 -----GlnGlnAlaValGluValTr 91
DB 1704 CCTCAGCTGACTCCAGAGTCCACTCCCTGATAGTGGGCGCAGAGCCGCTGAAAGTCTG 1763
OY 91 pGlnGlyLeuAlaLeuLeuSerGluAlaValLeuArgGlyGlnAlaLeuLeuValAsnSe 111
    |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 1764 GAGAGGCGCTGGCCCTGCTCGGAAGCTGCTCGGGGGCCAGAGCCCTGTGTGTAACAC 1823
OY 111 rSerGlnProTrpGluProLeuGlnLeuHisValAspLysAlaValSerGlyLeuArgSe 131
    |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 1824 TTCACAGCGGTGGAGCCCTCAGCTGATGTGATTAAGCGCTGACGCTTCGCGAG 1883
OY 131 rLeuThrTrpLeuLeuArgAlaLeuGlyAla----- 141
    |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 1884 CCTCAGCACTGTGCTTGGGCTGTGGAGAC-CCAGGTGATGAGAGCGACACTTCTGCT 1942
OY 141 ----- 141
DB 1943 TGCCTTTCTGAAGAGGAGAAAGGTCTGTGAAGAGTACAGAACTGCTGATT 2002
OY 142 -----GlnGlyGluAlaIle 146
DB 2003 CCTTCCCTTCTGTGGCACTGACGAGCCTCTGTTCTCTCTTGGCAGAGAAAGCCAT 2062
OY 146 eSerProProAlaAlaSerAlaAlaProLeuArgThrIleThrAlaAspThrPheAr 166
    |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 2063 CTCCCTCCAGATGGCGGCTCAGCTGCTCCTCCTCCCAACATCAGCTGACACATTCCG 2122
OY 166 gLysLeuPheArgValTyrSerAsnPhLeuArgGlyLysLeuLysLeuTyrThrGlyG1 186
    |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 2123 CAACCTCTCCAGATCTACTCCAAATTTCTCCGGGGAAGCTGAAGCTGTACACAGGGGA 2182
OY 186 uAlaCysArgThrGlyAspArg 193
    |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 2183 GGCCTGACAGACAGGGGACAGA 2204
OY 193 ----- 193

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RESULT 2
 US-10-011-858-1
 Sequence 1, Application US/10011858
 Patent No. US20020137145A1
 GENERAL INFORMATION:
 APPLICANT: POWELL, Jerry S.
 TITLE OF INVENTION: HUMAN ERYTHROPOIETIN GENE: HIGH LEVEL
 EXPRESSION IN STABLY TRANSFECTED MAMMALIAN CELLS
 NUMBER OF SEQUENCES: 6
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Dorsey & Whitney, LLP
 STREET: Suite 3400, 1420 Fifth Avenue, U. S. Bank Centre
 CITY: Seattle
 STATE: Washington
 COUNTRY: USA

```

1      ZIP: 98101
2
3      COMPUTER READABLE FORM:
4
5      MEDIUM TYPE: Floppy disk
6
7      COMPUTER: IBM PC compatible
8
9      OPERATING SYSTEM: PC-DOS/MS-DOS
10     SOFTWARE: MS-WORD
11
12     CURRENT APPLICATION DATA:
13
14     APPLICATION NUMBER: US/10/011,858
15
16     FILING DATE: 05-NO. US20020137145A1-2001
17
18     ATTORNEY/AGENT INFORMATION:
19
20     NAME: Roberts, Mark W.
21
22     REGISTRATION NUMBER: 46,160
23
24     REFERENCE/DOCKET NUMBER: 500582.13
25
26     TELECOMMUNICATION INFORMATION:
27
28     TELEPHONE: 206-903-8728
29
30     TELEFAX: 206-903-8820
31
32     INFORMATION FOR SEQ ID NO: 1:
33
34     SEQUENCE CHARACTERISTICS:
35
36     LENGTH: 2426 base pairs
37
38     TYPE: nucleic acid
39
40     STRANDEDNESS: single
41
42     TOPOLOGY: linear
43
44     MOLECULE TYPE: DNA (genomic)
45
46     SEQUENCE DESCRIPTION: SEQ ID NO: 1:
47
48     US-10-011-858-1

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Alignment Scores:

Pred. No.:	2,93e-78	Length:	2422
Score:	709.00	Matches:	186
Percent Similarity:	33.80%	Conservative:	3
Best Local Similarity:	35.23%	Mismatches:	4
Query Match:	71.04%	Indels:	337
DB:	12	Gaps:	3

US-09-813-775C-2 (1-193) X US-10-011-858-1 (1-2426)

QY	1	MetIyvalHistGlycysProAlaIleuTTPLeuTTPLeuLeuSerLeuLeuSerLeuPro	20
Db	625	CTATCTTCTTACAAATGCTCCGCTGGCTGGCTTCTCTCTCTCTGCTGCTCTCT	684
QY	21	LeuGIyLeuProValLeuGlyAlaProProArgLeuIleCysAspSerArgValLeuGlu	40
Db	685	CTGGGCTCCCACTCCGCGGGCCCCACCAACGCTCATCTGTGACAGCGAGTCTTGAG	744
QY	41	ArgTylLeuLeuGlyAlaIalysGluIalGluAsnIleThr-----	53
Db	745	AGGTACTCTTGGAGGGCCAAAGAGCCGAGAAATATCAGCGTGAAGACCCCTTCCCAACAC	804
QY	53	-----	53
Db	805	ATTCCACAGAACTACGCTCAGGGCTTCAGGGAACCTCTCCAGATCAGGAACCTGSCA	864
QY	53	-----	53
Db	865	CTTGGTTGGGGGTGGAGTTGGGAAGCTAGACACACTGCCCCCTACATAAGAATAACTCGG	924
QY	53	-----	53
Db	925	TGGCCCCAAACATACCTGGAAACTGAGCAAGAGCAAGACAGATCTACGCTGT	984
QY	54	-----ThrG1	55
Db	985	GGCCAGGGCCAGAGCCTTAGGAGCCCTTGACTCCCGGGCTGTGTGCATTTCACACGGG	1044
QY	55	YcysAlaGluHisCysSerLeuAsnGluAsnIleThrValProAspThrIysValAsnPh	75
Db	1045	CTGTGCTGCAACACTGCAGCTTGATGATGAGATATCATCTGTCCAGACCAACCAAGTTAAATT	1104
QY	75	eTyrAlaTrpIysArgMetGluValArg-----	84
Db	1105	CTATGCTGGAAAGAGATGAGAGTGAG-TTCCTTTTTCCTTTTTCCTTTTCCTTTTGG	1163
QY	84	-----	84

Db	1164	GAATCATTTCGGAGCGCCTGATTTTGTGATGAAGGAGAAATGATGAGGAAGGTAAA	1223
Qy	84	-----	84
Db	1224	TGGAGACAGAGATGAGGCTGCTGGGGCAGAGGCTCACCTCTATTAATCCAGGCTGA	1283
Qy	84	-----	84
Db	1284	GATGGCGGAANTGGGAGATTGCTTACGCCCGGAGATTTCAGACCACCTTAGCAGCATTA	1343
Qy	84	-----	84
Db	1344	GTGAGATCCCCCATCTCTCTACAAACATTTAAAAAAATATGTCAGTGGAAGTGGTGCAATGCT	1403
Qy	84	-----	84
Db	1404	GGTAGTCCAGATATTTTGGAAGGCTGAGCGGGAGGATCCGTGAGAGCCAGGAATTTTGAC	1463
Qy	84	-----	84
Db	1464	GCTGCAGTGAAGCTGTGATCACACCACTGAATCTCAGGCTCAGTGCAGAGATGAGGCCCTG	1523
Qy	84	-----	84
Db	1524	TCTCAAAAAAGAAAAAGAAAAAATATAGAGGCTGTATGGAATACGTTCAATTATT	1583
Qy	84	-----	84
Db	1584	CATTCACTCACTCACTCACTCATTCATTCAATTCATTCAACAAGCTTATTGCAATAC	1643
Qy	84	-----	84
Db	1644	CTTCTGTTTGTGCTAGCTTGCTGCTTGGGGCTGCTGAGGGGACGAGGAGGCTGACAT	1703
Qy	85	-----Ginglinalavalgluvaltr 91	
Db	1704	CCCTCAGCTGACATCCCGAGACTCACCCTGTAAGTTCGGGCGACGAGGCCGTAGAAGCTCG	1763
Qy	91	pglnglyleuAlaleuLeuSerGluAlaValleuArglyGlnAlaleuLeuValasnE 111	
Db	1764	GCAGGGCGCTGGCCCTGCTGTGCGAACCCTGCTCGGGGCCAGGCCCTGTGTGGAATC	1823
Db	1824	TTCCAGACCGTGGAGGCCCTGAGAGCTGCATGTGATTAAGCCGTCACTGGCCTTCGCAG	1883
Qy	131	rleuThrThrleuLeuArgAlaleuGlyAla-----141	
Db	1884	CCTCACACACTCTGCTTCGGGCTCTGGGAGC--CCAGGTAGTAGAGCGGACGACCTTGCT	1942
Qy	141	-----141	
Db	1943	TGCCCTTTCGTAAAGAGGGAGAAAGGCTTGTAAAGAGTACAGCACTGTCGGATTT	2002
Qy	142	-----GlnysGluAla11 146	
Db	2003	CCTTCCCTTCTGTGGCACTGCAGGCACTCTGTTTCTCTCTTGTGGCAAGGAAGCCAT	2062
Qy	146	eserProProAspAlaAlaSerAlaAlaProleuArgThrIleThrAlaAspThrPhear 166	
Db	2063	CTCCCTCCAGATGCGGCTCCACCTGCTCCACCTCGAACAATCACTGCTGACACTTCCG	2122
Qy	166	glyLeuPhearValTyrSerAsnPheluArgGlyLeuLeuLeuTyrThrArgly 186	
Db	2123	CAAACTCTTCGAGCTACTACCAATTTCTCCGGGAAAAAGCTGAAGCTGTACACAGGGGA	2182
Qy	186	uAlaCyArgThrGlyAspArg 193	
Db	2183	GGCTGCAAGACAGGGGACAGA 2204	
RESULT 3			
RS-09-864 -761-16087/c			

Sequence 16087, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aecm1ca-X-1
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US/09/864,761
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 16087
LENGTH: 423
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AF053356.1
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.93
US-09-864-761-16087

Alignment Scores:
Pred. No.: 6,638-32 Length: 423
Score: 327.00 Matches: 78
Percent Similarity: 62.40% Conservative: 0
Best Local Similarity: 62.40% Mismatches: 2
Query Match: 32.77% Indels: 46
DB: 10 Gaps: 1

US-09-813-775c-2 (1-193) x US-09-864-761-16087 (1-423)

QY 83 VALARGINGLALVALGLVALTRPGINGLYLEUALALEUENSERG1UALAVALLEU 102
DB 376 GTGGGAGACGACGCGCTAAGCTCTGGAGGCGCTGGCTCTGTGCGAAGCTGTCTG 317

QY 103 ARGGLYLALALEUVALANSERSEGINPIOTRPLUPLROEUNG1LNUH1SVAL 122
DB 316 CGGGGCCAGACCCCTGTGGTCAACTCTCCAGCGGTGGAGCCCTGCAGCTGATGTG 257
QY 123 ASPLVALVALSERGLYLEUARISERLEUTHRTHLEULNARGVALALEU1YALA 141
DB 256 GATTAAGCCGTAGTGGCCCTTCGACCCACACCTCTCTGGGCTGTGGAGC-CCA 198
QY 141 141
DB 197 GGTGATAGAGCGGACACTTCTGCTGGCTTTCTGTAAAGAGGAGAGAGGCTTTC 138
QY 141 141
DB 137 TAAGAGTACAGGAAGTCTGCTATCTCTCTGTGTGACATGACGACCTCTG 78
QY 142 142
DB 77 TTTTCTCTTGGCAGAGGACCATCTCCCTCGAGATGGGCTTCAGCTCTCCATCTC 18
QY 158 ARGTHRIETHRALA 162
DB 17 CGAACAATCACTGCT 3

RESULT 4
US-09-864-761-32584/C
Sequence 32584, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
FILE REFERENCE: Aecm1ca-X-1
CURRENT FILING DATE: US/09/864,761
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203

PRIOR FILING DATE: 2001-01-29
 NUMBER OF SEQ ID NOS: 49117
 SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
 SEQ ID NO 32584
 LENGTH: 191

TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 OTHER INFORMATION: MAP TO AF053356.1
 OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.93
 OTHER INFORMATION: NT HIT: AF202314.1, EVALUATE 1.00e-104
 OTHER INFORMATION: EST_HUMAN HIT: AA662379.1, EVALUATE 4.00e-57
 OTHER INFORMATION: SWISSPROT HIT: P01588, EVALUATE 1.00e-27
 US-09-864-761-32584

Alignment Scores:
 Pred. No.: 2,51e-27 Length: 191
 Score: 286.00 Matches: 59
 Percent Similarity: 98.33% Conservative: 0
 Best Local Similarity: 98.33% Mismatches: 1
 Query Match: 28.66% Indels: 0
 Gaps: 0

US-09-813-775C-2 (1-193) x US-09-864-761-32584 (1-191)

QY 83 ValArgGlnGlnAlaValAlaGluValTTPGInGlyLeuAlaLeuSerGluAlaValLeu 102
 Db 180 GTGGGAGAGAGAGCCGTAGAACTGTGGAGGCGCTGGCTGTGTGGAAAGCTGTCTG 121
 QY 103 ArgGlyGlnAlaLeuLeuValAsnSerSerGlnProTTPGInProLeuGlnLeuHisVal 122
 Db 120 CGGGGCCAGGCGCTGTGTGCAACTCTCCACCGCGAGCCCGCCGACCTGCATGTG 61
 QY 123 AspLysAlaValAsnSerGlyLeuArgSerLeuThrThrLeuLeuArgAlaLeuGlyAlaGln 142
 Db 60 GATAAAGCCCTCATGTGGCCCTTCGACGCTCACCATCTGCTTGGGCTCTGGAGCCAG 1

RESULT 5
 US-09-729-674-127

Sequence 127, Application US/09729674
 Patent No. US20010039335A1
 GENERAL INFORMATION:
 APPLICANT: JACOBS, Kenneth
 APPLICANT: MCCOY, John M.
 APPLICANT: LAVALLIE, Edward R.
 APPLICANT: COLLINS-RACLE, Lisa A.
 APPLICANT: EVANS, Cheryl
 APPLICANT: MERBERG, David
 APPLICANT: TREACY, Maurice
 APPLICANT: AGOSTINO, Michael J.
 APPLICANT: STEINDINGER II, Robert J.
 APPLICANT: SPAULDING, Vikki
 APPLICANT: WONG, Gordon G.
 APPLICANT: CLARK, Hilary
 APPLICANT: FECHTEL, Kim
 APPLICANT: Genetics Institute, Inc.
 TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
 FILE REFERENCE: 6055-64X
 CURRENT APPLICATION NUMBER: US/09/729,674
 CURRENT FILING DATE: 2000-12-04
 PRIOR APPLICATION NUMBER: 09/539,330
 PRIOR FILING DATE: 2000-03-30
 NUMBER OF SEQ ID NOS: 283
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 127
 LENGTH: 3149
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-729-674-127

Alignment Scores:
 Pred. No.: 0.397 Length: 3149
 Score: 90.00 Matches: 48

Percent Similarity: 44.03% Conservative: 22
 Best Local Similarity: 30.19% Mismatches: 63
 Query Match: 9.02% Indels: 26
 Gaps: 9

US-09-813-775C-2 (1-193) x US-09-729-674-127 (1-3149)

QY 6 CysProAlaThrLeuThrLeuLeuLeuSerLeuSerLeu-----ProLeuGlyLeu 23
 Db 364 TGCCCT-----CTGTCACTTCTTCAAAATGGCTCCCAAGAGGCTG 405
 QY 24 ProValLeuGlyAlaProProAlaGlyLeuIleCysAspSerArgValLeuGlyAlaGlyTyrLeu 43
 Db 406 TGTCTCTTGGTTCGCTCCGCCCAACCTAATCTGTGAGAAACACCTACCAAGAACCTTA 465
 QY 44 LeuGluAlaLysGluAlaGlnIleThr-----ThrGlyLysAlaGlnHisCys 60
 Db 466 TTGGATATTTTGGCAGATGGCACCATTTTTGAAGTTTGAGTGGATGCTGCAGAGATGCC 525
 QY 61 Ser-----LeuAsnGluAsnIleThrValProAspThrLysValAsnPheTyrAlaTrp 78
 Db 526 AGCAAGCTTGTGAGATATATGGCTGTGTATGGGGGTGCTGGAACCTC----- 576
 QY 79 LysArgMetGluValArgGlnGlnAlaValAlaGluValTTPGInGlyLeuAlaLeu----- 96
 Db 577 CGATACCTAGCAGCAGCGCAGAAACAAATTTGCTGTATGGCGCTTAGCCTGAAGTCC 636
 QY 97 LeuSerGlnAlaValLeuValG-----GlyGlnAlaLeuValAsnSerSerGln 113
 Db 637 CTGCTGAGACTGTTTGAACCTTTCCCTTGACACAGTCCCTTCACTGCTGTAGCGTGAAGTCC 696
 QY 114 ProTTPGInProLeuGlnLeuHisValAspLysAlaValSerGlyLeuValG----- 130
 Db 697 ---TGGATGGTGAGACTCCACAGAGACAGGATATTTATGCTGGCAGAGGATGCCAG 753
 QY 131 ---SerLeuThrThrLeuLeuArgAlaLeuGlyAlaGlnLysGluAlaIleSerPro 148
 Db 754 ATTTCAGTGGCTCTTCTTTCATCTTGTGATACCTTTCTAGAACCTTTCTAGAACCTT 810

RESULT 6
 US-09-731-872-39

Sequence 39, Application US/09731872
 Patent No. US20020102604A1
 GENERAL INFORMATION:
 APPLICANT: DUMAS Milne Edwards, Jean Baptiste
 APPLICANT: BOUQUELIERET, Lydie
 APPLICANT: JOBERT, Severin
 TITLE OF INVENTION: FULL-LENGTH HUMAN CDNAS ENCODING POTENTIALLY SECRETED PROTEINS
 FILE REFERENCE: 78.US3.REG
 CURRENT APPLICATION NUMBER: US/09/731,872
 CURRENT FILING DATE: 2000-12-07
 PRIOR APPLICATION NUMBER: US 60/169,629
 PRIOR FILING DATE: 1999-12-08
 PRIOR APPLICATION NUMBER: US 60/187,470
 PRIOR FILING DATE: 2000-03-06
 NUMBER OF SEQ ID NOS: 482
 SOFTWARE: Patent.pm
 SEQ ID NO 39
 LENGTH: 2124
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 505..1590
 NAME/KEY: sig_peptide
 LOCATION: 505..624
 OTHER INFORMATION: Von Heijne matrix
 OTHER INFORMATION: score 8.5056444915604
 OTHER INFORMATION: seq VVMILMLTLVLG/MV
 US-09-731-872-39

Alignment Scores:
 Pred. No.: 1.22 Length: 2124

Score: 84.00 Matches: 49
 Percent Similarity: 38.25% Conservative: 34
 Best Local Similarity: 22.58% Mismatches: 71
 Query Match: 8.42% Indels: 63
 Gaps: 10

US-09-813-775c-2 (1-193) x US-09-731-872-39 (1-2124)

```

Oy 3 ValHisGluCysProAlaTrpLeuTrpLeuLeuSerLeuLeuSerLeuProLeuGly 22
    ::::: ||| ::::: ||| ::::: ||| ::::: ||| ::::: |||
Db 712 CTrCACTACATGATCTCTCTCTCTGGGCTTGTCTGCTCTCTGTTGATCTCACTGGGT 771
Oy 23 LeuPro--ValLeuGlyAlaProAlaGlyLeuIleCysAspSerArgValLeuGly 41
    ||| ::::: ||| ::::: ||| ::::: ||| ::::: |||
Db 772 CTGCCCCGAGTGTCTCTCTCTCACTGGGAGCTGTAGTCAAGCCCGCTCTGAGAGAC 831
Oy 42 TyrLeuLeuGluAlaLysGluAlaGlyLeuAsnIleThrThrGlyCysAlaGluHisCysSer 61
    ||||| ||||| ||| ::::: ||| ::::: |||
Db 832 -----CTGGAG-----GAGCAGCTGTACTGCTCAGCCCTTGAAGAGCAGCC 873
Oy 62 LeuAsnGluAsnIleThrValProAspThrLysValAsnPheTyrAlaTrpLysArgMet 81
    ||| ||| ||| ||| |||
Db 874 CTGACCCCGAGAGATCTGTATCTCACTTCC-----TGCCTGGCTGCCTTTA 918
Oy 82 GluVal----- 83
Db 919 GACATGAGAGCTCTACACAGACAGTCTGCTGCTGACAGACAGAGGCTCTGTAG 978
Oy 84 ArgGlnGlnAlaValAlaGlyValTrpGln-----GlyLeuAlaLeuLeuSer 98
    ::::: ||| |||||
Db 979 AAGAGCGGAGAGCTTCAAGCTGCGCAAGCAAGCTGCTACCCCTGCTATGCTGTGC 1038
Oy 99 GluAlaValLeuArgGlyGlnAlaLeuLeuValAsnSer--SerGlnProTrpGluProLe 118
    ||||| ||| ::::: ||| ::::: |||
Db 1039 TTGCTGCTGCTGACGCGCTGTCTGTCTGCTATGTCGCATTCACATCCTGG----- 1090
Oy 118 uGlnLeuHisValAspLysAlaValSerGlyLeuArgSerLeuThrThrLeuLeuArgAl 138
    ::::: ||| |||||
Db 1091 -----AGCTGCTCATGATGAGG----- 1108
Oy 138 AlenGlyAlaGlnLysGluAlaIleSerProAspAlaAlaSerAlaAlaProLeuArg 158
    ||| ::::: ||||| ||| ||| ::::: |||
Db 1109 -CTGCCATGCGCCGAGGAGCATGAGGATACCTCTTAGCCAGAGTCTCTCCAAAGCG 1167
Oy 158 gThrIleThrAlaAspThrPheArgLysLeuPheArgValTyrSerAsnPhe----- 175
    ::::: ||| ::::: ||||| |||||
Db 1168 GGCCTCTTGTGTCGCTCA-----TTCAAGTTGTACTCATCTTTAACTTAATG 1215
Oy 176 -----LeuArgGlyLysLeuLysLeuTyrThrGlyGluAlaCys 188
    ||| |||||
Db 1216 GTGTCTCATGTTGTGGCTTCTATAGCTCTCCAGCTCTCCGAGCCCTGC 1264

```

RESULT 7
 US-09-992-598-137 Application US/09992598
 Patent No. US20020160384A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.
 APPLICANT: Baker, Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan L.
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Fong, Sherman
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerlitsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
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 APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 FILE REFERENCE: P2730PIC20
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US-09-813-775C-2 (1-193) x US-09-992-598-137 (1-2300)

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US-09-989-293A-137
Sequence 137, Application US/09989293A
Patent No. US20020177164A1
GENERAL INFORMATION:
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APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PLC66
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40	PRIOR APPLICATION NUMBER:	60/092182
41	PRIOR FILING DATE:	1998-07-09

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US-09-09-813-775C-2 (1-193) x US-09-989-730-137 (1-2300)

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	898	CTGTACTACATGCATCTCCCTTCTGGGGTTCTGCTCTCTGTGTACTCCTATGGT	957
Db	23	LeuPro---ValLeuGlyAlaProProArgLeuLeuCysAspSerArgValLeuGly	41
	958	CTGCGCCGCATGTCTCCGTCACTGGGAGCTGTAGTCAACCCCGCTGTGGAGAAC	1017
Db	42	TyrLeuLeuGluAlaLysGluAlaGluAsnIleThrThrGlyCysAlaGluHisCysSer	61
QY	1018	---CTGGAG-----GAGCAGCTGTACTGCTCAAGCCTTTGAGGAGGACGCC	1055
Db	62	LeuAsnGluAsnIleThrValProAspTrpIrrLysValAsnPheTyrAlaTrpLysArgMet	81
QY	1060	CTGACCCCGCAGATCTGTAACTCTACTTCC-----TGTGGCTGCTCTTAA	1104
Db	82	GluVal-----	83
QY	1105	GACATGGAGCTGCTACACAGACAGGCTCTGGCTCTGCACACACAGAGGGTCCCTGGTAG	1164
Db	84	ArgGlnGlnAlaValGluValTrpGln-----GlyLeuAlaLeuLeuSer	98

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Qy 99 GluaIaValIeuArgIyGlIaIaIeuleuValaIaSer-SerGlnProTgIuProLe 118
Db 1225 TTGGTGGGCGAGGGGCTCTGTGCTCATTTGGGCATCCACATCTCTG----- 1276
Qy 118 uGlnLeuHisValaSplysAlaValSerGlyLeuArgSerLeuThrLeuLeuArgAl 138
Db 1277 -----ACCTGCTCATCGATGAGC----- 1294
Qy 138 aleuGlyAlaGlnIysGluAlaIleSerProProAspAlaIaIaSerAlaIaProLeuAr 158
Db 1295 -CTGCCATGCCCGAGGATCAGAGTACTCTTAGGCGAGTCTCTTCCAAAGCTG 1353
Qy 158 gThrIleThrAlaAspThrPheArgLysLeuPheArgValTyrSerAsnPe----- 175
Db 1354 GGCCTCTTGGTGGCGTCA-----TTGAGGTGTACTCATCTTTACTTAATG 1401
Qy 176 -----LeuArgGlyLysLeuLysLeuTyrThrGlyAlaLys 188
Db 1402 GTGTCTCATCTGTGGCTTCTATAGCTTCACCTCTTCGAGCGCTGC 1450
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; Publication No. US20020198148A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Matababe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
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APPLICANT: Gerber, Hanspeter
APPLICANT: Gertlisen, Mary E.
APPLICANT: Goddard, Audrey
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APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
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Search completed: January 8, 2003, 07:52:35
Job time : 70.4596 secs

GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus.p2n model

Run on: January 8, 2003, 05:14:09 ; Search time 43.546 Seconds
(without alignments)
1359.222 Million cell updates/sec

Title: US-09-813-775c-2

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Delop 6.0 , Delext 7.0	

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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- 6: /cgcn2.6/ptodata/1/ina/Backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	991	99.3	725	5	PCT-US94-04361-21 Sequence 21, Appl
2	991	99.3	788	2	US-08-883-795A-35 Sequence 35, Appl
3	991	99.3	823	2	US-08-785-750-1 Sequence 1, Appl
4	991	99.3	823	4	US-09-205-337-1 Sequence 1, Appl
5	991	99.3	1011	2	US-08-750-128-12 Sequence 12, Appl
6	899.5	90.1	5107	4	US-08-910-647-3 Sequence 3, Appl
7	899.5	90.1	5107	4	US-09-620-925-3 Sequence 3, Appl
8	871.5	87.3	681	5	PCT-US94-04361-22 Sequence 22, Appl
9	846	84.8	1239	4	US-09-366-009-39 Sequence 39, Appl
10	843	84.5	508	1	US-08-318-193-69 Sequence 69, Appl
11	821	82.3	945	2	US-08-750-128-7 Sequence 7, Appl
12	821	82.3	969	2	US-08-750-128-4 Sequence 4, Appl

13	792.5	79.4	681	5	PCT-US94-04361-27	Sequence 27, Appl
14	769.5	77.1	688	5	PCT-US94-04361-26	Sequence 26, Appl
15	767	76.9	678	5	PCT-US94-04361-24	Sequence 24, Appl
16	759.5	76.1	687	5	PCT-US94-04361-25	Sequence 25, Appl
17	755	75.7	679	5	PCT-US94-04361-23	Sequence 23, Appl
18	732.5	73.4	3601	3	US-09-017-631-23	Sequence 23, Appl
19	732.5	73.4	3602	2	US-08-883-795A-33	Sequence 33, Appl
20	732.5	73.4	3602	4	US-09-018-138-1	Sequence 1, Appl
21	178	17.8	286	5	PCT-US94-04361-10	Sequence 10, Appl
22	148	14.8	1302	3	US-08-932-823A-1	Sequence 1, Appl
23	134.5	13.5	288	5	PCT-US94-04361-17	Sequence 17, Appl
24	134.5	13.5	289	5	PCT-US94-04361-16	Sequence 16, Appl
25	133.5	13.4	290	5	PCT-US94-04361-11	Sequence 11, Appl
26	130.5	13.1	274	5	PCT-US94-04361-15	Sequence 15, Appl
27	123	12.3	288	5	PCT-US94-04361-13	Sequence 13, Appl
28	120.5	12.1	280	5	PCT-US94-04361-14	Sequence 14, Appl
29	114	11.4	283	5	PCT-US94-04361-19	Sequence 19, Appl
30	112	11.2	283	5	PCT-US94-04361-18	Sequence 18, Appl
31	106	10.6	65	2	US-08-883-795A-24	Sequence 24, Appl
32	105	10.5	58	2	US-08-883-795A-6	Sequence 6, Appl
33	105	10.5	58	2	US-08-883-795A-22	Sequence 22, Appl
34	101	10.1	59	2	US-08-883-795A-4	Sequence 4, Appl
35	100.5	10.1	286	5	PCT-US94-04361-12	Sequence 12, Appl
36	97	9.7	56	2	US-08-883-795A-5	Sequence 5, Appl
37	97	9.7	61	2	US-08-883-795A-8	Sequence 8, Appl
38	96.5	9.7	605	1	US-08-388-779A-3	Sequence 3, Appl
39	96.5	9.7	605	1	US-08-591-070A-3	Sequence 3, Appl
40	96.5	9.7	605	2	US-08-927-855-3	Sequence 3, Appl
41	96.5	9.7	1059	3	US-08-471-045-57	Sequence 3, Appl
42	96.5	9.7	1059	3	US-08-469-712A-57	Sequence 57, Appl
43	96.5	9.7	1059	4	US-08-446-871-57	Sequence 57, Appl
44	96.5	9.7	1059	4	US-08-468-910-57	Sequence 57, Appl
45	96.5	9.7	1059	4	US-08-761-907-57	Sequence 57, Appl

ALIGNMENTS

```

RESULT 1
PCT-US94-04361-21
; Sequence 21, Application PC/TUS9404361
;
; GENERAL INFORMATION:
; APPLICANT: Brigham and Women's Hospital
; APPLICANT: 75 Francis Street
; APPLICANT: Boston, MA 02115
; APPLICANT: Bunn, H. Franklin
; APPLICANT: Wen, Danyl
; APPLICANT: Showers, Mark O.
; TITLE OF INVENTION: Erythropoietin Mutelins With Enhanced
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/04361
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/049,802
; FILING DATE: 21-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Cimbalia, Michele A.
; REGISTRATION NUMBER: 33,851
; REFERENCE/DOCKET NUMBER: 0627.336PC01

```

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 371-2600
 TELEFAX: (202) 371-2540
 INFORMATION FOR SEQ ID NO: 21:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 725 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: both
 PCT-US94-04361-21

Alignment Scores:

Pred. No.:	2,596-119	Length:	725
Score:	991.00	Matches:	192
Percent Similarity:	99.48%	Conservative:	0
Best Local Similarity:	99.48%	Mismatches:	1
Query Match:	99.30%	Indels:	0
DB:	5	Gaps:	0

US-09-813-775c-2 (1-193) x PCT-US94-04361-21 (1-725)

QY 1 MetGlyValHisGluCysProAlaTrpLeuTrpLeuLeuSerLeuLeuSerLeuPro 20
 DB 11 ATGGGGGTCGACGAATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 70
 QY 21 LeuGlyLeuProValLeuGluAlaProProAlaGluLeuIleCysAspSerArgValLeuGlu 40
 DB 71 CTGGGGCTCCAGTCTCTGGGGCCGCCACACGCTCATCTGTGACAGCCGAGTCTGGAG 130
 QY 41 ArgTyrLeuLeuGluAlaLeuGluAlaGluAlaGluAlaGluAlaGluAlaGluAla 60
 DB 131 AGGTACTCTTGGAGGCCCAAGAGGCCGGAATATCAGACGGGCTGTCTGACACTGC 190
 QY 61 SerLeuAsnGluAsnIleThrValProAspThrLysValAsnPheTyrAlaTrpLysArg 80
 DB 191 ACCTGAATGAGAAATATCACTGTCGCCAGACCAAAATTATTTATGCTCGGAAGAG 250
 QY 81 MetGluValArgGlnGlnAlaValAlaGluValITrpgInGlyLeuAlaLeuLeuSerGluAla 100
 DB 251 ATGGAGGTCGGGACAGGCGCTGAGAAATCTGGCAGGGCTGGCCCTGCTGCGGAAGCT 310
 QY 101 ValLeuArgGlyGlnAlaLeuLeuValAsnSerSerGlnProTrpGlnProLeuGlnLeu 120
 DB 311 CTCCTCGGGGGCCAGGCCCTGTGGTCAACTCTTCCACCGCTGGAGGCCCTGCGAGCTG 370
 QY 121 HisValAspLysAlaValSerGlyLeuArgSerLeuThrThrLeuLeuArgAlaLeuGly 140
 DB 371 CATGGGATTAAGCCGTCAGTGGCTTCGACAGCTCACCACACTGCTGGGGCTGGGA 430
 QY 141 AlaGlnLysGluAlaIleSerProProAspAlaIleSerAlaIleProLeuArgThrIle 160
 DB 431 GCCCAAGAAAGAGCCATCTCCCTCCAGATGGGCTCAGCTGCTCCACTCCGAACAAATC 490
 QY 161 ThrAlaAspThrPheArgLysLeuPheArgValTyrSerAsnPheLeuArgGlyLysLeu 180
 DB 491 ACTGCTGACACTTCCGCAACTCTTCCAGTCTACTCTCAATTTCTCCGGGAAAGCTG 550
 QY 181 LysLeuTyrThrGlyGluAlaCysArgThrGlyAspArg 193
 DB 551 AAGCTGTACACAGGGAGGCTGACAGACAGGGGACAGA 589

RESULT 2

US-08-883-795A-35
 Sequence 35, Application US/08883795A

GENERAL INFORMATION:
 APPLICANT: Delcive, Genevieve
 APPLICANT: Awang, Gregor
 TITLE OF INVENTION: Recombinant DNA Molecules and Expression
 NUMBER OF SEQUENCES: 39
 CORRESPONDENCE ADDRESS:
 ADDRESS: BERESKIN & PARR

STREET: 40 King Street West
 CITY: Toronto
 STATE: Ontario
 COUNTRY: Canada
 ZIP: M5H 3Y2

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/883,795A

FILING DATE: 27-JUN-1997

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Gravelle, Micheline

REGISTRATION NUMBER: 40,261

REFERENCE/DOCKET NUMBER: 7841-062

TELECOMMUNICATION INFORMATION:

TELEPHONE: (416) 364-7311

TELEFAX: (416) 361-1398

INFORMATION FOR SEQ ID NO: 35:

SEQUENCE CHARACTERISTICS:

LENGTH: 788 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

IMMEDIATE SOURCE:

CLONE: EPOLong

US-08-883-795A-35

Alignment Scores:

Pred. No.:	2,966-119	Length:	788
Score:	991.00	Matches:	192
Percent Similarity:	99.48%	Conservative:	0
Best Local Similarity:	99.48%	Mismatches:	1
Query Match:	99.30%	Indels:	0
DB:	2	Gaps:	0

US-09-813-775c-2 (1-193) x US-08-883-795A-35 (1-788)

QY 1 MetGlyValHisGluCysProAlaTrpLeuTrpLeuLeuSerLeuLeuSerLeuPro 20
 DB 80 ATGGGGGTCGACGAATATCACTGTCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 139
 QY 21 LeuGlyLeuProValLeuGluAlaProProAlaGluLeuIleCysAspSerArgValLeuGlu 40
 DB 140 CTGGGGCTCCAGTCTCTGGGGCCGCCACACGCTCATCTGTGACAGCCGAGTCTGGAG 199
 QY 41 ArgTyrLeuLeuGluAlaLeuGluAlaGluAlaGluAlaGluAlaGluAlaGluAla 60
 DB 200 AGGTACTCTTGGAGGCCCAAGAGGCCGGAATATCAGACGGGCTGTCTGACACTGC 259
 QY 61 SerLeuAsnGluAsnIleThrValProAspThrLysValAsnPheTyrAlaTrpLysArg 80
 DB 260 ACCTGAATGAGAAATATCACTGTCGCCAGACCAAAATTATTTATGCTCGGAAGAG 319
 QY 81 MetGluValArgGlnGlnAlaValAlaGluValITrpgInGlyLeuAlaLeuLeuSerGluAla 100
 DB 320 ATGGAGGTCGGGACAGGCCCTGTAGAAATCTGGCAGGGCTGGCCCTGTCGGAAGCT 379
 QY 101 ValLeuArgGlyGlnAlaLeuLeuValAsnSerSerGlnProTrpGlnProLeuGlnLeu 120
 DB 380 CTCCTCGGGGGCCAGGCCCTGTGGTCAACTCTTCCACCGCTGGAGGCCCTGCGAGCTG 439
 QY 121 HisValAspLysAlaValSerGlyLeuArgSerLeuThrThrLeuLeuArgAlaLeuGly 140
 DB 440 CATGGGATTAAGCCGTCAGTGGCTTCGACAGCTCACCACACTGCTGCGGGCTCGGGA 499
 QY 141 AlaGlnLysGluAlaIleSerProProAspAlaIleSerAlaIleProLeuArgThrIle 160

|||||
Db 500 GCCCAGAGGAGCATTCTCCCTCCAGATGCGCTCAGCTGCTCCACTCCGAAACATC 559
Qy 161 ThrAlaAspThrPheArgLysLeuPheArgValTyrSerAsnPheLeuArgGlyLysLeu 180
Db 560 ACAGCTGACACTTTCGCCAACAACCTTCGAGTCTACTCCAAATTTCTCCGCGGAAAGCTG 619
Qy 181 LysLeuTyrThrGlyGluAlaCysArgThrGlyAspArg 193
Db 620 AACCTGTACACAGGAGGAGCTCCAGAGACAGCGGACAGA 658
RESULT 3
US-08-785-750-1
Sequence 1, Application US/08785750
Patent No. 5846528
GENERAL INFORMATION:
APPLICANT: PODSAKOFF, GREGORY M.
APPLICANT: KURTZMAN, GARY J.
TITLE OF INVENTION: METHODS OF TREATING ANEMIA USING
TITLE OF INVENTION: RECOMBINANT ADENO-ASSOCIATED VIRUS VARIATIONS
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROBINS & ASSOCIATES
STREET: 90 MIDDLEFIELD ROAD, SUITE 200
CITY: MENLO PARK
STATE: CA
COUNTRY: USA
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/785,750
FILING DATE: 16-JAN-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/588,355
FILING DATE: 18-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: MCCracken, THOMAS P.
REGISTRATION NUMBER: 38,548
REFERENCE/DOCKET NUMBER: 0800-0009.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 325-7812
TELEFAX: (415)325-7823
INFORMATION FOR SEQ. ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 823 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-785-750-1
Alignment Scores:
Pred. No.: 3,17e-119 Length: 823
Score: 991.00 Matches: 192
Percent Similarity: 99.488 Conservative: 0
Best Local Similarity: 99.488 Mismatches: 1
Query Match: 99.308 Indels: 0
Gaps: 0
US-09-813-775C-2 (1-193) x US-08-785-750-1 (1-823)
Qy 1 MetGlyValHisGluCysProAlaIlePheTyrPheLeuLeuSerLeuLeuSerLeuPro 20
Db 52 ATGGGGGTGCACCAATGCTCTGCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 111
Qy 21 LeuGlyLeuProValLeuGlyAlaProPheArgLeuLeuLeuGlyAspSerArgValLeuGlu 40
Db 112 CTGGGCTCCCACTCTCTCTGGGCGCCCAACAGCGCTCATCTGTGACACAGCGAGTCTGGAG 171

Qy 41 ArgTyrLeuLeuGluAlaLysGluAlaGluAsnIleThrThrGlyCysAlaGluHisCys 60
Db 172 AGGTAACCTCTTGGAGGCGCAAGAGCGCCAGACAATATCCAGACGGGCTGTGCTGAACACTGC 211
Qy 61 SerLeuAsnGluAsnIleThrValProAspThrLysValAsnPheTyrAlaIlePheLysArg 80
Db 232 AGCTTGAATGAGATACACTGCTCCAGACCAAAAGTTAATTTCTATGCTGTGAAGAGG 291
Qy 81 MetGlyValArgGlnGlnAlaValAlaGluValTyrGlnGlyLeuAlaLeuSerGluAla 100
Db 292 ATGGAGGTCCGGGACGACAGGCGCTGAGAGTCTGGCAGGCGCTGCGCTGTGGAAAGCT 351
Qy 101 ValLeuArgGlyGlnAlaLeuLeuValAsnSerSerGlnProTyrGluProLeuGlnLeu 120
Db 352 GTCTCGGGGCGCAGGCGCTGTGTGTAACCTCTTCCAGCGGAGGAGCCCTCGCAGAGCTG 411
Qy 121 HisValAspLysAlaValSerGlyLeuArgSerLeuThrThrLeuLeuArgAlaLeuGly 140
Db 412 CATGTGATTAAGCCGCTCACTGCTCCAGGCTCCACCTCTGCTTCCGGCTCTGGGA 471
Qy 141 AlaGlnGluGluAlaIleSerProProAlaAlaSerAlaAlaProLeuArgThrIle 160
Db 472 GCCCAGAGGAGCATTCTCCCTCCAGATGCGGCTCAGCTCTCCACTCCGAAACATC 531
Qy 161 ThrAlaAspThrPheArgLysLeuPheArgValTyrSerAsnPheLeuArgGlyLysLeu 180
Db 532 ACTGCTGACACTTTCGCCAACAACCTTCGAGTCTACTCCAAATTTCTCCGCGGAAAGCTG 591
Qy 181 LysLeuTyrThrGlyGluAlaCysArgThrGlyAspArg 193
Db 592 AACCTGTACACAGGAGGAGCTCCAGAGACAGCGGACAGA 630
RESULT 4
US-09-205-337-1
Sequence 1, Application US/09205337
Patent No. 6325998
GENERAL INFORMATION:
APPLICANT: PODSAKOFF, GREGORY M.
APPLICANT: KURTZMAN, GARY J.
TITLE OF INVENTION: METHODS OF TREATING ANEMIA USING
TITLE OF INVENTION: RECOMBINANT ADENO-ASSOCIATED VIRUS VARIATIONS
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROBINS & ASSOCIATES
STREET: 90 MIDDLEFIELD ROAD, SUITE 200
CITY: MENLO PARK
STATE: CA
COUNTRY: USA
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/205,337
FILING DATE: 04-Dec-1998
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/785,750
FILING DATE: <unknown>
ATTORNEY/AGENT INFORMATION:
NAME: MCCracken, THOMAS P.
REGISTRATION NUMBER: 38,548
REFERENCE/DOCKET NUMBER: 0800-0009.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 325-7812
TELEFAX: (415)325-7823
INFORMATION FOR SEQ. ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 823 base pairs
TYPE: nucleic acid


```

Oy      161  TTTTAAAPThrPheAagLySLenUPheArgValTYSerASnPheneunrgLYLysLeu 180
Db      481  ACTGCTGACACTTTCGCCAACACTTTCCTCCAGTCTACTCCAATTTCCTCGGGGAAGCTG 540
Oy      181  LysLeuTyrrThrGLYGuAlaCYAsrGTThGLYAsPaRg 193
Db      541  AAGCTGTACACAGGGAGGCGCTGCAGACACAGGGAGCAGA 579

RESULT 6
US-08-910-647-3
; Sequence 3, Application US/08910647
; Patent No. 6251433
GENERAL INFORMATION:
APPLICANT: Zuckermann et al.
TITLE OF INVENTION: Compositions and Methods for
POLYNUCLEOTIDE DELIVERY
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
STATE: California
COUNTRY: U.S.A.
ZIP: 94608-2916
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/910,647
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Fujita, Sharon M.
REGISTRATION NUMBER: 38,459
REFERENCE/DOCKET NUMBER: 1218.002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 923-2706
TELEFAX: (510) 655-3542
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5107 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-910-647-3

Alignment Scores:
Pred. No.: 4,64e-106 Length: 5107
Score: 899.50 Matches: 176
Percent Similarity: 95.34% Conservative: 8
Best Local Similarity: 91.19% Mismatches: 8
Query Match: 90.13% Indels: 1
Dbs: 4 Gaps: 1

US-09-813-775c-2 (1-193) x US-08-910-647-3 (1-5107)
Oy      1 MetIyVahHsgLucYSPRoAlATPLPeUleuSenSerleuSenSerleuPro 20
Db      1710 ATGGGGGTGCACGAMtCTCTGCTGGCTGGCTTCTCTCTCTCTCTGCGCTCCCT 1769
Oy      21 LeuGIyLeuProVaIlLeuGIyAlaPrOProArGLeuILeCYAsPSerArGYAlLeuGI 40
Db      1770 CTGGGCTCCCATGTCGCCGGGCGCCCAACACAGCGCTATCTGTACAGCGCGAGTCTTGAG 1822
Oy      41 ArgTYrLeuLeuGuAlaLYSGuAlaGuIAsnILeThrThGLYCYSAlaGUlnICYS 60
Db      1830 AGGTACCTCTTGAGGCCCAAGGAGGCCGAGAAATGTCACAGATGGCGTTCGCCAAGAGCTGC 1885
Oy      61 SerLeuAnSngLuSnILeThrValPROASPThrLYSVAlAsnPhETyrAlATrPLYSarG 80

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Db 1890 AGCTTGATATGAGATATACACCGCTCCAGACACCAAGTTAACTTCTATGCTGGAGACGG 1949
QY 81 MetGluValArgGlnGlnAlaValGluValTrrGlnGlyLeuAlaLeuSerGlnAla 100
Db 1950 ATGGAGATCGGCGCCAGCGGCTGTATGAAGTCTGGACAGCGCTGCGCTCTCTCAAGAACT 2009
QY 101 ValLeuArgGlyGlnAlaLeuLeuValAsnSerSerGlnProTrrGluProLeuGlnLeu 120
Db 2010 GTCTCTGGGGGGCCAGGCGCTGTGGGCAACTCTTCCACACCTTTCGACGCCCTCGACCTG 2069
QY 121 HisValAspLysAlaValSerGlyLeuArgSerLeuThrThrLeuLeuArgAlaLeuGly 140
Db 2070 CACATGGATTAAGGCATCATGTGGCTTCGAGCATACCACATCTGCTTGGGGCGTGGGA 2129
QY 141 AlaGlnLysGluAlaAlaLeuSerProAspAlaAlaSerAlaAlaProLeuArgThrLe 160
Db 2130 GCCCAG--GAAGGACATCTCCCTCCACATCGCGCTCGGCTGCTGCACCTCGGAACATC 2186
QY 161 ThrAlaAspThrPheArgGlyLeuPheArgValTyrSerAsnPheLeuArgGlyLysLeu 180
Db 2187 ACTGCTGACACTTTCGCAAAACCTTCCGACGCTACTCCAAATTTCTCTCGGGGAAACCTG 2246
QY 181 LysLeuArgThrGlnGluAlaGlyAsnGlyThrGlyAspArg 193
Db 2247 AAGCTGTACAGGGGGAGGCGCTCGACGAGAGAGGGGACAGA 2285

RESULT 7
US-09-620-925-3
Sequence 3, Application US/09620925
Patent No. 6468986
GENERAL INFORMATION:
APPLICANT: Zuckermann et al.
TITLE OF INVENTION: Compositions and Methods for
Poly-nucleotide Delivery
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
STATE: California
COUNTRY: U.S.A.
ZIP: 94608-2916
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/620,925
FILING DATE: 21-Jul-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/910,647
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Fujita, Sharon M.
REGISTRATION NUMBER: 38,459
REFERENCE/DOCKET NUMBER: 1218.002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 923-2706
TELEFAX: (510) 655-3542
SEQUENCE CHARACTERISTICS:
SEQUENCE ID NO: 3
LENGTH: 5107 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-620-925-3

Alignment Scores: 4..64e-106 Length: 5107

```


US-09-366-009-39
Sequence 39, Application US/09366009
Patent No. 6426042
GENERAL INFORMATION:
APPLICANT: Asada, Kiyozo
Uemori, Takashi
Koyama, No. 6426042uto
Hashino, Kimikazu
Kato, Ikunoshin
TITLE OF INVENTION: METHOD FOR GENE TRANSFER INTO TARGET
CELLS WITH RETROVIRUS
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: WEISER & ASSOCIATES
STREET: 230 South Fifteenth Street, Suite 500
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/366,009
FILING DATE: 02-Aug-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/809,156
FILING DATE: <Unknown>
APPLICATION NUMBER: JP 294382/1995
FILING DATE: 13-NOV-1995
APPLICATION NUMBER: JP 051847/1996
FILING DATE: 08-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Weiser, Gerard J.
REGISTRATION NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 977,6507P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-875-8383
TELEFAX: 215-875-8394
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 1239 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-09-366-009-39
Alignment Scores:
Pred. No.: 4,22e-100 Length: 1239
Score: 846.00 Matches: 165
Percent Similarity: 99.40% Conservative: 1
Best Local Similarity: 98.80% Mismatches: 1
Query Match: 84.77% Indels: 0
DB: 4 Gaps: 0
US-09-813-775C-2 (1-193) x US-09-366-009-39 (1-1239)
QY 27 G1YAlAProProlArgLeuIleCysAspSerArgValLeuGluArgTyrLeuLeuGluAla 46
|||||
Db 694 GGTGCCCCACACAGCCGCTGACAGCCGAGCTCTCGACAGAGTACCTCTTGAGAGCC 753
QY 47 LysGluAlaGluAsnIleThrThrGlyCysAlaGluHisCysSerLeuAsnGluAsnIle 66
|||||
Db 754 AAGGAGGCCGAGATATCAGCAGCGGCTGTGTGAACACTGACCTGGAATGACATATC 813
QY 67 ThValProAspThrIysValAsnPhetYrAlaTrpIysArgMetGluValArgGlnGln 86
|||||

Db 814 ACTGTCCACAGACCAAGTTAATTTCATGCTCGAAGAGATGAGTGTGGCCACAG 873
QY 87 AlAValGluValTrpGlnGlyLeuAlaLeuLeuSerGluAlaValLeuArgGlyGlnAla 106
|||||
Db 874 GCCGTAGAAGTCTGGCAGGGGCTGGCCCTGCTGTGCGAAGCTGTCTGGGGGCGACGCC 933
QY 107 LeuLeuValAsnSerSerGlnProTrpGluProLeuGlnLeuHisValAspLysAlaVal 126
|||||
Db 934 CTGTGTGTCAACTCTTCCAGCCGCTGGAGCCCTGCAGCTGATGTGATGAAGCCGCTG 993
QY 127 SerGlyLeuArgSerLeuThrThrLeuLeuArgAlaLeuGlyAlaGlnLysGluAlaIle 146
|||||
Db 994 AGTGCCCTTGCACAGCTCCACACCTCTCTGCGGCTGTGGAGCCGAGGAAGGACCATC 1053
QY 147 SerProAspAlaAlaSerAlaAlaProLeuArgThrIleThrAlaAspThrPheArg 166
|||||
Db 1054 TCCCTTCAGATGGGGGCTCAGCTGCTCCACTCGGAACATCACTGCTGACACTTCCGC 1113
QY 167 LysLeuPheArgValTyrSerAsnPhelLeuArgGlyLysLeuLysLeuTyrThrGlyGlu 186
|||||
Db 1114 AAACCTTCGAGCTCACTCAATTTCTCCGGGGAAGCTGAAGCTGTACACAGGGAG 1173
QY 187 AlaCysArgThrGlyAspArg 193
|||||
Db 1174 GCTGTGAGAGACGGGAGAGA 1194
RESULT 10
US-08-318-193-69
Sequence 69, Application US/08318193
Patent No. 5641663
GENERAL INFORMATION:
APPLICANT: GARVIN, Robert T.
TITLE OF INVENTION: AN EXPRESSION SYSTEM FOR THE SECRETION
TITLE OF INVENTION: OF BIOACTIVE HUMAN GRANULOCYTE MACROPHAGE COLONY
STIMULATING FACTOR (GM-CSF) AND OTHER HETEROLOGOUS
NUMBER OF SEQUENCES: 91
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/318,193
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,314
FILING DATE:
APPLICATION NUMBER: US 07/224,568
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 18740/116 CACO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 508 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
MOLECULE TYPE: linear
MOLECULE TYPE: other nucleic acid;

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; DESCRIPTION: Synthetic DNA oligonucleotide
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 5..502
; US-08-318-193-69
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; Alignment Scores:
;   Pred. No.: 2,46e-100      Length: 508
;   Score: 843.00             Matches: 165
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;   Best Local Similarity: 99.40%  Mismatches: 1
;   Query Match: 84.47%        Indels: 0
;   DB: 1                      Gaps: 0
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; US-09-813-775c-2 (1-193) x US-08-318-193-69 (1-508)
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; DB 5 GCGCGCGCGCGCTCATCTGCGACACCGCGCTCTCGAGCGGTACTGCTCGAGCGCAAG 64
;
; QY 48 GluAlaGluAsnIleThrThrGlyCysAlaGluHisCysSerLeuAsnGluAsnIleThr 67
; DB 65 GAGCGCGAGAAATATCAGCAGCGGGGTGCGCGAGCACTGCTCCCTCAACGAGAAATCAGC 124
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; QY 68 ValProAspThrLysValAsnPhenylAlaTyrPlyArgMetGluValArgGlnGlnAla 87
; DB 125 GTCCCGACACAGGTCACTTCTACGCTGGAAGCGCATGGAGGTGGCGCAGCAGCGCG 184
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; QY 88 ValGluValTrpGlnGlyLeuAlaLeuLeuSerGluAlaValLeuArgGlnAlaLeu 107
; DB 185 GTGAGAGTGTGGCAGGGGCTCGCGCTCTCTCGAGCGGTCTCGCGCGCGCGCGCTC 244
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; QY 108 LeuValAsnSerSerGlnProTrrpGluProLeuGlnLeuHisValAspLysAlaValSer 127
; DB 245 CTGGTGAACCTGCTCCAGCGCGTGGAGCGCGCTCCAGCTGACAGTGCACAAAGCGCTC 304
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; QY 128 GlyLeuArgSerLeuThrThrLeuLeuArgAlaLeuGluAlaGlnLysGluAlaIleSer 147
; DB 305 GGGCTGGTCTCTGACACGCTGTGCTGCGCTCGGTGGCCAGAGAGCGCATCTCG 364
;
; QY 148 ProProAspAlaAlaSerAlaAlaProLeuArgThrIleThrAlaAspThrPheArgLys 167
; DB 365 CCGCGCGAGCGCGCGCGCGCGCGCGCTGCGAGCATCAGCGCGAGCAGCTTCCGCAAG 424
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; QY 168 LeuPheArgValIlySerAsnPhenylArgLysLysLeuLysLeuTyrThrGlyGluAla 187
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;
; QY 188 CysArgThrGlyAspArg 193
; DB 485 TGCCGACGCGGCGCGCGG 502
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; RESULT 11
; US-08-750-128-7
; Sequence 7, Application US/08750128
; Patent No. 5916773
;
; GENERAL INFORMATION:
; APPLICANT: MELE Antonio,
; APPLICANT: DE SANTIS Rita,
; APPLICANT: CARLONI Cristina,
; APPLICANT: COSCARIELLA Annamaria
; TITLE OF INVENTION: Hybrid molecule of formula GM-CSF-L-EPO or
; TITLE OF INVENTION: EPO-L-GM-CSF for hematopoietic stimulation
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LOWE, PRICE, LEBLANC & BECKER
; STREET: 99 Canal Center Plaza, Suite 300
; CITY: Alexandria
; STATE: VIRGINIA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk, 3.50 inch.

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; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentia Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/750,128
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IT FI 94 A 000106
; FILING DATE: 27-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Robert L. Price
; REGISTRATION NUMBER: 22,685
; REFERENCE/DOCKET NUMBER: 2879-007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-684-1111
; TELEFAX: 703-684-1124
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 945 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; HYPOTHEICAL: NO
; US-08-750-128-7
;
; Alignment Scores:
;   Pred. No.: 4.83e-97      Length: 945
;   Score: 821.00             Matches: 162
;   Percent Similarity: 97.01%  Conservative: 0
;   Best Local Similarity: 97.01%  Mismatches: 5
;   Query Match: 82.26%        Indels: 0
;   DB: 2                      Gaps: 0
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; US-09-813-775c-2 (1-193) x US-08-750-128-7 (1-945)
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; QY 27 GlyAlaProProArgLeuIleCysAspSerArgValLeuGluArgTyrLeuGluAla 46
; DB 442 GGGGCGCGCGCTCACTCATCTGTGTGACAGCGAGTCTCGAGAGGTACTCTGGAGGCC 501
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; QY 47 LysGluAlaGluAsnIleThrThrGlyCysAlaGluHisCysSerLeuAsnGluAsnIle 66
; DB 502 AAGGAGCGCGAATAATATCAGCAGCGGTGTCTGAACACTGCAGCTTGATGAGAAATATC 561
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; QY 67 ThrValProAspThrLysValAsnPhenylArgLysLysLeuLysLeuTyrThrGlyGln 86
; DB 562 ACTGTCCCGACACCAAGTTAATTTCTATGCTTGGAGAGGATGAGGTGCGGCGCAG 621
;
; QY 87 AlaValGluValTrpGlnGlyLeuAlaLeuLeuSerGluAlaValLeuArgGlnAla 106
; DB 622 GCCGTAGAAGTGTGCGAGGGCTGCGCTGTGCGAAGCTGTCTCGGGGGCGAGGCC 681
;
; QY 107 LeuLeuValAsnSerSerGlnProTrrpGluProLeuGlnLeuHisValAspLysAlaVal 126
; DB 682 CTGTTGGTCAACTCTCCAGCGCGTGGAGCGCGCTGCACTGCAATGATTAACCCGTC 741
;
; QY 127 SerGlyLeuArgSerLeuThrThrLeuLeuArgAlaLeuGluAlaGlnLysGluAlaIle 146
; DB 742 AGTGCGCTTCCGAGCGCTACCACTGCTGCTCGGCTGTGGAGCCGAGAGAGCCATC 801
;
; QY 147 SerProProAspAlaAlaSerAlaAlaProLeuArgThrIleThrAlaAspThrPheArg 166
; DB 802 TCCCTCCGAGATGGCGCTCAGCTGCTGCTCGGCTGTGGAGCCGAGAGAGCCATC 861
;
; QY 167 LysLeuPheArgValIlySerAsnPhenylArgLysLysLeuLysLeuTyrThrGlyGlu 186
; DB 862 AAACCTTCGAGTCTACTCCCAATTTCTCCGCGGAAAGCTGAAGCTTACACAGGAGAG 921
;
; QY 187 AlaCysArgThrGlyAspArg 193
; DB 922 GCTCGAGAGCAGGGGAGCAGA 942

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RESULT 12
US-08-750-128-4
Sequence 4, Application US/08750128
Patent No. 5916773
GENERAL INFORMATION:
APPLICANT: MELE Antonio,
APPLICANT: DE SANTIS Rita,
APPLICANT: CARLONI Cristina,
APPLICANT: COSCARIELLA Annamaria
TITLE OF INVENTION: Hybrid molecule of formula GM-CSF-L-EPO or
TITLE OF INVENTION: EPO-L-GM-CSF for hematopoietic stimulation
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: LOWE, PRICE, LeBLANC & BECKER
STREET: 99 Canal Center Plaza, Suite 300
CITY: Alexandria
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk, 3.50 inch.
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/750,128
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IT FI 94 A 000106
FILING DATE: 27-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Robert L. Price
REGISTRATION NUMBER: 22,685
REFERENCE/DOCKET NUMBER: 2879-007
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-684-1111
TELEFAX: 703-684-1124
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 969 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
US-08-750-128-4
Alignment Scores:
Pred. No.: 5.03e-97 Length: 969
Score: 821.00 Matches: 162
Percent Similarity: 97.01% Conservative: 0
Best Local Similarity: 97.01% Mismatches: 5
Query Match: 82.26% Indels: 0
Gaps: 0
DB: 2
US-09-813-775C-2 (1-193) x US-08-750-128-4 (1-969)
Oy 27 GYALAPROPRoATrgLEuILECysAspSerArGValLEuGuIARgTYrLEuLEuLAla 46
Db 466 GGGGGGGGGGGCTCACTATCTGTGACAGCCGAGTCTGGAGAGGTACCTTGGAGGCG 525
Oy 47 LysGluAlaGluAsnLIeThrThrGlyCysAlaGluHisCysSerLeuAsnGluAsnLIe 66
Db 526 AAGGAGCGCCGGAATATACGACGCGGCTGTGTAACAACCTGCAGCTTGATGACGATATAC 585
Oy 67 ThrValProAspThrLysValAsnPhetYrAlaTrpLysAspMetGluValArgGlnGln 86
Db 586 ACTGTCCAGACACCAAGATTAAATTCTATGCTCGAAGAGGATGAGGTCCGCGCAGCAG 645
Oy 87 AlaValGluValTrpGlnGlyLeuAlaLeuLeuSerGluAlaValLeuArgGlyGlnAla 106
Db 646 GCCGTAGAAGTCTGGCAGGCGCTGGCTGTGTGGAAGCTGTCTGGGGGGCCAGGCC 705

Oy 107 LeuLeuValAsnSerSerGlnProTrpGluProLeuGlnLeuHisValAspLysAlaVal 126
Db 706 CTGTTGCTCAACTCTTCCACGCGGTGGAGCCCTCGACAGCTGATGATTAACCCCTC 765
Oy 127 SerGlyLeuArgSerLeuThrThrLeuLeuArgAlaLeuGlyAlaGlnGluAlaIle 146
Db 766 AATGGCTCTTCGACGCTCACCTCTGCTTCGGGCTGTGGAGCCAGAAAGGAAACCATC 825
Oy 147 SerProAspAlaAlaSerAlaAlaProLeuArgTrpLIEThrAlaAspThrPheArg 166
Db 826 TCCCTCCAGATGGGCGCTCAGCTGCTCCACTCCGAAACATACTGTGACCTTCCGC 885
Oy 167 LysLeuPheArgValTyrSerAsnPhetLeuArgGlyLysLeuLysLeuYrThrGlyGlu 186
Db 886 AAACCTTCCGAGCTGCTACGCCAATTTCCGCCGGAAGAGCTGAACCTGTACACAGGGAG 945
Oy 187 AlaCysArgThrGlyAspArg 193
Db 946 GCCTGCAGACAGGGGAGCAGA 966
RESULT 13
PCT-US94-04361-27
Sequence 27, Application PC/TUS9404361
GENERAL INFORMATION:
APPLICANT: Brigham and Women's Hospital
APPLICANT: 75 Francis Street
APPLICANT: Boston, MA 02115
APPLICANT: Bunn, H. Franklin
APPLICANT: Men, Danyi
APPLICANT: Showers, Mark O.
TITLE OF INVENTION: Erythropoietin Mutains With Enhanced
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/04361
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/049,802
FILING DATE: 21-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Cimdala, Michele A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 0627,336PC01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 681 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: both
PCT-US94-04361-27
Alignment Scores:
Pred. No.: 1.44e-93 Length: 681
Score: 792.50 Matches: 159
Percent Similarity: 88.36% Conservative: 8
Best Local Similarity: 84.13% Mismatches: 21

Query Match: 79, 418 Indels: 1
DB: 5 Gaps: 1

US-09-813-775C-2 (1-193) x PCT-US94-04361-27 (1-681)

QY 5 GlnCysProAlaIrrPleuTrrPleuLeuSerLeuSerLeuProLeuGlyLeuPro 24
DB 1 GAATGTCCTGCC--CTGCTGCTTGTCTGATCTTGTCTGCTGCTCCCTGGGCTCCCA 57
QY 25 ValLeuGlyAlaProProAlaGlyLeuIleCysAspSerArgValLeuGlyAlaGlyLeu 44
DB 58 GTCTGGGGGGCCCCCTGCTCCATCTGTGACAGCCGATCTCTGGAGAGTACATCTG 117
QY 45 GluAlaLysGluAlaGluAsnIleThrGlyCysAlaGluHisCysSerLeuAsnGlu 64
DB 118 GAGGCGAGGAGGCGCAAAATGTCACCATGCTGCTCAAGAGCTGACCTTCAGTACGAG 177
QY 65 AsnIleThrValProAspThrLysValAsnPheThrAlaIrrPlysArgMetGluValArg 84
DB 178 AATATCATCTCTCCAGACACCAAGTCACTTCTATACCTGGAAGAGATGACAGTGGG 237
QY 85 GlnGlnAlaValGluValTrrPngInGlyLeuAlaLeuLeuSerGluAlaValLeuArgGly 104
DB 238 CACGAGGCTGTGAGATCTGTGGAGGGCTGCTGCTGTGACAGAGCATCTGCGGGGCG 297
QY 105 GlnAlaLeuLeuValAsnSerSerGlnProTrrPgluProLeuGlnLeuHisValAspLys 124
DB 298 CAGGCGCTGCTGGCCAACTCTCCAGCCATCTGAGACCTGCGACGCTGATGGATGAAA 357
QY 125 AlaValSerGlyLeuArgSerLeuThrThrLeuLeuArgAlaLeuGlyAlaGlnLysGlu 144
DB 358 GCGGTACAGCGCTGCGACACCTCACTCTCTGCTGGACCTGGAGGCGCCGAGAGGAA 417
QY 145 AlaIleSerProProAspAlaAlaSerAlaAlaProLeuArgThrIleThrAlaAspThr 164
DB 418 GCCACCTCCCTTCAGAGGCAACCTGCTGCTGCCAATCATCTGCGAGTACT 477
QY 165 PheArgLysLeuPheArgValTyrSerAsnPheLeuArgGlyLysLeuLysLeuTyrThr 184
DB 478 TTGTGCAAACTTTTCGAAATCTACTCCCACTTCCTGGGGAAGAGTACGCTGACACA 537
QY 185 GlyGluAlaCysArgThrGlyAspArg 193
DB 538 GGGGAGGCTGCGGAGAGAGAGACAGG 564

RESULT 14
PCT-US94-04361-26
Sequence 26, Application PC/TUS9404361
GENERAL INFORMATION:
APPLICANT: Brigham and Women's Hospital
APPLICANT: 75 Francis Street
APPLICANT: Boston, MA 02115
APPLICANT: Bunn, H. Franklin
APPLICANT: Men, Danyl
APPLICANT: Showers, Mark O.
TITLE OF INVENTION: Erythropoietin Mutelins With Enhanced
NUMBER OF INVENTIONS: Activity
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/04361
FILING DATE: Herewith

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/049,802
FILING DATE: 21-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Cimbala, Michele A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 0627,336PC01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ. ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 688 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: both
PCT-US94-04361-26

Alignment Scores:
Pred. No.: 1,42e-90 Length: 688
Score: 769.50 Matches: 158
Percent Similarity: 86.91% Conservative: 8
Best Local Similarity: 82.72% Mismatches: 22
Query Match: 77.10% Indels: 3
DB: 5 Gaps: 2

US-09-813-775C-2 (1-193) x PCT-US94-04361-26 (1-688)

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DB 1 GAATGTCCTGCCGGGCTG--CTTGTGCTATCTTGTCTGCTGCTCTCTGGGCTCCCA 57
QY 25 ValLeuGlyAlaProProAlaGlyLeuIleCysAspSerArgValLeuGlyAlaGlyLeu 44
DB 58 GTCTGGGGGGCCCCCTGCTCCATCTGTGACAGCCGATCTCTGGAGAGTACATCTTG 117
QY 45 GluAlaLysGluAlaGluAsnIleThrGlyCysAlaGluHisCysSerLeuAsnGlu 64
DB 118 GAGGCGAGGAGGCGCAAAATGTCACCATGCTGCTGCGCAAGCTGACCTTCAGTACGAG 177
QY 65 AsnIleThrValProAspThrLysValAsnPheThrAlaIrrPlysArgMetGluValArg 84
DB 178 AATATCATCTCTCCAGACACCAAGTCACTTCTATGCTGGAAGAGATGAGGTGTCAG 237
QY 85 GlnGlnAlaValGluValTrrPngInGlyLeuAlaLeuLeuSerGluAlaValLeuArgGly 104
DB 238 CACGAGGCTGTGAGATCTGTGGAGGGCTGCTGCTGTGACAGAGCATCTGCGGGGCG 297
QY 105 GlnAlaLeuLeuValAsnSerSerGlnProTrrPgluProLeuGlnLeuHisValAspLys 124
DB 298 CAGGCGCTGTTGGCCAACTCTCCAGCCATCTGAGAGCCCTGCGACGCTGTCGACAAA 357
QY 125 AlaValSerGlyLeuArgSerLeuThrThrLeuLeuArgAlaLeuGlyAlaGlnLysGlu 144
DB 358 GCTGTACAGGCGCTGCGACCTCACTCTCTCTGCTGGGCTGGAGGCGCCGAGAGGAA 417
QY 145 AlaIleSerProProAspAla-----AlaSerAlaAlaProLeuArgThrIleThrAla 162
DB 418 GCATGCCCTTCACAGAGCATGCCCTCTCTGCGCACCCCATCTCGAATCTTGTGTT 477
QY 163 AspThrPheArgLysLeuPheArgValTyrSerAsnPheLeuArgGlyLysLeuLysLeu 182
DB 478 GATACTTGTGCAAACTTTTCGCAACTACTCCAAATTCCTCTGCGGGAAGAGTACGAG 537
QY 183 TyrThrGlyGluAlaCysArgThrGlyAspArg 193
DB 538 TACACTGAGAGGCTGCGAGAGAGAGGACAGG 570

RESULT 15
PCT-US94-04361-24
Sequence 24, Application PC/TUS9404361
GENERAL INFORMATION:

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 8, 2003, 00:53:52 ; Search time 51.61 Seconds
(without alignments)
498.302 Million cell updates/sec

Title: US-09-813-775C-2
Perfect score: 998
Sequence: 1 MGVECPAMWLLSLSLP.....NLRGKIKLYTGACRTGDR 193

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues
Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
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5	991	99.3	193	15	AA1997
6	991	99.3	193	16	AA1997
7	991	99.3	193	16	AA1997
8	991	99.3	193	16	AA1997
9	991	99.3	193	17	AA1997
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19	991	99.3	193	23	AA1997	Epo-IL-3 short, re
20	991	99.3	193	23	AA1997	Human erythropoiet
21	991	99.3	193	23	AA1997	Human erythropoiet
22	991	99.3	193	23	AA1997	Human erythropoiet
23	991	99.3	193	23	AA1997	Human erythropoiet
24	991	99.3	193	23	AA1997	Human erythropoiet
25	991	99.3	193	23	AA1997	Human erythropoiet
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43	991	99.3	193	23	AA1997	Human erythropoiet
44	991	99.3	193	23	AA1997	Human erythropoiet
45	991	99.3	193	23	AA1997	Human erythropoiet

ALIGNMENTS

RESULT 1	AA1997	standard; Protein: 194 AA.
ID	AA1997	
XX	AA1997	
AC	AA1997	
XX	AA1997	
DE	28-MAR-2001	(first entry)
XX	Chimpanzee erythropoietin SEQ ID NO: 2.	
XX	Chimpanzee erythropoietin; EPO; hybridisation probe; gene therapy;	
KW	mapping; therapeutic agent.	
KW		
XX		
OS	Pan sp.	
XX		
PN	W0200068376-A1.	
XX		
PD	16-NOV-2000.	
XX		
PF	05-MAY-2000; 2000WO-US12370.	
XX		
PR	07-MAY-1999; 99US-0307307.	
XX		
PR	28-MAR-2000; 2000US-0307307.	
XX		
PA	(GETH) GENENTECH INC.	
XX		
PI	Desauvage F, Henner DJ;	
XX		
DR	WPI: 2001-007393/01.	
XX	N-PSDB; AAC66881.	
PT	Nucleic acids encoding chimpanzee erythropoietin, useful for treatment of e.g. anemia, also derived proteins, antibodies and modulators -	

XX Claim 1; Fig 1; 109pp; English.
 PS The present invention provides the coding and protein sequences of
 CC chimpanzee erythropoietin (EPO). These sequences can be used in gene
 CC therapy, to block the activity of EPO, as hybridisation probes, in
 CC genetic and chromosome mapping and as therapeutic agents.
 XX
 SQ Sequence 194 AA:
 Query Match 100.0%; Score 998; DB 22; Length 194;
 Best Local Similarity 100.0%; Pred. No. 4,8e-100;
 Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGVHECPAMWMLLSLSPGLPVLGAPPRILCDSRVLERLYLLEAKENITTCGAHC 60
 DB 1 MGVHECPAMWMLLSLSPGLPVLGAPPRILCDSRVLERLYLLEAKENITTCGAHC 60
 QY 61 SLNENITVPDTKVFYAMKRMVEYRQOAVEWQGLALSEAVLRGQALLVNSSQPMPEPLQ 120
 DB 61 SLNENITVPDTKVFYAMKRMVEYRQOAVEWQGLALSEAVLRGQALLVNSSQPMPEPLQ 120
 QY 121 HDKAVSGLSLTLTLRALGAQKEAISPDAASAPLRTITADTFRKLFRVYSNFLRGKL 180
 DB 121 HDKAVSGLSLTLTLRALGAQKEAISPDAASAPLRTITADTFRKLFRVYSNFLRGKL 180
 QY 181 KLYTGEACRTGDR 193
 DB 181 KLYTGEACRTGDR 193
 RESULT 2
 AAB34979
 ID AAB34979 standard; Protein: 193 AA.
 AC AAB34979;
 DT 27-MAR-2001 (first entry)
 DE Chimpanzee erythropoietin SEQ ID NO: 5.
 KW Chimpanzee; erythropoietin; EPO; hybridisation probe; gene therapy;
 KM mapping; therapeutic agent.
 XX
 OS Pan sp.
 PN WO200068376-A1.
 PD 16-NOV-2000.
 PF 05-MAY-2000; 2000MO-US12370.
 PR 07-MAY-1999; 99US-0307307.
 PR 28-MAR-2000; 2000US-0307307.
 PA (GETH) GENEENTECH INC.
 PI Desauvage F, Henner DJ;
 DR WPI; 2001-007393/01.
 PT Nucleic acids encoding chimpanzee erythropoietin, useful for treatment
 CC of e.g. anemia, also derived proteins, antibodies and modulators -
 XX
 PS Disclosure; Fig 3; 109pp; English.
 CC The present invention provides the coding and protein sequences of
 CC chimpanzee erythropoietin (EPO). These sequences can be used in gene
 CC therapy, to block the activity of EPO, as hybridisation probes, in
 CC genetic and chromosome mapping and as therapeutic agents.
 XX
 SQ Sequence 193 AA:

Query Match 99.4%; Score 992; DB 22; Length 193;
 Best Local Similarity 99.5%; Pred. No. 2.2e-99;
 Matches 192; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MGVHECPAMWMLLSLSPGLPVLGAPPRILCDSRVLERLYLLEAKENITTCGAHC 60
 DB 1 MGVHECPAMWMLLSLSPGLPVLGAPPRILCDSRVLERLYLLEAKENITTCGAHC 60
 QY 61 SLNENITVPDTKVFYAMKRMVEYRQOAVEWQGLALSEAVLRGQALLVNSSQPMPEPLQ 120
 DB 61 SLNENITVPDTKVFYAMKRMVEYRQOAVEWQGLALSEAVLRGQALLVNSSQPMPEPLQ 120
 QY 121 HDKAVSGLSLTLTLRALGAQKEAISPDAASAPLRTITADTFRKLFRVYSNFLRGKL 180
 DB 121 HDKAVSGLSLTLTLRALGAQKEAISPDAASAPLRTITADTFRKLFRVYSNFLRGKL 180
 QY 181 KLYTGEACRTGDR 193
 DB 181 KLYTGEACRTGDR 193
 RESULT 3
 AAP50300
 ID AAP50300 standard; protein: 193 AA.
 AC AAP50300;
 DT 01-JAN-1980 (first entry)
 DE Human erythropoietin encoded by positive clone (phage lambda-hel)
 DE isolated from human fetal liver gene bank.
 KW Erythropoietin; red blood cell; erythrocyte; anaemia; blood;
 KM disorder; ss; phage lambda-hel; gene bank.
 XX
 OS Homo sapiens.
 PN WO8502610-A.
 PD 20-JUN-1985.
 PF 11-DEC-1984; 84MO-US02021.
 PR 30-NOV-1984; 84US-0675298.
 PR 13-DEC-1983; 83US-0561024.
 PR 21-FEB-1984; 84US-0582185.
 PR 28-SEP-1984; 84US-0655841.
 PA (KIRI-) KIRIN-AMGEN INC.
 DR WPI; 1985-159229/26.
 DR N-PSDB; AAN50347.
 PT New polypeptide having properties of erythropoietin - is prepd.
 PT by cultivation of transformed eucaryotic or procaryotic host
 XX
 PS Disclosure; Page 43; 113pp; English.
 CC Human erythropoietin encoded by a sequence encoded by this phage
 CC lambda-hel is essential for red blood cell formation and is used
 CC for the diagnosis and treatment of blood disorders such as anaemia.
 CC Large amounts of EPO may be obtained using recombinant DNA
 CC techniques in contrast to small amounts obtained from plasma
 CC and urine. This sequence is expressed in E. coli. See also
 CC AAN50345-6, AAN50348-50 and AAP50298-99, AAP50301.
 XX
 SQ Sequence 193 AA:
 Query Match 99.3%; Score 991; DB 6; Length 193;
 Best Local Similarity 99.5%; Pred. No. 2.8e-99;
 Matches 192; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MGVHECPAMWMLLSLSPGLPVLGAPPRILCDSRVLERLYLLEAKENITTCGAHC 60

D _b	1	MGVHECCPAMLWLLLSLLSLPTGLPVLAGAPRLICDSRYLERLLEAKEMENITTGCAEHC	60
Q _y	61	SLNEIITTPDRFVNVSYAKRMFVRQOAAVEVMGIALLSAVLRGQALLVNSSQPMWPIQL	120
D _b	61	SLNEIITTPDRFVNVSYAKRMFVRQOAAVEVMGIALLSAVLRGQALLVNSSQPMWPIQL	120
Q _y	121	HVDKAVSGIRSLTTLRLALGAQKEAISPDDAASAPLRTITADTFRKLFRRVSYNPLRGKTL	180
D _b	121	HVDKAVSGIRSLTTLRLALGAQKEAISPDDAASAPLRTITADTFRKLFRRVSYNPLRGKTL	180
Q _y	181	KLYTGEACRTGDR	193
D _b	181	KLYTGEACRTGDR	193

```

XX RESULT 4
XX AAP70256
XX ID AAP70256 standard; protein: 193 AA.
XX AAP70256:
XX
XX 19-FEB-1991 (first entry)
XX
XX DE Sequence of human erythropoietin (EPO).
XX
XX KW Renal anaemia therapy; hormone.
XX
XX OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX FT Peptide 1..27
XX FT /label=SIGNAL
XX FT protein 28..193
XX FT Region 81..97
XX FT /note="Fragment that probe AAN70361 is based on"
XX
XX EP232034-A.
XX
XX PD 12-AUG-1987.
XX
XX PF 19-JAN-1987; 87EP-0300399.
XX
XX PR 23-JAN-1986; 86JP-0012868.
XX
XX PA (SUMO ) SUMITOMO CHEM IND KK.
XX PA (SUMI-) SUMITOMI SEIYAKU KK.
XX
XX PI Yanagi H, Ogawa I, Okamoto M, Hozumi T, Soga A, Yoshima T;
XX PI Tsutsumi M;
XX
XX WP1: 1987-223006/32.
XX DR N-PSDB; AAN70360, AAN70361.
XX
XX PT Human erythropoietin Prodn. - by culturing human cells, esp.
XX PT Namalwa cells, transformed with DNA encoding human erythropoietin
XX
XX PS Disclosure: Fig 1; 22pp: English.
XX
XX A cDNA library was prepd. from the poly (A) RNA, which was isolated
XX from the erythropoietin-producing human hepatoma cell Hp-1. The cDNA
XX library was screened using the probes given in AAN70361 and AAN70362. A
XX plasmid (named as p58-220) was isolated. The nucleotide sequence of
XX the cDNA obtained from this clone is shown in AAN70360.
XX
XX Sequence 193 AA:
XX
XX Query Match 99.3%; Score 991; DB 8; Length 193;
XX Best Local Similarity 99.5%; Pred. No. 2,8e-99;
XX Matches 192; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1 MGVCPCPMWLWLLSLSLPLGCPVGVGAPPRICDSRVIERLVLEAKENITTCGAHC 60
XX

```

Db	1	MGVHECPAMLLLTSLTSLPGLPVLGAPPRLLCDNRVLERVLLLEAKKEMENITTGAEHC	60
QY	61	SLNENITVYPTDKVNFYFMKKREYRQQAENVYWGGLALISEAVLRGQALLVYNSSQWPEIQL	120
Db	61	SLNENITVYPTDKVNFYFMKKREYRQQAENVYWGGLALISEAVLRGQALLVYNSSQWPEIQL	120
QY	121	HYDAVSGLSRLTLLTLLAALGAQKEAISPPDAASNAPLRTTADTFPKLFRVYSNPLRGKL	180
Db	121	HYDAVSGLSRLTLLTLLAALGAQKEAISPPDAASNAPLRTTADTFPKLFRVYSNPLRGKL	180
QY	181	KLYTGEACRTGDR	193
Db	181	KLYTGEACRTGDR	193

Query Match	99.3%	Score 991	DB 15	Length 193
Best Local Similarity	99.5%	Pred. No. 2.8e-99		
Matches 192	Conservative 0	Mismatches 1	Indels 0	Gaps 0
1	MGVHCSPAMLWMLLSLSLPLGLGAPPLPGICDSRYLERLLEAKENITTCGAEHC	60		
1	MGVHCSPAMLWMLLSLSLPLGLGAPPLPGICDSRYLERLLEAKENITTCGAEHC	60		
61	SLNENITAPDTRKVNKRMKEVRQAAVEVMQIGALLSEAVLRGQALLVNSQPEPIQL	120		

```

Db 61 SLNENTVPTDKVNFYAMKRMVEYGOAVEWOGALLSEAVLRGQALLVNSSQPMPEIQL 120
QY 121 HDKAVSGLSRLTTLRALGAQKEAISPPDASAPLRTITADTFPKLFRVYSNFLRGKL 180
    |||
Db 121 HDKAVSGLSRLTTLRALGAQKEAISPPDASAPLRTITADTFPKLFRVYSNFLRGKL 180
QY 181 KLYTGEACRTGDR 193
    |||
Db 181 KLYTGEACRTGDR 193

RESULT 6
AAR81982
ID AAR81982 standard; protein: 193 AA.
AC AAR81982;
XX
XX 27-FEB-1996 (first entry)
DT
DE Human erythropoietin.
KW Erythropoietin; sialylation; sialic acid; glycosylation;
KM reticulocyte; red blood cell; erythrocyte; haematocrit.
XX
OS Homo sapiens.
FH Key Location/Qualifiers
FT Peptide 1..27
FT /label= sig_peptide 51
FT Modified-site /label= N-glycosylation_site 65
FT Modified-site /label= N-glycosylation_site 110
FT Modified-site /label= N-glycosylation_site 153
FT Modified-site /label= O-glycosylation_site
FT
PM EP668351-A1.
XX
XX 23-AUG-1995.
PD
XX 12-OCT-1990; 90EP-0101849.
PF
XX 09-OCT-1990; 90MO-US05758.
PR 13-OCT-1989; 89US-0421444.
XX
XX (AMGE-) AMGEN INC.
PA
XX
XX Byrne TE, Elliott SG;
PI
XX WPI; 1995-284791/38.
DR
XX
XX New human erythropoietin analogues with increased glycosylation -
PT have increased activity useful for increasing prodn. of
PT reticulocytes and red blood cells
PS
XX Disclosure: Fig 5, 31pp; English.
XX
XX Human urinary erythropoietin (AAR81982) is a glycoprotein contg. 3 N-
CC linked and 1 O-linked oligosaccharide chain. Erythropoietin
CC analogues (AAR81983-87) have been produced in which the number of
CC glycosylation sites is increased.
XX
SQ Sequence 193 AA;

```

```

QY 61 SLNENTVPTDKVNFYAMKRMVEYGOAVEWOGALLSEAVLRGQALLVNSSQPMPEIQL 120
    |||
Db 61 SLNENTVPTDKVNFYAMKRMVEYGOAVEWOGALLSEAVLRGQALLVNSSQPMPEIQL 120
QY 121 HDKAVSGLSRLTTLRALGAQKEAISPPDASAPLRTITADTFPKLFRVYSNFLRGKL 180
    |||
Db 121 HDKAVSGLSRLTTLRALGAQKEAISPPDASAPLRTITADTFPKLFRVYSNFLRGKL 180
QY 181 KLYTGEACRTGDR 193
    |||
Db 181 KLYTGEACRTGDR 193

RESULT 7
AAR71137
ID AAR71137 standard; protein: 193 AA.
AC AAR71137;
XX
XX 17-OCT-1995 (first entry)
DT
DE Human erythropoietin.
KW Human erythropoietin; glycosylation; sialic acid; solubility;
KM half-life; biological activity; proteolysis resistance; anaemia;
KW chronic renal failure.
XX
OS Homo sapiens.
FH Key Location/Qualifiers
FT Peptide 1..27
FT /label= sig_peptide 51
FT
PM W09505465-A.
XX
XX 23-FEB-1995.
PD
XX 16-AUG-1994; 94WO-US09257.
PF
XX 13-OCT-1989; 89US-0421444.
PR 17-AUG-1993; 93US-0108016.
XX
XX (AMGE-) AMGEN INC.
PA
XX
XX Byrne TE, Elliott SG;
PI
XX WPI; 1995-098764/13.
DR
XX
XX Erythropoietin (EPO) analogues having additional glycosylation
PT site(s) - to increase sialic acid content, thereby increasing
PT solubility, serum half-life, biological activity and resistance
PT to proteolysis.
PS
XX Disclosure: Pages 80-81; 108pp; English.
XX
XX AAR71137 describes the amino acid sequence of human erythropoietin
CC (EPO), from which the inventions novel human EPO analogues were
CC derived. The analogues have at least one additional glycosylation
CC site, this is used to increase the sialic acid content which in
CC turn increases the solubility, half-life, biological activity and
CC proteolysis resistance of the protein. The analogues are useful
CC in claimed compns. for the treatment of chronic renal failure
CC associated anaemia.
XX
SQ Sequence 193 AA;

```

```

Query Match 99.3%; Score 991; DB 16; Length 193;
Best Local Similarity 99.5%; Pred. No. 2.8e-99;
Matches 192; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 MGVHECPAMLMILSLISLPGLPVLAGAPRLICDSRVLERLLEAKENITTCGAENC 60
    |||
1 MGVHECPAMLMILSLISLPGLPVLAGAPRLICDSRVLERLLEAKENITTCGAENC 60

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Db      1  MGVHECPAMWLMLLSLSLPLGLPYLGAPPRLLICDSRYLERYLEAKAEENITTCGAHC 60
QY      61  SLNENITVPDTRKVNFRYAKRMREVRQOAVEVWQGLALSEAVLRGALLVNSSQPEPIQL 120
        |||
Db      61  SLNENITVPDTRKVNFRYAKRMREVRQOAVEVWQGLALSEAVLRGALLVNSSQPEPIQL 120
QY      121  HVDAVAGSLRSLTTLRALGQKEAISPDDAASAPLRTITADTFRKLFRRYSNPLRGL 180
        |||
Db      121  HVDAVAGSLRSLTTLRALGQKEAISPDDAASAPLRTITADTFRKLFRRYSNPLRGL 180
QY      181  KLYTGEACRTGDR 193
        |||
Db      181  KLYTGEACRTGDR 193

RESULT 8
AAR74141
ID  AAR74141 standard; Protein; 193 AA.
XX
AC  AAR74141;
XX
DT  30-OCT-1995 (first entry)
XX
DE  Human erythropoietin.
XX
KW  Erythropoietin; anemia; gene therapy; gene transfer; red blood cell;
KM  RBC; erythrocyte; transformation; myoblast; EPO.
XX
OS  Homo sapiens.
XX
PN  M09513376-A.
XX
PD  18-MAY-1995.
XX
PF  09-NOV-1994; 94WO-U513066.
XX
PR  07-OCT-1994; 94US-0320480.
PR  10-NOV-1993; 93US-0149871.
XX
PA  (AMGE-) AMGEN INC.
XX  (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI  Hamamori Y, Kedes LH, Samal BB;
XX
DR  WPI: 1995-194095/25.
DR  N-PSDB: AA092296.
XX
PT  Gene therapy for treatment of anaemia - and increasing red blood cell
PS  production by transforming red blood cells with the erythropoietin gene
XX
PS  Disclosure; Page 38-40; 51pp; English.
XX
CC  The amino acid sequence encoded by human EPO cDNA is given in AAR74141.
CC  Transfection of target cells, e.g. myoblasts, with EPO cDNA and
CC  implantation into muscle tissue provides increased RBC prodn.
XX
SQ  Sequence 193 AA;

Query Match          99.3%; Score 991; DB 16; Length 193;
Best Local Similarity 99.5%; Pred. No. 2.8e-99;
Matches 192; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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```

QY      181  KLYTGEACRTGDR 193
        |||
Db      181  KLYTGEACRTGDR 193

RESULT 9
AAR98397
ID  AAR98397 standard; Protein; 193 AA.
XX
AC  AAR98397;
XX
DT  15-SEP-1996 (first entry)
XX
DE  Human erythropoietin.
XX
KW  Erythropoietin; EPO; anaemia; gene therapy; vector;
KM  scaffold attachment region; SAR element; transgenic animal.
XX
OS  Synthetic.
XX
FH  Key Location/Qualifiers
FT  Peptide 1..27
FT  /label= Sig_peptide
FT  Protein 28..193
XX  /label= Mat_protein
XX
PN  M09619573-A1.
XX
PD  27-JUN-1996.
XX
PF  18-DEC-1995; 95WO-CA00696.
XX
PR  19-DEC-1994; 94US-0358918.
XX
PA  (CANG-) CANGENE CORP.
XX
PI  Delcuve G;
XX
DR  WPI: 1996-309587/31.
DR  N-PSDB: AAT31529.
DR  N-PSDB: AAT31532.
XX
PT  Recombinant DNA molecule expressing mammalian erythropoietin -
PS  useful to transform cell lines, and for gene therapy, e.g. of
XX  anaemia and other red blood cell disorders
XX
PS  Claim 3; Page 58; 84pp; English.
XX
CC  Human erythropoietin (EPO) (AAR98397) functions to promote erythroid
CC  development, to initiate haemoglobin biosynthesis and to stimulate
CC  proliferation of immature erythroid precursors. It can be obtd.
CC  by stable, long-term expression in mammalian cell hosts transfected
CC  with a vector carrying EPO cDNA (AAT31529) or genomic DNA (AAT31532)
CC  operably linked to an expression control sequence and to 5' and 3'
CC  human apolipoprotein scaffold attachment region (SAR) elements (see
CC  also AAT31530-31). Transgenic animals can be produced that express
CC  the recombinant EPO in their milk.
XX
SQ  Sequence 193 AA;

Query Match          99.3%; Score 991; DB 17; Length 193;
Best Local Similarity 99.5%; Pred. No. 2.8e-99;
Matches 192; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY 121 HDKAVSGLSLTTLLRALGAQKEAISPDDAASAPLRTTTADTFKRLFRVYSNPLRGKL 180
DB 121 HDKAVSGLSLTTLLRALGAQKEAISPDDAASAPLRTTTADTFKRLFRVYSNPLRGKL 180
QY 181 KLYTGEACRTGDR 193
DB 181 KLYTGEACRTGDR 193

RESULT 10
AAV94530
ID AAY94530 standard; protein; 193 AA.
XX AAY94530:
AC AAY94530:
XX
XX
XX 28-NOV-2000 (first entry)
DE Human erythropoietin protein.
XX
XX
XX Human; erythropoietin; Epo; glycosylation; anaemia;
KW chronic renal failure; myelosuppressive therapy; cancer;
KW viral infection; HIV; blood loss.
XX
XX Homo sapiens.
OS
FH Key Location/Qualifiers
FT Peptide 1..27
FT /label= Signal
FT Protein 28..193
FT /label= Erythropoietin
XX
XX WO200024893-A2.
XX
XX PD 04-MAY-2000.
XX
XX PF 18-OCT-1999; 99WO-US24435.
XX
XX PR 23-OCT-1998; 98US-0178292.
XX
XX PA (AMGE-) AMGEN INC.
XX
XX PI Egrle JC, Elliott SG, Brown JK;
XX WPI: 2000-350735/30.
XX
XX DR Raising and maintaining hematocrit in a mammal by administering an
XX PT effective amount of a hyperglycosylated analog of erythropoietin,
XX PT useful for treating anemia associated with myelosuppressive therapy or
XX PT excessive blood loss -
XX
XX PS Disclosure; Figure 1; 63pp; English.
XX
XX The present sequence is human erythropoietin (Epo). Epo is a
CC glycoprotein hormone necessary for the maturation of erythroid
CC progenitor cells into erythrocytes. It has been discovered that
CC hyperglycosylated Epo has a longer half-life and greater in vivo
CC activity than recombinant human Epo. Several hyperglycosylated
CC Epo mutants (AAY94531 to AAY94544) have been made by in vitro
CC mutagenesis. Hyperglycosylated Epo analogs are useful as they
CC may be used instead of recombinant Epo to increase and maintain
CC the level of red blood cells in mammals. The Epo analogs may be
CC used to treat or prevent anemia associated with chronic renal
CC failure, myelosuppressive therapy, certain cancers, viral disease
CC such as HIV and excessive blood loss.
XX
XX
SQ Sequence 193 AA:
Query Match 99.3%; Score 991; DB 21; Length 193;
Best Local Similarity 99.5%; Pred. No. 2.8e-99;
Matches 192; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGVHECPAULMLLSLSTPLGLPVGAPRRLICDSRVLEKKEAKENITTCGAHC 60
DB 1 MGVHECPAULMLLSLSTPLGLPVGAPRRLICDSRVLEKKEAKENITTCGAHC 60

DB 1 MGVHECPAULMLLSLSTPLGLPVGAPRRLICDSRVLEKKEAKENITTCGAHC 60
QY 61 SLNENITVPDTKYNFYAMKRMVEYRQOAVEWQGLALISEAVLRGQALLVNSSQPMWPIQL 120
DB 61 SLNENITVPDTKYNFYAMKRMVEYRQOAVEWQGLALISEAVLRGQALLVNSSQPMWPIQL 120
QY 121 HDKAVSGLSLTTLLRALGAQKEAISPDDAASAPLRTTTADTFKRLFRVYSNPLRGKL 180
DB 121 HDKAVSGLSLTTLLRALGAQKEAISPDDAASAPLRTTTADTFKRLFRVYSNPLRGKL 180
QY 181 KLYTGEACRTGDR 193
DB 181 KLYTGEACRTGDR 193

RESULT 11
AAY93638
ID AAY93638 standard; protein; 193 AA.
XX AAY93638:
AC AAY93638:
XX
XX
XX 25-SEP-2000 (first entry)
DE Amino acid sequence of a human erythropoietin polypeptide.
XX
XX
XX Human; erythropoietin; Epo; inhibitor; nuclear factor-kappaB; NF-kappaB;
KW multi-drug resistance gene; malignant hemopathy; solid tumour;
KW malignant blood disease; leukaemia; lymphoma; solid cancer.
XX
XX
XX Homo sapiens.
OS
XX
XX WO200030587-A2.
XX
XX PD 02-JUN-2000.
XX
XX PF 24-NOV-1999; 99WO-FR02897.
XX
XX PR 25-NOV-1998; 98FR-0014858.
XX
XX PA (CNRS) CENT NAT RECH SCI.
XX
XX PI Hirsch F, Haeflner A;
XX WPI: 2000-399901/34.
XX DR N-PSDB: AAA46697.
XX
XX DR Treatment of haematological or solid tumours using an inhibitor of the
XX PT activation of nuclear factor-kappaB, particularly to prevent
XX PT development of resistance to chemotherapeutics -
XX
XX PS Claim 11; Page 30; 30pp; French.
XX
XX The present sequence represents a human erythropoietin (EPO) polypeptide.
CC The human growth hormone protein is used as an inhibitor of the
CC activation of nuclear factor-kappaB (NF-kappaB). The inhibitor inhibits
CC activation of NF-kappaB, and thus transcription of the multi-drug
CC resistance gene (which contains binding sites for NF-kappaB within its
CC regulatory regions). The inhibitors are used to produce pharmaceuticals
CC which may be used in the treatment of malignant hemopathy or solid
CC tumours. The inhibitors are especially used to treat malignant blood
CC diseases (leukaemia, lymphoma) and solid cancers (of breast or ovary).
XX
XX
SQ Sequence 193 AA:
Query Match 99.3%; Score 991; DB 21; Length 193;
Best Local Similarity 99.5%; Pred. No. 2.8e-99;
Matches 192; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGVHECPAULMLLSLSTPLGLPVGAPRRLICDSRVLEKKEAKENITTCGAHC 60
DB 1 MGVHECPAULMLLSLSTPLGLPVGAPRRLICDSRVLEKKEAKENITTCGAHC 60

QY 61 SLNENITVPDTKYNFYAMKRMVEYRQOAVEWQGLALISEAVLRGQALLVNSSQPMWPIQL 120
DB 61 SLNENITVPDTKYNFYAMKRMVEYRQOAVEWQGLALISEAVLRGQALLVNSSQPMWPIQL 120

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Db      61 SLNENITVPDTKVFYAMKREVEGQAAVEWQGLALLSEAVLRQOALLVNSSQWPEPLQL 120
      121 HVDAVSGLSRLTTLRLALGAKQEAISPPDASAPLRTITADFERKLFRRYSNFLRGKL 180
      121 HVDAVSGLSRLTTLRLALGAKQEAISPPDASAPLRTITADFERKLFRRYSNFLRGKL 180
Qy      181 KLYTGEACRTGDR 193
      181 KLYTGEACRTGDR 193
Db      181 KLYTGEACRTGDR 193

RESULT 12
AA99704
ID      AAY99704 standard; protein: 193 AA.
XX
AC      AAY99704;
XX
DT      15-SEP-2000 (first entry)
XX
DE      Human non-glycosylated erythropoietin NGE.
XX
KM      Human; non-glycosylated erythropoietin; NGE: haematocrit;
KW      antihaemic; anaemia; erythropoiesis promoter.
XX
OS      Homo sapiens.
XX
PN      MO200032772-A2.
XX
PD      08-JUN-2000.
XX
PF      23-NOV-1999; 99WO-US27801.
XX
PR      30-NOV-1998; 98US-0110289.
XX
PA      (ELIL ) LILLY & CO ELI.
XX
PI      Beals JM, Glaesner W, Micanovic R, Milligan RL, Witcher DR;
XX
DR      WPI: 2000-412320/35.
XX
PT      Non-glycosylated erythropoietic compound useful for increasing
XX
PT      haematocrit level in mammal with insufficient haematocrit levels in
XX
PT      conditions such as anemia, comprises protein covalently bonded to
XX
PT      polymer -
XX
PS      Claim 1: Page 91-92; 94pp: English.
XX
CC      The present sequence is the non-glycosylated erythropoietin NGE.
XX
CC      The protein promotes erythropoiesis and can therefore be used to
XX
CC      increase haematocrit levels in mammals with conditions such as
XX
CC      anaemia, in which levels of haematocrit are insufficient. Mutants
XX
CC      derived from the present protein can also be used to treat such
XX
CC      conditions. The analogues, designated NGEAS, do not themselves cause a
XX
CC      significant increase in haematocrit but they acquire that property once
XX
CC      they are derivatised with polyethylene glycol polymers. The analogues
XX
CC      can be produced using a linkerless aldehyde modification process. They
XX
CC      show stability and bioactivity in vivo. The compounds can be
XX
CC      produced by recombinant DNA technology or by chemical procedures such as
XX
CC      solution or solid-phase peptide synthesis.
XX
SQ      Sequence 193 AA;

Query Match      99.3%; Score 991; DB 21; Length 193;
Best local Similarity 99.5%; Pred. No. 2.8e-99;
Matches 192; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Db      61 SLNENITVPDTKVFYAMKREVEGQAAVEWQGLALLSEAVLRQOALLVNSSQWPEPLQL 120
      121 HVDAVSGLSRLTTLRLALGAKQEAISPPDASAPLRTITADFERKLFRRYSNFLRGKL 180
      121 HVDAVSGLSRLTTLRLALGAKQEAISPPDASAPLRTITADFERKLFRRYSNFLRGKL 180
Qy      181 KLYTGEACRTGDR 193
      181 KLYTGEACRTGDR 193
Db      181 KLYTGEACRTGDR 193

RESULT 13
AA43398
ID      AAY43398 standard; protein: 193 AA.
XX
AC      AAY43398;
XX
DT      28-JAN-2000 (first entry)
XX
DE      Human erythropoietin protein sequence.
XX
KM      SAR element: scaffold attachment region: human: apolipoprotein B: tPA:
KW      tissue plasminogen activator; protein expression; gene therapy; lysis;
KW      occlusive coronary artery thrombi; transmural myocardial infarction;
KW      ventricular function; congestive heart failure; acute ischaemic stroke;
KW      acute massive pulmonary embolism; venous thrombosis; arterial thrombosis;
KW      embolism; arteriovenous cannulae occlusion; plasminogen activator;
KW      intravenous catheter clearance; blood clot; erythropoietin.
XX
OS      Homo sapiens.
XX
PN      US5985607-A.
XX
PD      16-NOV-1999.
XX
PF      27-JUN-1997; 97US-0883795.
XX
PR      19-DEC-1994; 94US-0358918.
XX
PA      (CANG-) CANGENE CORP.
XX
PI      Awang G, Delcuve G;
XX
DR      WPI: 2000-012788/01.
XX
DR      N-PSDB: AA237201.
XX
PT      Recombinant DNA molecules encoding tissue plasminogen activator
XX
PT      proteins, operatively linked to a scaffold attachment region, useful
XX
PT      for the production of tissue plasminogen activator both in vivo and in
XX
PT      vitro -
XX
PS      Example 2: Fig 3; 49pp: English.
XX
CC      This sequence represents the human erythropoietin protein.
XX
CC      The invention relates to a recombinant DNA molecule adapted for
XX
CC      expression of tissue plasminogen activator (tPA). The DNA molecule
XX
CC      comprise a sequence encoding tPA, an expression control sequence
XX
CC      operatively linked to the tPA sequence, and at least one human
XX
CC      apolipoprotein B scaffold attachment region (SAR) element (the SAR is not
XX
CC      a 5' proximal apolipoprotein B SAR). The SAR element is used to increase
XX
CC      the expression of the coding sequences. The recombinant nucleic acids may
XX
CC      be used for the recombinant production of tPA both in vitro or in vivo
XX
CC      (e.g. as part of a gene therapy procedure). tPA may be administered to
XX
CC      treat and remove blood clots. It is especially useful for the lysis of
XX
CC      occlusive coronary artery thrombi associated with evolving transmural
XX
CC      myocardial infarction to improve ventricular function and reduce the risk
XX
CC      of congestive heart failure. Additionally, it may be used in the
XX
CC      management of acute massive pulmonary embolism, venous thrombosis and
XX
CC      acute ischaemic stroke. Finally, tPA may be used in treating arterial
XX
CC      thrombosis or embolism, arteriovenous cannulae occlusion and intravenous
XX
CC      catheter clearance. In contrast to other plasminogen activators
XX
CC      (e.g. urokinase and streptokinase), the activity of tPA is relatively
XX
CC      localised and (in theory) is less likely to produce systemic haemorrhagic

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CC disorders.
XX Sequence 193 AA;
SQ Query Match 99.3%; Score 991; DB 21; Length 193;
Best local Similarity 99.5%; Pred. No. 2.8e-99;
Matches 192; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGVECPAMIMLLSLISPLGLPVGAPRLICDSRVLEKKEAENITGCAEHC 60
DB 1 MGVECPAMIMLLSLISPLGLPVGAPRLICDSRVLEKKEAENITGCAEHC 60
QY 61 SLNENITVPDTKYNFYAMKMEYRQQAWEVWGGLALISEAVLRGQALLVNSSQPMPELQL 120
DB 61 SLNENITVPDTKYNFYAMKMEYRQQAWEVWGGLALISEAVLRGQALLVNSSQPMPELQL 120
QY 121 HDKAVSGLRSLTTLRALGAOKEAISPPDAASAAPLRTTADTFKRLFRVYSNFLRGKL 180
DB 121 HDKAVSGLRSLTTLRALGAOKEAISPPDAASAAPLRTTADTFKRLFRVYSNFLRGKL 180
QY 181 KLYTGEACRTGDR 193
DB 181 KLYTGEACRTGDR 193

RESULT 14
AAB85573
ID AAB85573 standard; Protein: 193 AA.
XX AAB85573;
AC AAB85573;
XX 29-OCT-2001 (first entry)
DT 29-OCT-2001 (first entry)
XX Human erythropoietin (EPO) sequence.
DE Human erythropoietin (EPO) sequence.
XX Transgenic; pig; human; erythropoietin; EPO; milk; PMSG; hCG;
KM chorionic gonadotrophic hormone; WAP promoter.
XX Homo sapiens.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Peptide 1..27 /note="signal peptide"
FT Protein 28..193 /note="mature protein"
XX WO200159074-A1.
PN 16-AUG-2001.
PD 28-JUN-2000; 2000MO-KR00675.
XX 14-FEB-2000; 2000KR-0006888.
XX (KORE-) REPUBLIC KOREA.
PA Chang W, Park J, Seong H, Min K, Yang B, Im G, Lee Y, Lee C;
PI Kim J;
XX WPI: 2001-514656/56.
DR N-PSDB: AAH46972.
XX Producing transgenic porcine that secretes human erythropoietin (hEPO)
PT in milk. By introducing vector comprising hEPO gene into fertilized
PT eggs of porcine to which PMSG and hCG were administered, and developing
PT progeny -
XX Claim 4; Fig 3; 21pp; English.
XX The invention relates to producing transgenic pigs (P) that secrete
CC human erythropoietin (hEPO) in milk. The method involves administering
CC PMSG and human chorionic gonadotrophic hormone (hCG) into (P), collecting
CC fertilized eggs after mating, injecting expression vector containing a

CC 2.6 kb WAP promoter, hEPO genome and SV40 poly A DNA into male pronuclei,
CC transplanting them in surrogate mother pig and allowing it to give birth.
CC The method provides transgenic porcine capable of secreting hEPO in their
CC milk, thus producing the expensive useful medicine at a low cost with
CC stability on a large scale, giving a contribution to the improvement of
CC human health. The present sequence represents a human EPO sequence
CC incorporated into the genome of porcine.
XX Sequence 193 AA;
SQ Query Match 99.3%; Score 991; DB 22; Length 193;
Best local Similarity 99.5%; Pred. No. 2.8e-99;
Matches 192; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGVECPAMIMLLSLISPLGLPVGAPRLICDSRVLEKKEAENITGCAEHC 60
DB 1 MGVECPAMIMLLSLISPLGLPVGAPRLICDSRVLEKKEAENITGCAEHC 60
QY 61 SLNENITVPDTKYNFYAMKMEYRQQAWEVWGGLALISEAVLRGQALLVNSSQPMPELQL 120
DB 61 SLNENITVPDTKYNFYAMKMEYRQQAWEVWGGLALISEAVLRGQALLVNSSQPMPELQL 120
QY 121 HDKAVSGLRSLTTLRALGAOKEAISPPDAASAAPLRTTADTFKRLFRVYSNFLRGKL 180
DB 121 HDKAVSGLRSLTTLRALGAOKEAISPPDAASAAPLRTTADTFKRLFRVYSNFLRGKL 180
QY 181 KLYTGEACRTGDR 193
DB 181 KLYTGEACRTGDR 193

RESULT 15
AAB34978
ID AAB34978 standard; Protein: 193 AA.
XX AAB34978;
AC AAB34978;
XX 27-MAR-2001 (first entry)
DT 27-MAR-2001 (first entry)
XX Human erythropoietin SEQ ID NO: 4.
DE Human erythropoietin SEQ ID NO: 4.
XX Chimpanzee; erythropoietin; EPO; hybridisation probe; gene therapy;
KM mapping; therapeutic agent.
XX Homo sapiens.
OS Homo sapiens.
FH WO200068376-A1.
PN 16-NOV-2000.
PD 05-MAY-2000; 2000MO-US12370.
XX 07-MAY-1999; 99US-0307307.
XX 28-MAR-2000; 2000US-0307307.
XX (GETH) GENENTECH INC.
PA Desauvage F, Henner DJ;
PI Desauvage F, Henner DJ;
XX WPI: 2001-007393/01.
DR Nucleic acids encoding chimpanzee erythropoietin, useful for treatment
PT of e.g. anemia, also derived proteins, antibodies and modulators -
PT Disclosure; Fig 3; 109pp; English.
XX The present invention provides the coding and protein sequences of
CC chimpanzee erythropoietin (EPO). These sequences can be used in gene
CC therapy, to block the activity of EPO, as hybridisation probes, in
CC genetic and chromosome mapping and as therapeutic agents.
SQ Sequence 193 AA;

Query Match 99.3%; Score 991; DB 22; Length 193;
 Best Local Similarity 99.5%; Pred. No. 2.8e-99;
 Matches 192; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	MGVHECPAMLLLSLPLGLPVLCAPPRLICDSRVLERYLLEAKEAENITTCGAHC	60
Db	1	MGVHECPAMLLLSLPLGLPVLCAPPRLICDSRVLERYLLEAKEAENITTCGAHC	60
QY	61	SLNENITVPDTKYNFYAMKRMEVROQAVEYWGILALLSEAVLRGQALLVNSSQPEPLQL	120
Db	61	SLNENITVPDTKYNFYAMKRMEVROQAVEYWGILALLSEAVLRGQALLVNSSQPEPLQL	120
QY	121	HVDKAVSGLSLTTLLRALGAQKEAISPDAASAAPLRTTADTFKKLFVRYSNFLRGKL	180
Db	121	HVDKAVSGLSLTTLLRALGAQKEAISPDAASAAPLRTTADTFKKLFVRYSNFLRGKL	180
QY	181	KLYTGEACRTGDR	193
Db	181	KLYTGEACRTGDR	193

Search completed: January 8, 2003, 03:41:26
 Job time : 60.61 secs

PS Claim 34; Page 94; 109pp; English.

CC The present invention provides the coding and protein sequences of
CC chimpanzee erythropoietin (EPO). These sequences can be used in gene
CC therapy, to block the activity of EPO, as hybridisation probes, in
CC genetic and chromosome mapping and as therapeutic agents.

XX Sequence 166 AA;

Query Match 99.5%; Score 839; DB 22; Length 166;
Best Local Similarity 100.0%; Pred. No. 2e-86;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLYERLYLLEKKEAENITTCGAHCISLNEITVPDVKVNFYAMKRNKXSOQA 60

DB 1 APPRLICDSRVLYERLYLLEKKEAENITTCGAHCISLNEITVPDVKVNFYAMKRNKXSOQA 60

QY 61 VEWOGIALLSAVALRGQALLVNSSQWPEPLQHLVDKAVSGIRSLTTLRALGAQKEAIS 120

DB 61 VEWOGIALLSAVALRGQALLVNSSQWPEPLQHLVDKAVSGIRSLTTLRALGAQKEAIS 120

QY 121 PPDASAAPLRTITADTFERKLFRRVYSNPLRGKLYTGACRTGDR 166

DB 121 PPDASAAPLRTITADTFERKLFRRVYSNPLRGKLYTGACRTGDR 166

RESULT 2
AAB35002
ID AAB35002 standard; Protein; 193 AA.

XX AAB35002;

DT 27-MAR-2001 (first entry)

DE Chimpanzee erythropoietin fragment SEQ ID NO: 34.

XX Chimpanzee; erythropoietin; EPO; hybridisation probe; gene therapy;

KM mapping; therapeutic agent.

OS Pan sp.

PN WO200068376-A1.

PF 05-MAY-2000; 2000WO-US12370.

PR 07-MAY-1999; 99US-0307307.

PR 28-MAR-2000; 2000US-0307307.

PA (GETH) GENENTECH INC.

PI Desauvage F, Henner DJ;

DR WPI; 2001-007393/01.

PT Nucleic acids encoding chimpanzee erythropoietin, useful for treatment

PS of e.g. anemia, also derived proteins, antibodies and modulators -

XX Claim 35; Page 96; 109pp; English.

CC The present invention provides the coding and protein sequences of
CC chimpanzee erythropoietin (EPO). These sequences can be used in gene
CC therapy, to block the activity of EPO, as hybridisation probes, in
CC genetic and chromosome mapping and as therapeutic agents.

XX Sequence 193 AA;

Query Match 99.5%; Score 839; DB 22; Length 193;
Best Local Similarity 100.0%; Pred. No. 2.5e-86;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLYERLYLLEKKEAENITTCGAHCISLNEITVPDVKVNFYAMKRNKXSOQA 60

DB 28 APPRLICDSRVLYERLYLLEKKEAENITTCGAHCISLNEITVPDVKVNFYAMKRNKXSOQA 87

QY 61 VEWOGIALLSAVALRGQALLVNSSQWPEPLQHLVDKAVSGIRSLTTLRALGAQKEAIS 120

DB 61 VEWOGIALLSAVALRGQALLVNSSQWPEPLQHLVDKAVSGIRSLTTLRALGAQKEAIS 120

QY 121 PPDASAAPLRTITADTFERKLFRRVYSNPLRGKLYTGACRTGDR 166

DB 121 PPDASAAPLRTITADTFERKLFRRVYSNPLRGKLYTGACRTGDR 166

RESULT 3
AAB34988
ID AAB34988 standard; Protein; 166 AA.

XX AAB34988;

DT 27-MAR-2001 (first entry)

DE Chimpanzee erythropoietin fragment SEQ ID NO: 20.

XX Chimpanzee; erythropoietin; EPO; hybridisation probe; gene therapy;

KM mapping; therapeutic agent.

OS Pan sp.

PN WO200068376-A1.

PF 05-MAY-2000; 2000WO-US12370.

PR 07-MAY-1999; 99US-0307307.

PR 28-MAR-2000; 2000US-0307307.

PA (GETH) GENENTECH INC.

PI Desauvage F, Henner DJ;

DR WPI; 2001-007393/01.

PT Nucleic acids encoding chimpanzee erythropoietin, useful for treatment

PS of e.g. anemia, also derived proteins, antibodies and modulators -

XX Claim 34; Page 94; 109pp; English.

CC The present invention provides the coding and protein sequences of
CC chimpanzee erythropoietin (EPO). These sequences can be used in gene
CC therapy, to block the activity of EPO, as hybridisation probes, in
CC genetic and chromosome mapping and as therapeutic agents.

XX Sequence 166 AA;

Query Match 99.2%; Score 836; DB 22; Length 166;
Best Local Similarity 99.4%; Pred. No. 4.4e-86;
Matches 165; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLYERLYLLEKKEAENITTCGAHCISLNEITVPDVKVNFYAMKRNKXSOQA 60

DB 1 APPRLICDSRVLYERLYLLEKKEAENITTCGAHCISLNEITVPDVKVNFYAMKRNKXSOQA 60

QY 61 VEWOGIALLSAVALRGQALLVNSSQWPEPLQHLVDKAVSGIRSLTTLRALGAQKEAIS 120

DB 61 VEWOGIALLSAVALRGQALLVNSSQWPEPLQHLVDKAVSGIRSLTTLRALGAQKEAIS 120

QY 121 PPDASAAPLRTITADTFERKLFRRVYSNPLRGKLYTGACRTGDR 166

DB 121 PPDASAAPLRTITADTFERKLFRRVYSNPLRGKLYTGACRTGDR 166

RESULT 4
AAB35004


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ID AAB35004 standard. Protein; 193 AA.
XX
XX AAB35004;
AC
XX
XX 27-MAR-2001 (first entry)
DT
XX
XX Chimpanzee erythropoietin fragment SEQ ID NO: 36.
DE
XX
XX Chimpanzee; erythropoietin; EPO; hybridisation probe; gene therapy;
KM mapping; therapeutic agent.
XX
XX Pan sp.
OS
XX
XX WO200068376-A1.
PN
XX
XX 16-NOV-2000.
PD
XX
XX 05-MAY-2000; 2000MO-US12370.
PF
XX
XX 07-MAY-1999; 99US-0307307.
PR
XX
XX 28-MAR-2000; 2000US-0307307.
PS
XX
XX (GETH ) GENENTECH INC.
PI
XX
XX Desauvage F, Henner DJ;
DR
XX
XX WPI; 2001-007393/01.
DT
XX
XX Nucleic acids encoding chimpanzee erythropoietin, useful for treatment
PT of e.g. anemia, also derived proteins, antibodies and modulators -
XX
XX Claim 35; Page 96; 109pp; English.
PS
XX
XX The present invention provides the coding and protein sequences of
CC chimpanzee erythropoietin (EPO). These sequences can be used in gene
CC therapy, to block the activity of EPO, as hybridisation probes, in
CC genetic and chromosome mapping and as therapeutic agents.
XX
XX Sequence 193 AA;
SQ
XX
XX Query Match 99.2%; Score 836; DB 22; Length 193;
XX Best Local Similarity 99.4%; Pred. No. 5.4e-86;
XX Matches 165; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 APPRLICDSRVLEERYLLEAKAEENITTCGAHCSLNNITVPDTKVFYAMKRNXSXQA 60
DB 28 APPRLICDSRVLEERYLLEAKAEENITTCGAHCSLNNITVPDTKVFYAMKRNXTXQA 87
XX
XX 61 VEVWQGLALISEAVLRGQALLVNSQWPPEPLQLHVDKAVSGLSLTTLLRALGAQKEAIS 120
DB 88 VEVWQGLALISEAVLRGQALLVNSQWPPEPLQLHVDKAVSGLSLTTLLRALGAQKEAIS 147
XX
XX 121 PPDAASAAPLRTTADTFKRLFRVYSNFLRGKLIKLYTGEACRTGDR 166
DB 148 PPDAASAAPLRTTADTFKRLFRVYSNFLRGKLIKLYTGEACRTGDR 193
XX
XX RESULT 5
XX AAB34987
XX ID AAB34987 standard. Protein; 166 AA.
XX
XX AAB34987;
AC
XX
XX 27-MAR-2001 (first entry)
DT
XX
XX Chimpanzee erythropoietin fragment SEQ ID NO: 19.
DE
XX
XX Chimpanzee; erythropoietin; EPO; hybridisation probe; gene therapy;
KM mapping; therapeutic agent.
XX
XX Pan sp.
OS
XX
XX WO200068376-A1.
PN

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XX
XX 16-NOV-2000.
PD
XX
XX 05-MAY-2000; 2000MO-US12370.
PF
XX
XX 07-MAY-1999; 99US-0307307.
PR
XX
XX 28-MAR-2000; 2000US-0307307.
PS
XX
XX (GETH ) GENENTECH INC.
PI
XX
XX Desauvage F, Henner DJ;
DR
XX
XX WPI; 2001-007393/01.
DT
XX
XX Nucleic acids encoding chimpanzee erythropoietin, useful for treatment
PT of e.g. anemia, also derived proteins, antibodies and modulators -
XX
XX Claim 34; Page 94; 109pp; English.
PS
XX
XX The present invention provides the coding and protein sequences of
CC chimpanzee erythropoietin (EPO). These sequences can be used in gene
CC therapy, to block the activity of EPO, as hybridisation probes, in
CC genetic and chromosome mapping and as therapeutic agents.
XX
XX Sequence 166 AA;
SQ
XX
XX Query Match 99.1%; Score 835; DB 22; Length 166;
XX Best Local Similarity 99.4%; Pred. No. 5.7e-86;
XX Matches 165; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 APPRLICDSRVLEERYLLEAKAEENITTCGAHCSLNNITVPDTKVFYAMKRNXSXQA 60
DB 1 APPRLICDSRVLEERYLLEAKAEENITTCGAHCSLNNITVPDTKVFYAMKRNXTXQA 60
XX
XX 61 VEVWQGLALISEAVLRGQALLVNSQWPPEPLQLHVDKAVSGLSLTTLLRALGAQKEAIS 120
DB 61 VEVWQGLALISEAVLRGQALLVNSQWPPEPLQLHVDKAVSGLSLTTLLRALGAQKEAIS 120
XX
XX 121 PPDAASAAPLRTTADTFKRLFRVYSNFLRGKLIKLYTGEACRTGDR 166
DB 121 PPDAASAAPLRTTADTFKRLFRVYSNFLRGKLIKLYTGEACRTGDR 166
XX
XX RESULT 6
XX AAB35003
XX ID AAB35003 standard. Protein; 193 AA.
XX
XX AAB35003;
AC
XX
XX 27-MAR-2001 (first entry)
DT
XX
XX Chimpanzee erythropoietin fragment SEQ ID NO: 35.
DE
XX
XX Chimpanzee; erythropoietin; EPO; hybridisation probe; gene therapy;
KM mapping; therapeutic agent.
XX
XX Pan sp.
OS
XX
XX WO200068376-A1.
PN
XX
XX 16-NOV-2000.
PD
XX
XX 05-MAY-2000; 2000MO-US12370.
PF
XX
XX 07-MAY-1999; 99US-0307307.
PR
XX
XX 28-MAR-2000; 2000US-0307307.
PS
XX
XX (GETH ) GENENTECH INC.
PI
XX
XX Desauvage F, Henner DJ;
DR
XX
XX WPI; 2001-007393/01.
PN

```

PT Nucleic acids encoding chimpanzee erythropoietin, useful for treatment of e.g. anemia, also derived proteins, antibodies and modulators -

XX Claim 35; Page 96; 109pp; English.

CC The present invention provides the coding and protein sequences of chimpanzee erythropoietin (EPO). These sequences can be used in gene therapy, to block the activity of EPO, as hybridisation probes, in genetic and chromosome mapping and as therapeutic agents.

XX

SQ Sequence 193 AA;

Query Match 99.1%; Score 835; DB 22; Length 193;
Best Local Similarity 99.4%; Pred. No. 7e-86;
Matches 165; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 APPRLICDSRVLELYLLEAKEENITTCGAHCISLNIENITVPDTKVNPFAMKRNKXQQA 60
DB 28 APPRLICDSRVLELYLLEAKEENITTCGAHCISLNIENITVPDTKVNPFAMKRNKXQQA 87
OY 61 VEWOGGLALLSEAVLRGALLVNSSQPWEPLQLHVDKAVSGLSRSLTTLRALGAQKEAIS 120
DB 88 VEWOGGLALLSEAVLRGALLVNSSQPWEPLQLHVDKAVSGLSRSLTTLRALGAQKEAIS 147
OY 121 PPDASAAPLRTITADTFRKLFRRVSNFLRGKILKLYTGACRTGDR 166
DB 148 PPDASAAPLRTITADTFRKLFRRVSNFLRGKILKLYTGACRTGDR 193

RESULT 7
AAB34989
ID AAB34989 standard; Protein: 166 AA.

XX AAB34989;

XX 27-MAR-2001 (first entry)

DE Chimpanzee erythropoietin fragment SEQ ID NO: 21.

XX

KW Chimpanzee; erythropoietin; EPO; hybridisation probe; gene therapy;
mapping; therapeutic agent.

XX

OS Pan sp.

XX

PN WO200068376-A1.

XX

PD 16-NOV-2000.

XX

PF 05-MAY-2000; 2000WO-US12370.

XX

PR 07-MAY-1999; 99US-0307307.
28-MAR-2000; 2000US-0307307.

XX

PA (GETH) GENENTECH INC.

XX

PI Desauvage F, Hennen DJ;

XX

DR WPI: 2001-007393/01.

XX

PT Nucleic acids encoding chimpanzee erythropoietin, useful for treatment of e.g. anemia, also derived proteins, antibodies and modulators -

XX

PS Claim 34; Page 94; 109pp; English.

XX

CC The present invention provides the coding and protein sequences of chimpanzee erythropoietin (EPO). These sequences can be used in gene therapy, to block the activity of EPO, as hybridisation probes, in genetic and chromosome mapping and as therapeutic agents.

XX

SQ Sequence 166 AA;

Query Match 98.7%; Score 832; DB 22; Length 166;
Best Local Similarity 98.8%; Pred. No. 1.2e-85;

Matches 164; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 APPRLICDSRVLELYLLEAKEENITTCGAHCISLNIENITVPDTKVNPFAMKRNKXQQA 60
DB 1 APPRLICDSRVLELYLLEAKEENITTCGAHCISLNIENITVPDTKVNPFAMKRNKXQQA 87
OY 61 VEWOGGLALLSEAVLRGALLVNSSQPWEPLQLHVDKAVSGLSRSLTTLRALGAQKEAIS 120
DB 61 VEWOGGLALLSEAVLRGALLVNSSQPWEPLQLHVDKAVSGLSRSLTTLRALGAQKEAIS 120
OY 121 PPDASAAPLRTITADTFRKLFRRVSNFLRGKILKLYTGACRTGDR 166
DB 121 PPDASAAPLRTITADTFRKLFRRVSNFLRGKILKLYTGACRTGDR 166

RESULT 8
AAB35005
ID AAB35005 standard; Protein: 193 AA.

XX AAB35005;

XX 27-MAR-2001 (first entry)

DE Chimpanzee erythropoietin fragment SEQ ID NO: 37.

XX

KW Chimpanzee; erythropoietin; EPO; hybridisation probe; gene therapy;
mapping; therapeutic agent.

XX

OS Pan sp.

XX

PN WO200068376-A1.

XX

PD 16-NOV-2000.

XX

PF 05-MAY-2000; 2000WO-US12370.

XX

PR 07-MAY-1999; 99US-0307307.
28-MAR-2000; 2000US-0307307.

XX

PA (GETH) GENENTECH INC.

XX

PI Desauvage F, Hennen DJ;

XX

DR WPI: 2001-007393/01.

XX

PT Nucleic acids encoding chimpanzee erythropoietin, useful for treatment of e.g. anemia, also derived proteins, antibodies and modulators -

XX

PS Claim 35; Page 96; 109pp; English.

XX

CC The present invention provides the coding and protein sequences of chimpanzee erythropoietin (EPO). These sequences can be used in gene therapy, to block the activity of EPO, as hybridisation probes, in genetic and chromosome mapping and as therapeutic agents.

XX

SQ Sequence 193 AA;

Query Match 98.7%; Score 832; DB 22; Length 193;
Best Local Similarity 98.8%; Pred. No. 1.5e-85;
Matches 164; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 APPRLICDSRVLELYLLEAKEENITTCGAHCISLNIENITVPDTKVNPFAMKRNKXQQA 60
DB 28 APPRLICDSRVLELYLLEAKEENITTCGAHCISLNIENITVPDTKVNPFAMKRNKXQQA 87
OY 61 VEWOGGLALLSEAVLRGALLVNSSQPWEPLQLHVDKAVSGLSRSLTTLRALGAQKEAIS 120
DB 88 VEWOGGLALLSEAVLRGALLVNSSQPWEPLQLHVDKAVSGLSRSLTTLRALGAQKEAIS 147
OY 121 PPDASAAPLRTITADTFRKLFRRVSNFLRGKILKLYTGACRTGDR 166
DB 148 PPDASAAPLRTITADTFRKLFRRVSNFLRGKILKLYTGACRTGDR 193

CC with chronic renal failure, myelosuppressive therapy, certain cancers,
 CC viral disease such as HIV and excessive blood loss.
 CC Note: The present sequence is not shown in the specification but is
 CC derived from the wild-type erythropoietin shown in Figure 1 (AAV94530).
 XX

SO Sequence 193 AA;

Query Match 98.0%; Score 826; DB 21; Length 193;
 Best Local Similarity 97.6%; Pred. No. 7.3e-85;
 Matches 162; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 APRRLICDSRVLELYLLEAKAEKNTTGCACHCISNENITVPDTKVNPFAMKRNKXQQA 60
 DB 28 APRRLICDSRVLELYLLEAKAEKNTTGCACHCISNENITVPDTKVNPFAMKRNKXQQA 87
 QY 61 VEWMOGLALLSEAVLRGQALLVNSSQPMPEPLQHLVDKAVSGLSLITLLRALGAQKEAIS 120
 DB 88 VEWMOGLALLSEAVLRGQALLVNSSQPMPEPLQHLVDKAVSGLSLITLLRALGAQKEAIS 147
 QY 121 PPDASAAPLRTITADTFKRLFRVYSNPLRGKRLKLYTGEACRTGDR 166
 DB 148 PPDASAAPLRTITADTFKRLFRVYSNPLRGKRLKLYTGEACRTGDR 193

RESULT 11

AA070398
 ID AAP70398 standard; Protein; 166 AA.

XX AC AAP70398;

XX DT 19-FEB-1991 (first entry)

XX DE Sequence of human erythropoietin (EPO).

KW Mega-karyocyte-platelet growth factor; hormone;
 KW mega-karyocyte colony stimulating factor; therapy;
 KW small acetyl cholinesterase positive cell;
 KW erythrocyte growth effect.

XX OS Homo sapiens.

XX PN JP62149624-A.

XX PD 03-JUL-1987.

XX PF 15-AUG-1986; 86JP-0191542.

XX PR 13-SEP-1985; 85JP-0203049.

XX PR 15-AUG-1986; 86JP-0191542.

XX PA (KAWA)/ KAWAKITA M.

XX DR WPI: 1987-224837/32.

XX PT Megakaryocyte-platelet growth factor - contains as active
 PT component human erythropoietin and is used to treat diseases
 PT caused by decrease in platelets

XX PS Disclosure: Page 181; 8pp; Japanese.

XX All of the Cys residues in the SO are labelled "SH". Megakaryocyte-
 CC platelet growth factor contains human EPO as an active principle.
 CC Human EPO has a megakaryocyte colony-stimulating activity and
 CC increases the ratio of small acetyl cholinesterase positive cell
 CC (Schner) which is immature megakaryocyte. Human EPO effects
 CC megakaryocyte-platelet system other than an erythrocyte growth
 CC effect. Megakaryocyte-platelet growth is usable as a remedy for
 CC diseases caused by a platelet decrease.

SO Sequence 166 AA;

Query Match 97.9%; Score 825; DB 8; Length 166;
 Best Local Similarity 97.6%; Pred. No. 7.6e-85;

Matches 162; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 APRRLICDSRVLELYLLEAKAEKNTTGCACHCISNENITVPDTKVNPFAMKRNKXQQA 60
 DB 1 APRRLICDSRVLELYLLEAKAEKNTTGCACHCISNENITVPDTKVNPFAMKRNKXQQA 60
 QY 61 VEWMOGLALLSEAVLRGQALLVNSSQPMPEPLQHLVDKAVSGLSLITLLRALGAQKEAIS 120
 DB 61 VEWMOGLALLSEAVLRGQALLVNSSQPMPEPLQHLVDKAVSGLSLITLLRALGAQKEAIS 120
 QY 121 PPDASAAPLRTITADTFKRLFRVYSNPLRGKRLKLYTGEACRTGDR 166
 DB 121 PPDASAAPLRTITADTFKRLFRVYSNPLRGKRLKLYTGEACRTGDR 166

RESULT 12

AA023593
 ID AAR23593 standard; Protein; 166 AA.

XX AC AAR23593;

XX DT 20-OCT-1992 (first entry)

XX DE Recombinant hematopoietic molecule portion 2.

KW Erythropoietin; EPO; erythrocytes; IL-3; haematopoiesis.

XX OS Homo sapiens.

XX PN WO9206116-A.

XX PD 16-APR-1992.

XX PF 26-SEP-1991; 91WO-US07053.

XX PR 28-SEP-1990; 90US-0589958.

XX PA (ORTH) ORTHO PHARM CORP.

XX PI Rosen JI;

XX DR WPI: 1992-150819/18.

XX PT Recombinant haematopoietic molecules useful in treating
 PT anaemia(s) - comprise IL-3 or GM-CSF, EPO, G-CSF, IL-5 or M-CSF
 PT and has early and later myeloid differentiation activity

XX PS Disclosure: Page 32; 82pp; English.

XX This protein sequence given comprises the entire amino acid sequence
 CC of human erythropoietin (EPO). EPO leads to the maturation of
 CC erythrocytes and is therefore designated as a late myeloid
 CC differentiation factor (MDF). Within the scope of the invention
 CC hybrid molecules were produced which contain at least a portion of an
 CC early MDF and at least a portion of a late MDF covalently linked. The
 CC EPO sequence given is effective within the scope of the invention in
 CC full or in a truncated version. Amino acids 7-161 act as a
 CC late MDF when recombined with an early MDF eg. IL-3.
 CC These compounds can be used to promote hematopoiesis in a patient.
 CC The bonding of the early and late factors allows a very high conc. of
 CC late MDF at the surface of a cell which the early MDF is bound. It
 CC also allows the early MDA to act more specifically to stimulate only
 CC the desired lineage, thus reducing undesirable effects. These
 CC compounds are useful for treating anaemias of various origins eg. renal
 CC failure and AIDS. It is easier to produce and administer one
 CC recombinant molecule rather than two separate molecules.

SO Sequence 166 AA;

Query Match 97.9%; Score 825; DB 13; Length 166;
 Best Local Similarity 97.6%; Pred. No. 7.6e-85;
 Matches 162; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY	1	APPRILCSRYLERLLLEAKKAEKENTTGCACFKCSINENITVPDTKYVNFYAMKRNAXSQOA	60
Db	1	APPRILCSRYLERLLLEAKKAEKENTTGCACFKCSINENITVPDTKYVNFYAMKRMVEGQOA	60
QY	61	VEWMOGLALLSAVLRGQALLVNSSOPMPEPQLDHYDKAVSGLSRLITLLRALGAQKEAIS	12
Db	61	VEWMOGLALLSAVLRGQALLVNSSOPMPEPQLDHYDKAVSGLSRLITLLRALGAQKEAIS	12
QY	121	PPDASAAPLRTITADTFRKLFRVYSNFLRGKSLKLYTSEACRTGDR	166
Db	121	PPDASAAPLRTITADTFRKLFRVYSNFLRGKSLKLYTSEACRTGDR	166
RESULT 13			
AAW77780	ID	AAW77780 standard; Protein: 166 AA.	
XX	XX	AAW77780;	
AC	XX	24-NOV-1998 (first entry)	
XX	XX		
DE	XX	Human EPO receptor agonist polypeptide.	
XX	XX		
KM	XX	Haematopoietic receptor agonist; erythropoietin receptor agonist;	
KW	XX	EPO; human; chimeric protein; stem cell expansion; tumour;	
KM	XX	infection; autoimmune disease; haematopoietic disorder; therapy;	
KM	XX	dendritic cell.	
OS	XX		
XX	XX	Homo sapiens.	
FA	FA	Key	
FA	FA	Misc-difference 1..6	
FA	FA	/note= "1-6 amino acids of the N-terminus are	
FA	FA	optionally deleted"	
FA	FA	Misc-difference 162..166	
FA	FA	/note= "1-5 amino acids of the C-terminus are	
FA	FA	optionally deleted"	
FA	FA	Misc-difference 23..24	
FA	FA	/note= "possible positions of new C- and N-termini"	
FA	FA	Misc-difference 24..25	
FA	FA	/note= "possible positions of new C- and N-termini"	
FA	FA	Misc-difference 25..26	
FA	FA	/note= "possible positions of new C- and N-termini"	
FA	FA	Misc-difference 26..27	
FA	FA	/note= "possible positions of new C- and N-termini"	
FA	FA	Misc-difference 27..28	
FA	FA	/note= "possible positions of new C- and N-termini"	
FA	FA	Misc-difference 28..29	
FA	FA	/note= "possible positions of new C- and N-termini"	
FA	FA	Misc-difference 29..30	
FA	FA	/note= "possible positions of new C- and N-termini"	
FA	FA	Misc-difference 30..31	
FA	FA	/note= "possible positions of new C- and N-termini"	
FA	FA	Misc-difference 31..32	
FA	FA	/note= "possible positions of new C- and N-termini"	
FA	FA	Misc-difference 32..33	
FA	FA	/note= "possible positions of new C- and N-termini"	
FA	FA	Misc-difference 33..34	
FA	FA	/note= "possible positions of new C- and N-termini"	
FA	FA	Misc-difference 34..35	
FA	FA	/note= "possible positions of new C- and N-termini"	
FA	FA	Misc-difference 35..36	
FA	FA	/note= "possible positions of new C- and N-termini"	
FA	FA	Misc-difference 36..37	
FA	FA	/note= "possible positions of new C- and N-termini"	
FA	FA	Misc-difference 37..38	
FA	FA	/note= "possible positions of new C- and N-termini"	
FA	FA	Misc-difference 38..39	
FA	FA	/note= "possible positions of new C- and N-termini"	
FA	FA	Misc-difference 39..40	
FA	FA	/note= "possible positions of new C- and N-termini"	
FA	FA	Misc-difference 40..41	
FA	FA	/note= "possible positions of new C- and N-termini"	

[illegible]

FT	/note-	"possible positions of new C- and N-termi"
FT	Misc-difference	118..119
FT	/note-	"possible positions of new C- and N-termi"
FT	Misc-difference	119..120
FT	/note-	"possible positions of new C- and N-termi"
FT	Misc-difference	120..121
FT	/note-	"possible positions of new C- and N-termi"
FT	Misc-difference	121..122
FT	/note-	"possible positions of new C- and N-termi"
FT	Misc-difference	122..123
FT	/note-	"possible positions of new C- and N-termi"
FT	Misc-difference	123..124
FT	/note-	"possible positions of new C- and N-termi"
FT	Misc-difference	124..125
FT	/note-	"possible positions of new C- and N-termi"
FT	Misc-difference	125..126
FT	/note-	"possible positions of new C- and N-termi"
FT	Misc-difference	126..127
FT	/note-	"possible positions of new C- and N-termi"
FT	Misc-difference	127..128
FT	/note-	"possible positions of new C- and N-termi"
FT	Misc-difference	128..129
FT	/note-	"possible positions of new C- and N-termi"
FT	Misc-difference	129..130
FT	/note-	"possible positions of new C- and N-termi"
FT	Misc-difference	130..131
FT	/note-	"possible positions of new C- and N-termi"
FT	Misc-difference	131..132
FT	/note-	"possible positions of new C- and N-termi"
XX	MO9817810-A2.	
XX		
XX	30-APR-1998.	
XX		
XX	23-OCT-1997:	97MO-US20037.
XX		
XX	25-OCT-1996:	96US-0029629.
XX		
XX	(SEAR)	SEARLE & CO G D.
XX		
PI	Feng Y, McKearn JP, McWhorter CA, Minnerly JC, Minster NI;	
PI	Staten NR, Streeter PR, Summers NL, Wouffe SL;	
XX		
XX	WPI: 1998-261504/23.	

Pt Multi-functional chimeric haematopoietic receptor agonist - useful
Pt to treat haematopoietic disorders, tumours, infections or autoimmune
Pn diseases

Px Claim 1; Page 762; 841pp; English.

Xx A human erythropoietin (Epo) receptor agonist polypeptide comprises
xx a modified Epo amino acid sequence of the formula provided in
cc AA077780, in which the N-terminus is joined to the C-terminus directly
cc or via a linker, the polypeptide having new C- and N-terminals at one
cc of the positions indicated. Novel claimed multi-functional chimeric
cc haematopoietic receptor agonists (see AA077812-22) have the formula
cc R1-I-L-R2, R2-I-L-R1, R1-R2 or R2-R1, where L is a linker and R1 and
cc R2 are independently selected from: (a) The human Epo receptor
cc agonist; (b) a human stem cell factor receptor agonist polypeptide
cc (see AA077781); (c) a human flit-3 receptor agonist polypeptide (see
cc AA077782); (d) a modified human granulocyte colony stimulating factor
cc (G-CSF) polypeptide (see AA077783); (e) modified human interleukin-3
cc polypeptide (see AA077784); (f) modified human c-mpl ligand polypeptide
cc (see AA077785); and (g) a factor selected from the group consisting of
cc a CSF, a cytokine, a lymphokine, an interleukin and a haematopoietic
cc growth factor, provided that at least R1 or R2 is selected from (a),
cc (b) or (c) as above. The multi-functional chimeric haematopoietic
cc receptor agonist can be used to stimulate the production of

Query Match 97.9%; Score 825; DB 19; Length 166;
Best Local Similarity 97.6%; Pred. No. 7.6e+5;
Matches 162; Conservative 0; Mismatches 4; Indels 0; Gaps 0

Qy	1	APPRICDSRYLERLLLEAKAEENITTCGACHCSCJNINITYPDTKYVFMKRNXXQQA	60
Db	1	APPRICDSRYLERLLLEAKAEENITTCGACHCSCJNINITYPDTKYVFMKRNXXQQA	60
Qy	61	VEVWQGLALLSEAVLRGQALLVNSSQPEWPEQLQHVDAVGSGLSTLTLLRALGAOKPAIS	120
Db	61	VEVWQGLALLSEAVLRGQALLVNSSQPEWPEQLQHVDAVGSGLSTLTLLRALGAOKPAIS	120
Qy	121	PPDASAPPLRTITADTFRKLLFRYYNFFLRGKLTLYTGEACRTGDR	166
Db	121	PPDASAPPLRTITADTFRKLLFRYYNFFLRGKLTLYTGEACRTGDR	166

RESULT 14	
AAW58404	
ID	AAW58404 standard; Protein; 166 AA

AC AAW58404;

DT 12-OCT-1998 (first entry)

Human erythropoietin.

KW Erythropoietin receptor agonist; EPO; human; anaemia; thrombopoietic deficiency; megakaryocyte; platelet

KW	haematopoietic deficiency; red blood cell; erythroid progenitor;
KW	bone marrow suppression.
XY	

OS Homo sapiens

PN WO9818926-A1
XX

PD 07-MAY-1998.

PF 23-OCT-1997; 97WO-US18703.
VY

PR	25-OCT-1996;	96US-0034044.
YY		

PA (SEAR) SEARLE & CO G D.
YY

PI Feng Y, McWhorter CA, Summers N;
xy

DR N-PSDB; AAV31031.

PT Human erythropoietin receptor agonist polypeptide - used to stimulate the production of red blood cells in a patient

PS Claim 1; Page 93; 112pp; English.

A claimed human erythropoietin (EPO) receptor agonist polypeptide comprises a modified EPO amino acid sequence given in AAWS5404, where (a) optionally 1-6 amino acids from the N-terminus and 1-5 from the C-terminus can be deleted, (b) the N-terminus is joined to the C-terminus directly or through a linker (see AAWS58405-12) capable of joining the N-terminus to the C-terminus, (c) there are new C- and N-terminal at any two consecutive amino acids from amino acids 23-24 to 38-39, 40-41 to 41-42, 43-44 to 48-49, 50-51 to 57-58, 77-78 to 82-83, 84-85 to 88-89, and 108-109 to 131-132, and (d) optionally the agonist polypeptide is preceded by Met, Ala, or Met-Ala. 60 of these circularly permuted EPO receptor agonists (see AAWS6413-72) are claimed. Also claimed are: nucleic acid molecules (see AAWS0971-V31030) encoding novel EPO receptor agonists; a method of producing an EPO receptor agonist using transformed or transfected host cells; and methods for stimulating the production of haematopoietic cells, for selective ex vivo expansion of erythroid progenitors, and treating patients having a haematopoietic disorder using the EPO receptor agonists. The EPO receptor agonists retain one or more activities of native EPO and may also show improved haematopoietic cell-stimulating activity and/or an improved activity profile which may include reduction of undesirable biological activities associated with native EPO and/or have improved physical properties such as increased solubility,

CC stability and refold efficiency.

XX Sequence 166 AA;

Query Match 97.9%; Score 825; DB 19; Length 166;
Best Local Similarity 97.6%; Pred. No. 7.6e-85;
Matches 162; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 APPRLICDSRYLERYLLEAKAEENITTCGAHCSLNENITVPDTKVNPFYAMKRNXSXQQA 60
DB 1 APPRLICDSRYLERYLLEAKAEENITTCGAHCSLNENITVPDTKVNPFYAMKRNVEVGQA 60
QY 61 VEWQGIALLSEAVLRGQALLVNSSQWPBPLQLHVDKAVSGLSLTLLRALGAQKEAIS 120
DB 61 VEWQGIALLSEAVLRGQALLVNSSQWPBPLQLHVDKAVSGLSLTLLRALGAQKEAIS 120
QY 121 PPDASAPLRTITADTFRKLFVYSNPLRGKCLKLYTGEACRTGDR 166
DB 121 PPDASAPLRTITADTFRKLFVYSNPLRGKCLKLYTGEACRTGDR 166

RESULT 15

ABB07030 standard; Protein; 166 AA.

AC ABB07030;
DT 21-JUN-2002 (first entry)

DE Modified erythropoietin related gene protein sequence.

KW Modified erythropoietin; EPO.

OS Unidentified.

PN KRL45802-B1.

PD 01-AUG-1998.

PF 31-MAY-1994; 94KR-0012082.

PR 31-MAY-1994; 94KR-0012082.

PA (GLDS) LG CHEM CO LTD.

PI Kim C, Song Y, Lee T;

DR WPI: 2000-234250/20.

DR N-PSDB; ABL50878.

PT MODIFIED ERYTHROPOIETIN GENE AND EXPRESSION VECTORS THEREOF -

PS Disclosure; Page 14; 15pp; Korean.

CC The present invention describes modified erythropoietin (EPO) genes

CC and expression vectors comprising the genes. The present sequence

CC represents a protein sequence from the present invention.

XX Sequence 166 AA;

Query Match 97.9%; Score 825; DB 21; Length 166;
Best Local Similarity 97.6%; Pred. No. 7.6e-85;
Matches 162; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 APPRLICDSRYLERYLLEAKAEENITTCGAHCSLNENITVPDTKVNPFYAMKRNXSXQQA 60
DB 1 APPRLICDSRYLERYLLEAKAEENITTCGAHCSLNENITVPDTKVNPFYAMKRNVEVGQA 60
QY 61 VEWQGIALLSEAVLRGQALLVNSSQWPBPLQLHVDKAVSGLSLTLLRALGAQKEAIS 120
DB 61 VEWQGIALLSEAVLRGQALLVNSSQWPBPLQLHVDKAVSGLSLTLLRALGAQKEAIS 120
QY 121 PPDASAPLRTITADTFRKLFVYSNPLRGKCLKLYTGEACRTGDR 166

DB 121 PPDASAPLRTITADTFRKLFVYSNPLRGKCLKLYTGEACRTGDR 166

Search completed: January 8, 2003, 03:41:28
Job time : 46.39 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 8, 2003, 02:35:14 ; Search time 26.8802 Seconds
(without alignments) 690.245 Million cell updates/sec

Title: US-09-813-775C-2

Perfect score: 998

Sequence: 1 MGVECPAMWLILLSLSLP.....NFLRGKIKLYTGACRTGDR 193

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	991	99.3	193	1 ZUHU	erythropoietin pre
2	899.5	90.1	192	1 ZU0173	erythropoietin pre
3	894.5	89.6	192	1 I84613	erythropoietin pre
4	794.5	79.6	188	1 I46083	erythropoietin pre
5	778.5	78.0	182	1 S28148	erythropoietin pre
6	773.5	77.1	194	1 I46401	erythropoietin pre
7	769.5	76.0	190	2 I46578	erythropoietin - p
8	758.5	75.0	192	1 A24902	erythropoietin pre
9	731	73.2	195	2 JC7699	erythropoietin - r
10	714.5	71.6	175	2 I46199	erythropoietin - d
11	107	10.7	353	2 G02729	thrombopoietin - h
12	96.5	9.7	353	2 I80105	thrombopoietin pre
13	93.5	9.4	286	2 A55530	megakaryocyte grow
14	90	9.0	356	2 S45330	thrombopoietin - m
15	87.5	8.8	346	2 AE0959	Solute binding rec
16	87	8.7	323	2 AB0323	ribonucleoside-dip
17	86.5	8.7	326	2 JC4135	thrombopoietin pre
18	86.5	8.7	622	2 T02244	probable DNA repl
19	85.5	8.6	897	2 A54696	EGF receptor subst
20	85	8.5	339	2 A83274	UDP-N-acetylpyruvo
21	84.5	8.5	2201	2 AH0095	probable sideroph
22	84	8.4	235	2 JC4227	thrombopoietin pre
23	83.5	8.4	475	2 D84064	succinate-semialde
24	83	8.3	451	2 S75569	hypothetical prote
25	82.5	8.3	296	2 AI0443	probable 2-hydroxy
26	82.5	8.3	480	2 S56639	ribosomal protein
27	82.5	8.3	3033	1 GNMVJ8	genome polypeptide
28	82	8.2	1336	2 T18288	AAC transport prot
29	82	8.2	1980	2 S54307	myosin heavy chain

30	81	8.1	813	2 AF0526	ATP-dependent heli
31	79.5	8.0	929	2 B41863	two-component regu
32	79	7.9	623	2 T03800	anthranilate synth
33	79	7.9	1089	2 S53978	PSI protein - yea
34	78.5	7.9	1829	2 T35681	probable sensory h
35	78	7.8	282	2 B37994	KR2 protein - salm
36	78	7.8	743	2 D75590	methyl-accepting c
37	77.5	7.8	242	2 AD1928	hypothetical prote
38	77.5	7.8	896	2 S43074	epidermal growth f
39	77	7.7	304	2 A87258	hypothetical prote
40	77	7.7	637	2 S75772	hypothetical prote
41	76.5	7.7	249	2 G87105	probable amidotran
42	76.5	7.7	567	2 T08405	hypothetical prote
43	76.5	7.7	925	2 E83529	sensor/response re
44	76	7.6	384	2 AI2962	cellulose synthesi
45	76	7.6	389	2 E98320	hypothetical prote

ALIGNMENTS

RESULT 1

ZUHU
Erythropoietin precursor [validated] - human
C:Species: Homo sapiens (man)
C:Date: 27-Nov-1985 #sequence_revision 27-Nov-1985 #text_change 08-Dec-2000
C:Accession: A01855; A24744; A25384; A22210; S56178
R:Jacobs, K.; Shoemaker, C.; Ruderdorf, R.; Neill, S.D.; Kaufman, R.J.; Mifson, A.; Nature 313, 806-810, 1985
A:Title: Isolation and characterization of genomic and cDNA clones of human erythropo
A:Reference number: A01855; MUID:85137899; PMID:3838366
A:Accession: A01855
A:Molecule type: RNA: DNA
A:Residues: 1-193 <I>A01855</I>
A:Cross-references: GB:X02157; GB:X02158
R:Lin, F.K.; Suggs, S.; Lin, C.H.; Browne, J.K.; Smalling, R.; Egrie, J.C.; Chen, K.K
Proc. Natl. Acad. Sci. U.S.A. 82, 7580-7584, 1985
A:Title: Cloning and expression of the human erythropoietin gene.
A:Reference number: A24744; MUID:86067948; PMID:3865178
A:Accession: A24744
A:Molecule type: DNA
A:Residues: 1-193 <I>A01855</I>
A:Cross-references: GB:M11319; MUID:9182197; PIDN:AAA52400.1; PID:9182198
R:Iat, P.H.; Everett, R.; Wang, F.F.; Arakawa, T.; Goldwasser, E.
J. Biol. Chem. 261, 3116-3121, 1986
A:Title: Structural characterization of human erythropoietin.
A:Reference number: A25384; MUID:86140080; PMID:3949763
A:Accession: A25384
A:Molecule type: protein
A:Residues: 28-86, 'Q', 87-193 <I>A01855</I>
A:Experimental source: urine
A:Note: forms without the carboxyl-terminal residue and the four carboxyl-terminal re
R:Yanagawa, S.; Hirade, K.; Ohnata, H.; Sasaki, R.; Chiba, H.; Goto, M.
J. Biol. Chem. 259, 2707-2710, 1984
A:Title: Isolation of human erythropoietin with monoclonal antibodies.
A:Reference number: A22210; MUID:84135751; PMID:6698989
A:Accession: A22210
A:Molecule type: protein
A:Residues: 28-29, 'X', 31-33, 'L', 35-50, 'X', 52-53, 'D', 55, 'G', 57 <I>A01855</I>
R:Matsumoto, S.; Ikura, K.; Ueda, M.; Sasaki, R.
Plant Mol. Biol. 27, 1163-1172, 1995
A:Title: Characterization of a human glycoprotein (erythropoietin) produced in cultur
A:Reference number: S56178; MUID:95284365; PMID:7766897
A:Accession: S56178
A:Molecule type: protein
A:Residues: 28-33, 'X', 35-37 <I>A01855</I>
C:Comment: Erythropoietin is produced by kidney or liver of adult mammals and by live
C:Genetics:
A:Gene: GDB:EPO
A:Cross-references: GDB:119110; OMIM:133170
A:Map position: 7q21.3-7q22.1
A:Introns: 5/1; 53/3; 82/3; 142/3
C:Function:

A:Description: the primary inducer of erythrocyte formation
 C:Superfamily: erythropoietin
 C:Keywords: erythropoiesis; glycoprotein; hormone; kidney; liver
 F:1-27/Domain: signal sequence #status predicted <SIG>
 F:28-193/Product: erythropoietin #status experimental <MAT>
 F:34-187,56-60/Disulfide bonds: #status experimental
 F:51,65,110/Binding site: carbohydrate (Ser) (covalent) #status experimental
 F:153/Binding site: carbohydrate (Ser) (covalent) #status experimental

Query Match 99.3%; Score 991; DB 1; Length 193;
 Best local Similarity 99.5%; Pred. No. 1.7e-85;
 Matches 192; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 MGVECPAMWMLLSLSPGLGPGVPGAPRLICDSRYLERLYLLEKAEENITTCGAHC 60
 |||||
 Db 1 MGVECPAMWMLLSLSPGLGPGVPGAPRLICDSRYLERLYLLEKAEENITTCGAHC 60
 |||||
 Oy 61 SLNENITVPPTKYNFYAMKMEYRQOAVEWQGLALISEAVLNGOALLVNSQPPWEPLOL 120
 |||||
 Db 61 SLNENITVPPTKYNFYAMKMEYRQOAVEWQGLALISEAVLNGOALLVNSQPPWEPLOL 120
 |||||
 Oy 121 HDKAVSGLSLTTLRALGAQKEAISPPDASAPLRTTADTFKRLFRVYSNPLRGKL 180
 |||||
 Db 121 HDKAVSGLSLTTLRALGAQKEAISPPDASAPLRTTADTFKRLFRVYSNPLRGKL 180
 |||||
 Oy 181 KLYTGEACRTGDR 193
 |||||
 Db 181 KLYTGEACRTGDR 193

RESULT 2

Oy0173
 erythropoietin precursor - crab-eating macaque
 C:Species: Macaca fascicularis (crab-eating macaque)
 C>Date: 07-Sep-1990 #sequence_revision 15-Nov-1996 #text_change 22-Jun-1999
 C:Accession: J00173
 R:Lin. F.K.: Lin. C.H.: Lai, P.H.; Browne, J.K.; Egrie, J.C.; Smalling, R.; Fox, G.M.; C
 Gene 44, 201-209, 1986
 A:Title: Monkey erythropoietin gene: cloning, expression and comparison with the human
 A:Reference number: J00173; MUID:87055236; PMID:2877922
 A:Accession: J00173
 A:Molecule type: mRNA
 A:Residues: 1-192 <LIN>
 A:Cross-references: GB:M18189; GB:M15818; GB:M15819; GB:M18188; NID:9342093; PIDN:AAA368
 A:Experimental source: kidney
 C:Comment: This protein is the principal hormone involved in the regulation of erythrocy
 C:Comment: Erythropoietin is produced by kidney or liver of adult mammals and by liver C
 C:Function:
 A:Description: the primary inducer of erythrocyte formation
 C:Superfamily: erythropoietin
 C:Keywords: erythropoiesis; glycoprotein; hormone; kidney; liver
 F:1-27/Domain: signal sequence #status predicted <SIG>
 F:28-192/Product: erythropoietin #status predicted <MAT>
 F:34-187,56-60/Disulfide bonds: #status predicted
 F:51,65,110/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:152/Binding site: carbohydrate (Ser) (covalent) #status predicted

Query Match 90.1%; Score 899.5; DB 1; Length 192;
 Best local Similarity 91.2%; Pred. No. 6.4e-77;
 Matches 176; Conservative 8; Mismatches 8; Indels 1; Gaps 1;

Oy 1 MGVECPAMWMLLSLSPGLGPGVPGAPRLICDSRYLERLYLLEKAEENITTCGAHC 60
 |||||
 Db 1 MGVECPAMWMLLSLSPGLGPGVPGAPRLICDSRYLERLYLLEKAEENITTCGAHC 60
 |||||
 Oy 61 SLNENITVPPTKYNFYAMKMEYRQOAVEWQGLALISEAVLNGOALLVNSQPPWEPLOL 120
 |||||
 Db 61 SLNENITVPPTKYNFYAMKMEYRQOAVEWQGLALISEAVLNGOALLVNSQPPWEPLOL 120
 |||||
 Oy 121 HDKAVSGLSLTTLRALGAQKEAISPPDASAPLRTTADTFKRLFRVYSNPLRGKL 180
 |||||
 Db 121 HDKAVSGLSLTTLRALGAQKEAISPPDASAPLRTTADTFKRLFRVYSNPLRGKL 179

Oy 181 KLYTGEACRTGDR 193
 |||||
 Db 180 KLYTGEACRTGDR 192

RESULT 3

184613
 erythropoietin precursor - rhesus macaque
 C:Species: Macaca mulatta (rhesus macaque)
 C>Date: 02-Aug-1996 #sequence_revision 15-Nov-1996 #text_change 22-Jun-1999
 C:Accession: I84613
 R:Men D.: Boissel, J.
 Blood 82, 1507-1516, 1993
 A:Title: Erythropoietin structure-function relationships: High degree of sequence hom
 A:Reference number: I46083; MUID:93372347; PMID:8364201
 A:Accession: I84613
 A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA
 A:Residues: 1-192 <RES>
 A:Cross-references: GB:L10609; NID:9342095; PIDN:AAA36842.1; PID:9342096
 C:Comment: Erythropoietin is produced by kidney or liver of adult mammals and by live
 C:Function:
 A:Description: the primary inducer of erythrocyte formation
 C:Superfamily: erythropoietin
 C:Keywords: erythropoiesis; glycoprotein; hormone; kidney; liver
 F:1-27/Domain: signal sequence #status predicted <SIG>
 F:28-192/Product: erythropoietin #status predicted <MAT>
 F:34-187,56-60/Disulfide bonds: #status predicted
 F:51,65,110/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:152/Binding site: carbohydrate (Ser) (covalent) #status predicted

Query Match 89.6%; Score 894.5; DB 1; Length 192;
 Best local Similarity 90.2%; Pred. No. 1.9e-76;
 Matches 174; Conservative 10; Mismatches 8; Indels 1; Gaps 1;

Oy 1 MGVECPAMWMLLSLSPGLGPGVPGAPRLICDSRYLERLYLLEKAEENITTCGAHC 60
 |||||
 Db 1 MGVECPAMWMLLSLSPGLGPGVPGAPRLICDSRYLERLYLLEKAEENITTCGAHC 60
 |||||
 Oy 61 SLNENITVPPTKYNFYAMKMEYRQOAVEWQGLALISEAVLNGOALLVNSQPPWEPLOL 120
 |||||
 Db 61 SLNENITVPPTKYNFYAMKMEYRQOAVEWQGLALISEAVLNGOALLVNSQPPWEPLOL 120
 |||||
 Oy 121 HDKAVSGLSLTTLRALGAQKEAISPPDASAPLRTTADTFKRLFRVYSNPLRGKL 180
 |||||
 Db 121 HDKAVSGLSLTTLRALGAQKEAISPPDASAPLRTTADTFKRLFRVYSNPLRGKL 179
 |||||
 Oy 181 KLYTGEACRTGDR 193
 |||||
 Db 180 KLYTGEACRTGDR 192

RESULT 4

I46083
 erythropoietin precursor - cat (fragment)
 C:Species: Felis silvestris catus (domestic cat)
 C>Date: 16-Aug-1996 #sequence_revision 15-Nov-1996 #text_change 22-Jun-1999
 C:Accession: I46083
 R:Men, D.: Boissel, J.
 Blood 82, 1507-1516, 1993
 A:Title: Erythropoietin structure-function relationships: High degree of sequence hom
 A:Reference number: I46083; MUID:93372347; PMID:8364201
 A:Accession: I46083
 A:Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA
 A:Residues: 1-188 <MEN>
 A:Cross-references: GB:L10606; NID:9163820; PIDN:AAA30807.1; PID:9163821
 C:Comment: Erythropoietin is produced by kidney or liver of adult mammals and by live
 C:Function:
 A:Description: the primary inducer of erythrocyte formation
 C:Superfamily: erythropoietin
 C:Keywords: erythropoiesis; glycoprotein; hormone; kidney; liver
 F:1-22/Domain: signal sequence (fragment) #status predicted <SIG>

```
F:23-188/Prouct: eiythropoietin #status predicted <MA>
F:29-183,51-55/Disulfide bonds: #status predicted
F:46,60,105/Binding site: carboxylate (Asn) (covalent) #status predicted
F:148/Binding site: carboxylate (Ser) (covalent) #status predicted
```

Query Match	79.68;	Score 794.5;	DB 1;	Length 188;
Best Local Similarity	84.18;	Pred. NO. 4.3e-67;		
Matches 159;	Conservative 9;	Mismatches 20;	Indels 1;	Gaps 1.

Qy	5	ECPPAWMLLISLSPICLPVLGAPPRICISRYLERLLLEAKKAENITGCAHCISLNE	64
Db	1	ECPPA-LILLISLULLPLQLPVLGAPPRICISRYLERLLEAKKAENITGCAHCISFSE	59
Qy	65	NIIVPDTRKVFNYAMKRMEYRQOAVEVMQGLALLSEAVLRGOALLVNSSQPMPEQLHVDK	124
Db	60	NIIVPDTRKVFNYETKRMIDVGQOAVEVMQGLALLSEAILRGALLANSSQPMETQLHVDK	119
Qy	125	AVSGIRSLTLLLRALGAKKEAISPDDAASAPPLRTITADPFRKLFERYYSNFLRCKLKYT	184
Db	120	AVSSLRSLTSLLRALGAKKEATSLPEATSAAPPLRTFTVVDLCKLFRIYYSNFLRCKLKYT	179
Qy	185	GEACRTGDR	193
Db	180	GEACRGDR	188

RESULT 5

erythropoietin precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 22-Nov-1993 #sequence_revision 15-Nov-1996 #text_change 21-Jul-2000
C:Accession: S28148; I62743
R:Naevo, M.; Suga, H.; Okano, M.; Masuda, S.; Narita, H.; Ikura, K.; Sasaki, R.
Biochim. Biophys. Acta 1171, 99-102, 1992
A:Title: Nucleotide sequence of rat erythropoietin.
A:Reference number: S28148; MUID:93042015; PMID:1420369
A:Accession: S28148
A:Molecule type: mRNA
A:Residues: 1-192 <NMG>
A:Cross-references: GB:D10763; NID:g220735; PIDN:BAAO1593.1; PID:g220736
R:Wen, D.; Boltsel, J.
Blood 82, 1507-1516, 1993
A:Title: Erythropoietin structure-function relationships: High degree of sequence homology.
A:Reference number: I46083; MUID:93372347; PMID:8364201
A:Accession: 162743
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 4-192 <RES>
A:Cross-references: GB:I10608; NID:g204060; PIDN:AAA41126.1; PID:g204061
C:Comment: Erythropoietin is produced by kidney or liver of adult mammals and by liver c
A:Function:
A:Description: the primary inducer of erythrocyte formation
C:Superfamily: erythropoietin
C:Keywords: erythropoiesis; glycoprotein; hormone; kidney; liver
F:1-56/Domain: signal sequence #status predicted <SIG>
F:27-192/Product: erythropoietin #status predicted <MAT>
E:33-187,55-165/Disulfide bonds: #status predicted
E:50,64,109/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match	78.0%;	Score 778.5;	DB 1;	Length 192;
Best Local Similarity	80.8%;	Pred. NO. 1.4e-65;		
Matches 156;	Conservative 14;	Mismatches 22;	Indels 1;	Gaps 1;

```

Oy      1 MGVEHCAPMELLLSTLLSTPLGELVPLCAPPLIDSDVRELYELEANEAKNITGGCAEHG 60
        1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db      1 MGVEPERPL-LLLSLTLLPLIGLPLVPCAPPLIDSDKRLERYELEANEAEVNTMGCAECP 59
        1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Oy      61 SLNENITVPDTRKNVNFYAMKRMEVBOQAEVEMOGLALISEAALRGCAOLLVNSSQPEPDLTOL 120
        1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db      60 RLSEKITVPTDKRVNFYAMKRMRKVEQAEVEMOGLSTLSEALIQAOVLQANSSQPEPDLTOL 119
        1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Oy      121 HYDAKAVGLSRSLTILLRLALGAQKEAISEPDAASAPLRTTTADTFRKLFRVYSNFLRGKL 180
        1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

```

D_b 120 HIDAI SOLRSLTSLRYLGAQKELMSPDPATOAPLRTLTADTFCKLFRVYSNFLRGKL 179

Q_Y 181 KLYTGEACRTGDR 193
|||||
180 KLYTGEACRGRDR 192

RESULT 6

erythropoietic precursor - sheep
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 16-Aug-1996 #sequence_revision 15-Nov-1996 #text_change 22-Jun-1999
C:Accession: I46401; I47077
R:Fu, P.; Evans, B.; Lim, G.B.; Moritz, K.; Wintour, E.M.
Mol. Cell. Endocrinol. 93, 107-116, 1993
A:Title: The sheep erythropoietin gene: molecular cloning and effect of hemorrhage on
A:Reference number: I46401; MUID:93351736; PMID:8349021
A:Accession: I46401
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-194 <PUX>
A:Cross-references: EMBL:Z24681; NID:9395049; PIDN:CAA80848.1; PID:9395050
R:Wen, D.; Bolssel, J.
Blood 82, 1507-1516, 1993
A:Title: Erythropoietin structure-function relationships: High degree of homology
A:Reference number: I46083; MUID:93372347; PMID:8364201
A:Accession: I47077
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 4-15, 'L', 17-107, 'P', 109-194 <MEN>
A:Cross-references: GB:I10610; NID:9165876; PIDN:AAA31518.1; PID:9165877
C:Comment: Erythropoietin is produced by kidney or liver of adult mammals and by liver
C:Function:
A:Description: the primary inducer of erythrocyte formation
C:Superfamily: erythropoietin
C:Keywords: erythropoiesis; glycoprotein; hormone; kidney; liver
F:1-27/Domin: signal sequence #status predicted <SIG>
F:28-194/Product: erythropoietin #status predicted <MAT>
F:34-189, 56-60/Disulfide bonds: #status predicted
F:31,65,110/Binding site: carbohydrate (Ser) (covalent) #status predicted
F:154/Binding site: carbohydrate (Ser) (covalent) #status predicted

Query Match	77.5%	Score 773.5	DB 1	Length 194
Best Local Similarity	79.4%	Pred. No. 4.2e-65		
Matches 154	Conservative 11	Mismatches 28	Indels 1	Gaps 1

QY	1	MGVHECPAMWLLLSLLSLPLGLFVLICAPRLLICDSVLEVEYLLEANEANITGCAEHC	60	
		1		
		1	MGARICPPLLLLLLSFLPLFGLFVLICAPRLLICDSVLEVEYLLEANEANITGCAEHC	60
		1		
QY	61	SLNENITVPDTRVNFVYAMKRMEEVROQAVEVWQGLALLSEAVLRGQALLVNSQCPPELOT	120	
		1		
		1	SFSENIITVPDTRVNFVYAMKRMEEVROQAVEVWQGLALLSEAVLRGQALLVNSQCPPELOT	120
		1		
Db	61	SFSENIITVPDTRVNFVYAMKRMEEVROQAVEVWQGLALLSEAVLRGQALLVNSQCPPELOT	120	
		1		
QY	121	HYDKAVSGLSLSTLLLRALGAQKEAISPDDAA-SAAPLRITVADTFPKLLFRVYSNPLRGK	179	
		1		
		1	HYDKAVSGLSLSTLLLRALGAQKEAISPDDAA-SAAPLRITVADTFPKLLFRVYSNPLRGK	179
		1		
Db	121	HYDKAVSGLSLSTLLLRALGAQKEAISPDDAA-SAAPLRITVADTFPKLLFRVYSNPLRGK	180	
		1		
QY	180	LKLYTGECACRTGDR	193	
		1		
Db	181	LTLVTGGECACRTGDR	194	

RESULT 7

erythropoietin pig (fragment)
C.Species: Sus scrofa domestica (domestic pig)
C.Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 16-Jul-1999
C.Accession: I46578
R.Wen, D.: Boissel, J.
Blood 82, 1507-1516, 1993
A.Title: Erythropoietin structure-function relationships: High degree of sequence hom
Reference number: I46083; MUID:53372347; PMID:8354201

C:Genetics:
A:Gene: MGDF
A:Map position: 3q26.3
C:Keywords: alternative splicing; cytokine

Query Match 9.4%; Score 93.5; DB 2; Length 286;
Best Local Similarity 27.1%; Pred. No. 0.39; Mismatches 82; Indels 23; Gaps 6;
Matches 46; Conservative 19;

OY 12 LILSLISLPGLVLPGLPRLICDSRVLEKAEENITTCGAHCSLNENTIVPDT 71
DB 11 MLITRRLTSSP---APP--ACDLRLVLSKLRSDSHVLSRSCQCEVHPPLPVLPRV 65
OY 72 KNEFYAMKREYVROQAVEVWQGLLSEAVL--RGOALLVNSSQPEWPIQLHYDKAVSGL 129
DB 66 DESLGEWKTQTEQSKADILGAVTLLEGVMAARGOLGPTCLSSILGQLSQVRLILGAL 125
OY 130 RSLITTLRLGAKQKALISPPDASAPLRITITADTFRKLFERYVSNFLRGLK 179
DB 126 QSL-----LGTQ-----LPPQG-----RTTAHKDPNALFLSPHLLRGL 159

RESULT 14

S45330
thrombopoietin - mouse
C:Species: Mus musculus (house mouse)
C:Date: 10-Dec-1994 #sequence_revision 17-Nov-1995 #text_change 08-Oct-1999
C:Accession: S45330
R:Lox, S.; Koushansky, K.; Holly, R.D.; Kuiper, J.L.; Lofton-Day, C.E.; Oort, P.J.; Grä
unkard, D.; Ching, A.F.T.; Mathewes, S.L.; Bailey, M.C.; Forstrom, J.W.; Buddle, M.M.; C
Nature 369, 565-568, 1994
A:Title: Cloning and expression of murine thrombopoietin cDNA and stimulation of platele
A:Reference number: S45330; MUID:94261207; PMID:8202158
A:Accession: S45330
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-356 <LOK>
A:Cross-references: GB:L34169; NID:9508540; PIDN:AAA40436.1; PID:9508541

Query Match 9.0%; Score 90; DB 2; Length 356;
Best Local Similarity 25.1%; Pred. No. 1.1;

Matches 44; Conservative 29; Mismatches 78; Indels 24; Gaps 6;

OY 12 LILSLISLPGLVLPGLPRLICDSRVLEKAEENITTCGAHCSLNENTIVPDT 71
DB 6 LLLAAMLAVALRLTSSPYAPACDPRLNKLRLSDSHLSRSCQCPDVPDLSIPVLPRV 65
OY 72 KNEFYAMKREYVROQAVEVWQGLLSEAVL--RGOALLVNSSQPEWPIQLHYDKAVSGL 129
DB 66 DESLGEWKTQTEQSKADILGAVTLLEGVMAARGOLGPTCLSSILGQLSQVRLILGAL 125
OY 130 RSLITTLRLGAKQKALISPPDASAPLRITITADTFRKLFERYVSNFLRGLK 181
DB 112 GOLSGOVRLILGALGGLL-----GTQLPLOGRTTAHKDPNALFLSLQQLRGRV 161

RESULT 15

AE0959

Solute binding receptor protein [imported] - Salmonella enterica subsp. enterica serovar
C:Species: Salmonella enterica subsp. enterica serovar Typh
A:Note: this species has also been called Salmonella typhi
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001

C:Accession: AE0959

R:Parthill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Conerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001

A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A:Reference number: AB0502; PMID:11677608

A:Accession: AE0959
A>Status: preliminary
A:Molecule type: DNA

A:Residues: 1-346 <PAR>
A:Cross-references: GB:AL513382; PIDN:CAD03169.1; PID:q16504804; GSPDB:GN00176
C:Genetics:
A:Gene: SPY3952

Query Match 8.8%; Score 87.5; DB 2; Length 346;
Best Local Similarity 26.7%; Pred. No. 1.8;
Matches 44; Conservative 22; Mismatches 48; Indels 51; Gaps 9;

OY 37 RVLEKRLLEKAEENITTCG--CAHCSLNE--NITVPDTRKVNPAKREYVROQAVEVWQ 92
DB 217 RNLLQEMLEKHPDANVYASATIAEAAKMGGRNLTPLTIVSYFL-----THQYTR 267
OY 93 GLALLSEAVLRGOALLVNSSQ--PWEPIQLHYDKAVSGLRSLTTLRLALGAQ--KEAISP 149
DB 268 GLK-----RGHILMALSDQAMQ-----GELATQSIKVLGQGPVPENISPP 309
OY 150 -----DAASAAPLRITITADTFRKLFERYVSNFLRGLKLYTGEA 187
DB 310 VLLITHNNADSAVRRLSLSPGFRPY-----LYQYTSSEA 344

Search completed: January 8, 2003, 05:14:55
Job time : 41.8802 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 8, 2003, 00:55:32 ; Search time 13.4401 Seconds
(without alignments) 595.600 Million cell updates/sec

Title: US-09-813-775C-2
Sequence: 1 MGHECPAMWILLSLSLP.....NFLRGLKLYTGEACRTGDR 193

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	991	99.3	193	1	EPO_HUMAN
2	899.5	90.1	192	1	EPO_MACRA
3	894.5	89.6	192	1	EPO_MACMU
4	793.5	79.5	192	1	EPO_FELCA
5	778.5	78.0	192	1	EPO_RAT
6	773.5	77.5	194	1	EPO_SHEEP
7	769.5	77.1	190	1	EPO_PIG
8	766.5	76.8	192	1	EPO_MOUSE
9	761.5	76.3	192	1	EPO_BOVIN
10	714.5	71.6	175	1	EPO_CANFA
11	124.5	12.5	352	1	TPO_CANFA
12	96.5	9.7	353	1	TPO_HUMAN
13	90	9.0	356	1	TPO_MOUSE
14	86.5	8.7	326	1	TPO_RAT
15	86.5	8.7	622	1	FAGG_HUMAN
16	85.5	8.6	897	1	EP15_MOUSE
17	82.5	8.3	3033	1	POLG_HCVJ8
18	82	8.2	1980	1	MY9B_RAT
19	79.5	8.0	907	1	GACS_PSESY
20	79	7.9	1007	1	SAL2_HUMAN
21	79	7.9	1089	1	IMB3_YEAST
22	78	7.8	548	1	CH60_BUCMP
23	77.5	7.8	896	1	EP15_HUMAN
24	77	7.7	551	1	CH60_BUCAP
25	77	7.7	778	1	RG12_MOUSE
26	75.5	7.6	381	1	MODD_MYCAV
27	75.5	7.6	3164	1	TEG0_HSV11
28	74.5	7.5	353	1	NEDG_YERPE
29	74.5	7.5	388	1	TRAG_BURCE
30	74.5	7.5	543	1	CH60_BARBA
31	74.5	7.5	552	1	CH60_PSEST
32	74.5	7.5	830	1	GCL2_MOUSE
33	74.5	7.5	837	1	GCL2_HUMAN

34	74	7.4	552	1	CH60_COXBU
35	73.5	7.4	468	1	T10A_HUMAN
36	73.5	7.4	3010	1	POLG_HCVJA
37	73	7.3	342	1	TORT_ECO57
38	73	7.3	342	1	TORT_ECOLI
39	73	7.3	548	1	CH60_BUCAI
40	73	7.3	3010	1	POLG_HCVJT
41	72.5	7.3	486	1	BAF1_KIOLA
42	72	7.2	224	1	MER1_HUMAN
43	72	7.2	263	1	YH25_DEIRA
44	72	7.2	809	1	HRPB_ECOLI
45	71.3	7.2	347	1	CH60_LEGPN

ALIGNMENTS

RESULT 1	EPO_HUMAN	STANDARD:	PRT:	193 AA.
AC	P01588; Q9UHA0; Q9UEZ5; Q9UDZ0;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Erythropoietin precursor (Epoetin).			
GN	EPO.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=85137899; PubMed=3838366;			
RA	Jacobs K., Shoemaker C., Ruderstorf R., Neill S.D., Kaufman R.J.,			
RA	Mutson A., Seehra J., Jones S.S., Hewick R., Fritsch E.F.,			
RA	Kawakita M., Shimizu T., Miyake T.,			
RT	"Isolation and characterization of genomic and cDNA clones of human			
RL	erythropoietin."			
RN	Nature 313:806-810(1985).			
[2]				
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=86067948; PubMed=3865178;			
RA	Lin F.-K., Suggs S., Lin C.-H., Browne J.K., Smalling R., Egrie J.C.,			
RA	Chen K.K., Fox G.M., Martin F., Stabinsky Z., Badrawi S.M., Lai P.-H.,			
RA	Goldwasser E.;			
RT	"Cloning and expression of the human erythropoietin gene."			
RL	Proc. Natl. Acad. Sci. U.S.A. 82:7580-7584(1985).			
[3]				
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=99018118; PubMed=9799793;			
RA	Gloechner G., Scherer S., Schattevoy R., Boright A., Weber J.,			
RA	Tsui L.-C., Rosenthal A.;			
RT	"Large-scale sequencing of two regions in human chromosome 7q22:			
RL	analysis of 650 kb of genomic sequence around the Epo and CUTL1 loci			
RT	reveals 17 genes."			
RL	Genome Res. 8:1060-1073(1998).			
[4]				
RP	SEQUENCE FROM N.A.			
RA	Rupert J.L., Hochachka P.W.;			
RT	"Erythropoietin gene sequence in the Quechua, a high altitude native			
RL	population."			
RN	submitted (NOV-1999) to the EMBL/Genbank/DBJ databases.			
[5]				
RP	SEQUENCE OF 58-193 FROM N.A., AND VARIANTS HEPATOCELLULAR CARCINOMA.			
RA	Funakoshi A., Muta H., Bada T., Shimizu S.;			
RT	"Gene expression of mutant erythropoietin in hepatocellular			
RL	carcinoma."			
RN	Biochem. Biophys. Res. Commun. 195:717-722(1993).			
[6]				
RP	SEQUENCE OF 28-193, AND DISULFIDE BONDS.			
RC	TISSUE=Urine;			
RX	MEDLINE=86140080; PubMed=3949763;			

DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-AUG-1988 (Rel. 08, last sequence update)
 DT 16-OCT-2001 (Rel. 40, last annotation update)
 DE Erythropoietin precursor.
 GN EPO.
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Macaca.
 NC NCBI_Taxid=9541;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=67055236; PubMed=2877922;
 RA Lin F.-K., Lin C.-H., Lai P.-H., Browne J.K., Egrie J.C., Smalling R.,
 RA Fox G.M., Chen K.K., Castro M., Suggs S.;
 RT "Monkey erythropoietin gene: cloning, expression and comparison with
 RT the human erythropoietin gene.";
 RL Gene 44:201-209(1986)
 CC -1- FUNCTION: ERYTHROPOIETIN IS THE PRINCIPAL HORMONE INVOLVED IN THE
 CC REGULATION OF ERYTHROCYTE DIFFERENTIATION AND THE MAINTENANCE OF A
 CC PHYSIOLOGICAL LEVEL OF CIRCULATING ERYTHROCYTE MASS.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: PRODUCED BY KIDNEY OR LIVER OF ADULT MAMMALS
 CC AND BY LIVER OF FETAL OR NEONATAL MAMMALS.
 CC -1- SIMILARITY: BELONGS TO THE EPO / TPO FAMILY.
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 CC -----
 DR EMBL: M18189; AAA36841.1; -;
 DR PIR: J00173; J00173.
 DR HSSP: P01588; ICN4.
 DR InterPro: IPR001323; EPO_TPO.
 DR Pfam: PF00758; EPO_TPO; 1.
 DR PRINTS: PR00272; ERYTHROPTN.
 DR PROSITE: PS00817; EPO_TPO; 1.
 DR Erythrocyte maturation; Glycoprotein; Hormone; Signal.
 KW SIGNAL.
 FT CHAIN 1 27
 FT DISULFID 28 192
 FT DISULFID 34 187
 FT DISULFID 56 60
 FT CARBOHYD 51 51
 FT CARBOHYD 65 65
 FT CARBOHYD 110 110
 FT CARBOHYD 152 152
 SQ SEQUENCE 192 AA; 21113 MW; E8A900F442AD4522 CRC64;
 Query Match. 90.1%; Score 899.5; DB 1; Length 192;
 Best Local Similarity 91.2%; Pred. No. 2.2e-78;
 Matches 176; Conservative 8; Mismatches 8; Indels 1; Gaps 1;
 QY 1 MGVEHCFAWMLLLSLPLGLPVLGAPPRLLICDSRYLERLYLEAKEAENITGCAEHC 60
 DB 1 MGVEHCFAWMLLLSLPLGLPVLGAPPRLLICDSRYLERLYLEAKEAENITGCAEHC 60
 QY 61 SLNENITVPDTKVNFAWKREVRQQAWEVQGLALLSEAVLRQOALLVNSQFPEPLQL 120
 DB 61 SLNENITVPDTKVNFAWKREVRQQAWEVQGLALLSEAVLRQOALLVNSQFPEPLQL 120
 QY 121 HVDKAVSGLRSLTTLRLALGAKAISPPDAASAAPLRTTAQDFRRLFRYNSFLRGKL 180
 DB 121 HMDKAISGLRSITTLRLALGAKAISPPDAASAAPLRTTAQDFRRLFRYNSFLRGKL 180
 QY 181 KLYTGACRTGDR 193
 DB 180 KLYTGACRTGDR 192

RESULT 3
 EPO_MACMU
 ID EPO_MACMU STANDARD; PRT; 192 AA.
 AC 028513;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, last sequence update)
 DT 16-OCT-2001 (Rel. 40, last annotation update)
 DE Erythropoietin precursor.
 GN EPO.
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Macaca.
 NC NCBI_Taxid=9544;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93372347; PubMed=8364201;
 RA Wen D., Boissel J.P.R., Tracy T.E., Gruninger R.H., Mulcahy L.S.,
 RA Celusniak J., Goodman M., Bunn H.F.;
 RT "Erythropoietin structure-function relationships: high degree of
 RT sequence homology among mammals.";
 RL Blood 82:1507-1516(1993).
 CC -1- FUNCTION: ERYTHROPOIETIN IS THE PRINCIPAL HORMONE INVOLVED IN THE
 CC REGULATION OF ERYTHROCYTE DIFFERENTIATION AND THE MAINTENANCE OF A
 CC PHYSIOLOGICAL LEVEL OF CIRCULATING ERYTHROCYTE MASS.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: PRODUCED BY KIDNEY OR LIVER OF ADULT MAMMALS
 CC AND BY LIVER OF FETAL OR NEONATAL MAMMALS.
 CC -1- SIMILARITY: BELONGS TO THE EPO / TPO FAMILY.
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 DR EMBL: L10609; AAA36842.1; -;
 DR HSSP: P01588; ICN4.
 DR InterPro: IPR001323; EPO_TPO.
 DR Pfam: PF00758; EPO_TPO; 1.
 DR PRINTS: PR00272; ERYTHROPTN.
 DR PROSITE: PS00817; EPO_TPO; 1.
 DR Erythrocyte maturation; Glycoprotein; Hormone; Signal.
 KW SIGNAL.
 FT CHAIN 1 27
 FT DISULFID 28 192
 FT DISULFID 34 187
 FT DISULFID 56 60
 FT CARBOHYD 51 51
 FT CARBOHYD 65 65
 FT CARBOHYD 110 110
 FT CARBOHYD 152 152
 SQ SEQUENCE 192 AA; 21081 MW; 275560A264628CD1 CRC64;
 Query Match. 89.6%; Score 894.5; DB 1; Length 192;
 Best Local Similarity 90.2%; Pred. No. 6.4e-78;
 Matches 174; Conservative 10; Mismatches 8; Indels 1; Gaps 1;
 QY 1 MGVEHCFAWMLLLSLPLGLPVLGAPPRLLICDSRYLERLYLEAKEAENITGCAEHC 60
 DB 1 MGVEHCFAWMLLLSLPLGLPVLGAPPRLLICDSRYLERLYLEAKEAENITGCAEHC 60
 QY 61 SLNENITVPDTKVNFAWKREVRQQAWEVQGLALLSEAVLRQOALLVNSQFPEPLQL 120
 DB 61 SLNENITVPDTKVNFAWKREVRQQAWEVQGLALLSEAVLRQOALLVNSQFPEPLQL 120
 QY 121 HVDKAVSGLRSLTTLRLALGAKAISPPDAASAAPLRTTAQDFRRLFRYNSFLRGKL 180
 DB 121 HMDKAISGLRSITTLRLALGAKAISPPDAASAAPLRTTAQDFRRLFRYNSFLRGKL 179

FT DISULFID 33 187 BY SIMILARITY.
 FT CARBOHYD 50 50 N-LINKED (GLCNAC. . .) (BY SIMILARITY).
 FT CARBOHYD 64 64 N-LINKED (GLCNAC. . .) (BY SIMILARITY).
 FT CARBOHYD 109 109 N-LINKED (GLCNAC. . .) (BY SIMILARITY).
 SO SEQUENCE 192 AA; 21286 MW; 3EA632737ED2443 CRC64;

Query Match 78.0%; Score 778.5; DB 1; Length 192;
 Best Local Similarity 80.8%; Pred. No. 6.8e-67;
 Matches 156; Conservative 14; Mismatches 22; Indels 1; Gaps 1;

QY 1 MGVECPAMLLSLPLGLPLGAPPLICDSRYLELYLEAKAEENITGCAEHC 60
 DB 1 MGVECPAMLLSLPLGLPLGAPPLICDSRYLELYLEAKAEENITGCAEHC 59
 QY 61 SLNENITVPDTKVFYANKRMEVROQAVEVWOGIALLSAVALRGQALLVNSSQPEPIQL 120
 DB 60 RLSENITVPDTKVFYANKRMEVROQAVEVWOGIALLSAVALRGQALLVNSSQPEPIQL 119
 QY 121 HYDKAVSGSLRTTLRLALGAKAISPDAASAPLRTITADTFRLFRVYSNFLRGKL 180
 DB 120 HIDKAVSGSLRTTLRLALGAKAISPDAASAPLRTITADTFRLFRVYSNFLRGKL 179
 QY 181 KLYTGEACRTGDR 193
 DB 180 KLYTGEACRTGDR 192

RESULT 6
 EPO_SHEEP STANDARD; PRT; 194 AA.
 ID EPO_SHEEP
 AC P33709; 028572;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Erythropoietin precursor.
 GN EPO.
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 NC NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=93372347; PubMed=8349021;
 RA Fu P., Evans B., Jim G.B., Moritz K., Wintour M.E.;
 RA Men D., Boissel J.P.R., Tracy T.E., Gruninger R.H., Mulcahy L.S.,
 RT "Erythropoietin structure-function relationships: high degree of
 RT hemorhage on plasma erythropoietin and renal/liver messenger RNA in
 RT adult sheep.";
 RL Mol. Cell. Endocrinol. 93:107-116(1993).
 RN [2]
 RP SEQUENCE OF 4-194 FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=93372347; PubMed=8364201;
 RA Men D., Boissel J.P.R., Tracy T.E., Gruninger R.H., Mulcahy L.S.,
 RT "Erythropoietin structure-function relationships: high degree of
 RT sequence homology among mammals.";
 RL Blood 82:1507-1516(1993).
 RN [1]
 RP FUNCTION: ERYTHROPOIETIN IS THE PRINCIPAL HORMONE INVOLVED IN THE
 CC REGULATION OF ERYTHROCYTE DIFFERENTIATION AND THE MAINTENANCE OF A
 CC PHYSIOLOGICAL LEVEL OF CIRCULATING ERYTHROCYTE MASS.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: PRODUCED BY KIDNEY OR LIVER OF ADULT MAMMALS
 CC AND BY LIVER OF FETAL OR NEONATAL MAMMALS.
 CC -1- SIMILARITY: BELONGS TO THE EPO / TPO FAMILY.
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 CC -----
 DR EMBL: Z24681; CA80848.1; -
 DR EMBL: L10610; AAA31518.1; -
 DR HSSP: P01588; ICN4
 DR InterPro: IPR001323; EPO_TPO.
 DR InterPro: IPR003013; Erythroptn.
 DR Pfam: PF00758; EPO_TPO.1.
 DR PRINTS: PR00272; ERYTHROPTN.
 DR PROSITE: PS00817; EPO_TPO.1.
 KM Erythrocyte maturation; Glycoprotein; Hormone; Signal.
 FT SIGNAL 1 27
 FT CHAIN 28 194
 FT ERYTHROPOIETIN.
 FT DISULFID 34 189
 FT DISULFID 56 60 BY SIMILARITY.
 FT CARBOHYD 51 51 BY SIMILARITY.
 FT CARBOHYD 65 65 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 110 110 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 16 16 F -> L (IN REF. 2).
 FT CONFLICT 108 108 L -> P (IN REF. 2).
 SO SEQUENCE 194 AA; 21335 MW; C025AAB0528131A9 CRC64;

Query Match 77.5%; Score 773.5; DB 1; Length 194;
 Best Local Similarity 79.4%; Pred. No. 2.1e-66;
 Matches 154; Conservative 11; Mismatches 28; Indels 1; Gaps 1;

QY 1 MGVECPAMLLSLPLGLPLGAPPLICDSRYLELYLEAKAEENITGCAEHC 60
 DB 1 MGVECPAMLLSLPLGLPLGAPPLICDSRYLELYLEAKAEENITGCAEHC 60
 QY 61 SLNENITVPDTKVFYANKRMEVROQAVEVWOGIALLSAVALRGQALLVNSSQPEPIQL 120
 DB 61 SLENITVPDTKVFYANKRMEVROQAVEVWOGIALLSAVALRGQALLVNSSQPEPIQL 120
 QY 121 HYDKAVSGSLRTTLRLALGAKAISPDAASAPLRTITADTFRLFRVYSNFLRGKL 179
 DB 121 HYDKAVSGSLRTTLRLALGAKAISPDAASAPLRTITADTFRLFRVYSNFLRGKL 180
 QY 180 KLYTGEACRTGDR 193
 DB 181 KLYTGEACRTGDR 194

RESULT 7
 EPO_PIG STANDARD; PRT; 190 AA.
 ID EPO_PIG
 AC P49157;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Erythropoietin precursor (Fragment).
 GN EPO.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
 NC NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=93372347; PubMed=8364201;
 RA Men D., Boissel J.P.R., Tracy T.E., Gruninger R.H., Mulcahy L.S.,
 RA Czelusniak J., Goodman M., Bunn H.F.;
 RT "Erythropoietin structure-function relationships: high degree of
 RT sequence homology among mammals.";
 RL Blood 82:1507-1516(1993).
 RN [1]
 RP FUNCTION: ERYTHROPOIETIN IS THE PRINCIPAL HORMONE INVOLVED IN THE
 CC REGULATION OF ERYTHROCYTE DIFFERENTIATION AND THE MAINTENANCE OF A
 CC PHYSIOLOGICAL LEVEL OF CIRCULATING ERYTHROCYTE MASS.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: PRODUCED BY KIDNEY OR LIVER OF ADULT MAMMALS
 CC AND BY LIVER OF FETAL OR NEONATAL MAMMALS.
 CC -1- SIMILARITY: BELONGS TO THE EPO / TPO FAMILY.
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CC EMBL: L10607; AAA31029.1; -
 DR HSSP: P01588; ICN4.
 DR InterPro: IPR001323; EPO_TPO.
 DR Pfam: PF00758; EPO_TPO; 1.
 DR PROSITE: PS00817; EPO_TPO; 1.
 KW Erythrocyte maturation; Glycoprotein; Hormone; Signal.
 FT MON_TER 1 1
 FT SIGNAL <1 22
 FT CHAIN 23 190 ERYTHROPOIETIN.
 FT DISULFID 29 185 BY SIMILARITY.
 FT DISULFID 51 55
 FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 60 60 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 105 105 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 168 168 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 190 AA; 20888 MW; A75BD6CCE5077E2A CRC64;

Query Match 77.1%; Score 769.5; DB 1; Length 190;
 Best Local Similarity 82.7%; Pred. No. 4,8e-66;
 Matches 158; Conservative 8; Mismatches 22; Indels 3; Gaps 2;

OY 5 ECPAWMLLTLSTLPLGLPVLCAPRLICDSRVLEKAEKENTTTCGAHC 64
 DB 1 ECPARL-LTLSTLPLGLPVLCAPRLICDSRVLEKAEKENTTTCGAHC 59
 OY 65 NITVPDTKYVNFYAMKREYVQQAWEVWGIALSEAVLRGQALLVNSSPWEPLQL 124
 DB 60 NITVPDTKYVNFYAMKREYVQQAWEVWGIALSEAVLRGQALLVNSSPWEPLQL 119
 OY 125 AVSGRLSTLTLRALGAKAEISPPDA--ASAAPLRTTADTFKRLFRYSNFKRLK 182
 DB 120 AVSGRLSTLTLRALGAKAEISPPDA--ASAAPLRTTADTFKRLFRYSNFKRLK 179
 OY 183 YTGECRTGDR 193
 DB 180 YTGECRTGDR 190
 RESULT 8
 EPO_MOUSE
 ID EPO_MOUSE STANDARD; PRT; 192 AA.
 AC P07321;
 DT 01-APR-1988 (Rel. 07, Created)
 DT 01-APR-1988 (Rel. 07, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Erythropoietin precursor.
 GN EPO.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=87039105; PubMed=3773894;
 RT "Murine erythropoietin gene: cloning, expression, and human gene
 RT homology.";
 RL Mol. Cell. Biol. 6:849-858(1986).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=87039104; PubMed=3022133;
 RA McDonald J.D., Lin F.-K., Goldwasser E.;
 RT "Cloning, sequencing, and evolutionary analysis of the mouse
 RT erythropoietin gene.";
 RL Mol. Cell. Biol. 6:842-848(1986).

RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/Sv;
 RX MEDLINE=21138439; PubMed=11239002;
 RA Wilson M.D., Riemer C., Martindale D.W., Schnupf P., Boright A.P.,
 RA Cheung T.L., Hardy D.M., Schwartz S., Scherer S.W., Tsui L.-C.,
 RA Miller W., Koop B.F.;
 RT "Comparative analysis of the gene-dense Ache/TFE2 region on human
 RT chromosome 7q22 with the orthologous region on mouse chromosome 5.";
 RL Nucleic Acids Res. 29:1352-1365(2001).
 RN [4]

RP SEQUENCE OF 1-52 FROM N.A.
 RC STRAIN=ICN;
 RA MEDLINE=98030528; PubMed=9365246;
 RA Chretien S., Duprez V., Maouche L., Gisselbrecht S., Mayeux P.,
 RA Lacombe C.;
 RT "Abnormal erythropoietin (Epo) gene expression in the murine
 RT erythroleukemia IKS2 cells results from a rearrangement between the
 RT G-protein beta2 subunit gene and the Epo gene.";
 RL Oncogene 15:1995-1999(1997).
 CC -1- FUNCTION: ERYTHROPOIETIN IS THE PRINCIPAL HORMONE INVOLVED IN THE
 CC REGULATION OF ERYTHROCYTE DIFFERENTIATION AND THE MAINTENANCE OF A
 CC PHYSIOLOGICAL LEVEL OF CIRCULATING ERYTHROCYTE MASS.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: PRODUCED BY KIDNEY OR LIVER OF ADULT MAMMALS
 CC AND BY LIVER OF FETAL OR NEONATAL MAMMALS.
 CC -1- SIMILARITY: BELONGS TO THE EPO / TPO FAMILY.

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DR EMBL: M12482; AAA37568.1; -
 DR EMBL: M12950; AAA37570.1; -
 DR EMBL: AF312033; AAK28825.1; -
 DR EMBL: Y11971; CAAY22707.1; -
 DR PIR: A24901; A24901.
 DR PIR: A24902; A24902.
 DR HSSP: P01588; ICN4.
 DR MGD: MGI:95407; EPO.
 DR InterPro: IPR001323; EPO_TPO.
 DR InterPro: IPR003013; Erythroptn.
 DR Pfam: PF00758; EPO_TPO; 1.
 DR PRINTS: PR00272; ERYTHROPTN.
 DR PROSITE: PS00817; EPO_TPO; 1.
 KW Erythrocyte maturation; Glycoprotein; Hormone; Signal.
 FT SIGNAL 1 26
 FT CHAIN 27 192 ERYTHROPOIETIN.
 FT DISULFID 33 187 BY SIMILARITY.
 FT CARBOHYD 50 50 N-LINKED (GLCNAC. . .) (BY SIMILARITY).
 FT CARBOHYD 64 64 N-LINKED (GLCNAC. . .) (BY SIMILARITY).
 FT CARBOHYD 109 109 N-LINKED (GLCNAC. . .) (BY SIMILARITY).
 SQ SEQUENCE 192 AA; 21365 MW; 65F94E214E0DEF2E CRC64;

Query Match 76.8%; Score 766.5; DB 1; Length 192;
 Best Local Similarity 78.8%; Pred. No. 9.4e-66;
 Matches 152; Conservative 15; Mismatches 25; Indels 1; Gaps 1;

OY 1 MGVECPAWMLLTLSTLPLGLPVLCAPRLICDSRVLEKAEKENTTTCGAHC 60
 DB 1 MGVECPAWMLLTLSTLPLGLPVLCAPRLICDSRVLEKAEKENTTTCGAHC 59
 OY 61 SLNENITVPDTKYVNFYAMKREYVQQAWEVWGIALSEAVLRGQALLVNSSPWEPLQL 120
 DB 60 RLSNENITVPDTKYVNFYAMKREYVQQAWEVWGIALSEAVLRGQALLVNSSPWEPLQL 119
 OY 121 HYDKAVSGRLSTLTLRALGAKAEISPPDA--ASAAPLRTTADTFKRLFRYSNFKRLK 180
 DB 120 HYDKAVSGRLSTLTLRALGAKAEISPPDA--ASAAPLRTTADTFKRLFRYSNFKRLK 179

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OY 181 KLYTGEACRTGDR 193
Db 180 KLYTGEACRTGDR 192

RESULT 9
EPO_BOVIN
ID EPO_BOVIN STANDARD: PRT: 192 AA.
AC P48617:
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Erythropoietin precursor.
GN EPO.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bozan; Tissue=Kidney;
RX MEDLINE=96257233; PubMed=8666286;
RA Sulman H.B., Majwa P.A.O., Feldman B.F., Mertens B.,
RA Logan-Henfrey L.L.;
RT "Cloning of a cDNA encoding bovine erythropoietin and analysis of its
RT transcription in selected tissues.";
RL Gene 171:275-280(1996).

CC -1- FUNCTION: ERYTHROPOIETIN IS THE PRINCIPAL HORMONE INVOLVED IN THE
CC REGULATION OF ERYTHROCYTE DIFFERENTIATION AND THE MAINTENANCE OF A
CC PHYSIOLOGICAL LEVEL OF CIRCULATING ERYTHROCYTE MASS.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: PRODUCED BY KIDNEY OR LIVER OF ADULT MAMMALS
CC AND BY LIVER OF FETAL OR NEONATAL MAMMALS.
CC -1- SIMILARITY: BELONGS TO THE EPO / TPO FAMILY.

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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: I41354; AAB41268.1; -
DR EMBL: U44762; AAA86653.1; -
DR HSSP: P01588; ICN4.
DR InterPro: IPR001323; EPO_TPO.
DR InterPro: IPR001323; Erythropo.
DR Pfam: PF00758; EPO_TPO.1.
DR PRINTS: PR00272; ERYTHROP.
DR PROSITE: PS00817; EPO_TPO.1.
KW Erythrocyte maturation; Glycoprotein; Hormone; Signal.
FT SIGNAL 1 25 POTENTIAL.
FT CHAIN 26 192 ERYTHROPOIETIN.
FT DISULFID 32 187 BY SIMILARITY.
FT DISULFID 32 187 BY SIMILARITY.
FT CARBOHYD 49 49 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 63 63 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 108 108 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 192 AA; 21075 MW; DBC419022F7B483A CRC64;

Query Match 76.3%; Score 761.5; DB 1; Length 192;
Best Local Similarity 78.9%; Pred. No. 2.8e-65;
Matches 153; Conservative 11; Mismatches 27; Indels 3; Gaps 2;

OY 1 MGVHECPAMWLILSLPLGLVGLGAPRLICDSRVLEERYLLLEAKDAENITTCGAEHC 60
Db 1 MGVHECPAMWLILSLPLGLVGLGAPRLICDSRVLEERYLLLEAKDAENITTCGAEHC 58
OY 61 SLNNTITVPDTRKVNPFYAMKRMHEVQOALEFWOGALLSEAILRGQALLVNSSQPEPIQL 120
Db 61 SLNNTITVPDTRKVNPFYAMKRMHEVQOALEFWOGALLSEAILRGQALLVNSSQPEPIQL 120

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Db 59 SFENITVPDTRKVNPFYAMKRMHEVQOALEFWOGALLSEAILRGQALLVNSSQPEPIQL 118
OY 121 HDKAVSGLSRLSTLLRALGAQKEAISPDDAA-SAAPRLTTADTRFKLFVRYNSFLRGK 179
Db 119 HDKAVSGLSRLSTLLRALGAQKEAISPDDAA-SAAPRLTTADTRFKLFVRYNSFLRGK 178
OY 180 KLYTGEACRTGDR 193
Db 179 LLYTGEACRTGDR 192

RESULT 10
EPO_CANFA
ID EPO_CANFA STANDARD: PRT: 175 AA.
AC P33707:
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Erythropoietin precursor (Fragment).
GN EPO.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93372347; PubMed=8364201;
RA Wen D., Boissel J.P.R., Tracy T.E., Gruninger R.H., Mulcahy L.S.,
RA Czeglusniak J., Goodman M., Bunn H.F.;
RT "Erythropoietin structure-function relationships: high degree of
RT sequence homology among mammals.";
RL Blood 82:1507-1516(1993).

CC -1- FUNCTION: ERYTHROPOIETIN IS THE PRINCIPAL HORMONE INVOLVED IN THE
CC REGULATION OF ERYTHROCYTE DIFFERENTIATION AND THE MAINTENANCE OF A
CC PHYSIOLOGICAL LEVEL OF CIRCULATING ERYTHROCYTE MASS.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: PRODUCED BY KIDNEY OR LIVER OF ADULT MAMMALS
CC AND BY LIVER OF FETAL OR NEONATAL MAMMALS.
CC -1- SIMILARITY: BELONGS TO THE EPO / TPO FAMILY.

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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: L13027; AAA30842.1; -
DR HSSP: P01588; ICN4.
DR InterPro: IPR001323; EPO_TPO.
DR Pfam: PF00758; EPO_TPO.1.
DR PROSITE: PS00817; EPO_TPO.1.
KW Erythrocyte maturation; Glycoprotein; Hormone; Signal.
FT NON_TER 1 1
FT SIGNAL 1 22 BY SIMILARITY.
FT CHAIN 23 >175 ERYTHROPOIETIN.
FT DISULFID 29 >175 BY SIMILARITY.
FT DISULFID 51 55 BY SIMILARITY.
FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 60 60 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 105 105 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT NON_TER 175 175
SQ SEQUENCE 175 AA; 19193 MW; B504F8DE8676BF4 CRC64;

Query Match 71.6%; Score 714.5; DB 1; Length 175;
Best Local Similarity 81.2%; Pred. No. 7.3e-61;
Matches 143; Conservative 13; Mismatches 19; Indels 1; Gaps 1;

OY 5 ECPAMWLILSLPLGLVGLGAPRLICDSRVLEERYLLLEAKDAENITTCGAEHCISINE 64
Db 5 ECPAMWLILSLPLGLVGLGAPRLICDSRVLEERYLLLEAKDAENITTCGAEHCISINE 59

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OY 65 NITVPDKVNFYAKRMEVQOAVEVQGLALLSEAVLRQALLVNSQPEPQLHVK 124
 DB 60 NITVPDKVNFYAKRMEVQOAVEVQGLALLSEAVLRQALLVNSQPEPQLHVK 119
 OY 125 AVSGLSLTLRALGAKQEAISPPDASAPLRTTADTFKLFPRYSNFKRL 180
 DB 120 AVSLSLTLRALGAKQEAISPPDASAPLRTTADTFKLFPRYSNFKRL 175

RESULT 11
 TPO_CANFA
 ID TPO_CANFA STANDARD: PRT: 352 AA.

AC P42705;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Thrombopoietin precursor (Megakaryocyte colony stimulating factor)
 DE (C-MPL ligand) (MPL) (Megakaryocyte growth and development factor)
 DE (MGDF).
 GN THPO OR TPO.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 24-44.
 RC TISSUE=Kidney;
 RA Bartley T.D., Bogenberger J., Hunt P., Li Y.-S., Lu H.S., Martin F.,
 Chang M.-S., Samal B.B., Nichol J.L., Swift S., Johnson M.J.,
 Hsu R.-Y., Parker V.P., Suggs S., Skrine J.D., Merewether L.A.,
 Clogson C., Hsu E., Hokom M.M., Hornkohl A., Choi E., Pangelinan M.,
 Sun Y., Mar V., McNich J., Simonet L., Jacobsen F., Xie C.,
 Shutter J., Chute H., Basu R., Selander L., Trollinger D., Siew L.,
 Padilla D., Trail G., Elliott G., Izumi R., Covey T., Crouse J.,
 Garcia A., Xu W., del Castillo J., Biron J., Cole S., Hu M.C.-T.,
 Pacifici R., Ponting I., Sarris C., Wen D., Yung Y.P., Lin H.,
 Bosselman R.A.;
 RA "Identification and cloning of a megakaryocyte growth and development
 factor that is a ligand for the cytokine receptor Mpl.";
 RT Cell 77:1117-1117(1994).
 RL [2]
 CC -1- FUNCTION: LINEAGE-SPECIFIC CYTOKINE AFFECTING THE PROLIFERATION
 AND MATURATION OF MEGAKARYOCYTES FROM THEIR COMMITTED PROGENITOR
 CELLS. IT ACTS AT A LATE STAGE OF MEGAKARYOCYTE DEVELOPMENT. IT
 MAY BE THE MAJOR PHYSIOLOGICAL REGULATOR OF CIRCULATING PLATELETS.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- DOMAIN: TWO-DOMAIN STRUCTURE WITH AN ERYTHROPOIETIN-LIKE N-
 TERMINAL AND A SER/PRO/THR-RICH C-TERMINAL.
 CC -1- SIMILARITY: BELONGS TO THE EPO / TPO FAMILY.
 DR InterPro: IPR001323; EPO_TPO.
 DR InterPro: IPR003978; Thrombopoietin.
 DR Pfam: PF00758; EPO_TPO; 1.
 DR PRINTS: PRO1485; THROMBOPTN.
 DR PROSITE: PS00817; EPO_TPO; 1.
 KW Cytokine; Glycoprotein; Hormone; Signal.

FT CHAIN 1 23
 FT SIGNAL 24 352
 FT DISULFID 28 172
 FT DISULFID 50 106
 FT CARBOHYD 185 185
 FT CARBOHYD 197 197
 FT CARBOHYD 206 206
 FT CARBOHYD 234 234
 FT CARBOHYD 255 255
 FT CARBOHYD 332 332
 FT CARBOHYD 347 347
 FT CARBOHYD 37641 MW; 024F3B41B061PBD8 CRG64;
 SQ SEQUENCE 352 AA;

Query Match 12.5%; Score 124.5; DB 1: Length 352;
 Best Local Similarity 25.5%; Pred. No. 0.0002;
 Matches 47; Conservative 26; Mismatches 68; Indels 43; Gaps 6;

OY 12 LILSLSLPLGL-PVLGAPRLICDSRVLEKLEAKENITTCGAHCSCNMENTVDP 70

DB 7 LILVLMLLTARLDPCLPAP--ACDPRLLNKMRLDSVLSRISOCEDIVLPSTVLLPA 64
 OY 71 TKVNFYAKRMEVQOAVEVQGLALLSEAVLRQALLVNSQPEPQLHVKAVSG 128
 DB 65 VDSLSGEMTKQKQKQTRAKQDVGAVALLDVLARGOL-----G 103
 OY 129 LRSITLTLRALGAKQEAISPPDASAPLRTTADTFKLFPRYSNFKRL 177
 DB 104 PCLSSLLGQLSGQVRLLAGLGLGTQLPQG-----RTTHDPNMFISFQOLLR 157
 OY 178 GKLR 181
 DB 158 GKVR 161

RESULT 12
 TPO_HUMAN
 ID TPO_HUMAN STANDARD: PRT: 353 AA.
 AC P40225; Q13020; Q15790; Q15791; Q15792;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Thrombopoietin precursor (Megakaryocyte colony stimulating factor)
 DE (Myeloproliferative leukemia virus oncogene ligand) (C-mpl ligand)
 DE (ML) (Megakaryocyte growth and development factor) (MGDF).
 GN THPO.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Fetal liver;
 RA MEDLINE-94291202; PubMed-8202154;
 RA de Sauvage F.J., Hass P.E., Spencer S.D., Malloy B.E., Gurney A.L.,
 Oles K.J., Hultgren B., Solberg L.A., Jr., Goeddel D.V., Eaton D.L.;
 RA "Stimulation of megakaryocytopoiesis and thrombopoiesis by the c-Mpl
 ligand.";
 RT Nature 369:533-538(1994).
 RL [2]
 CC -1- FUNCTION: LINEAGE-SPECIFIC CYTOKINE AFFECTING THE PROLIFERATION
 AND MATURATION OF MEGAKARYOCYTES FROM THEIR COMMITTED PROGENITOR
 CELLS. IT ACTS AT A LATE STAGE OF MEGAKARYOCYTE DEVELOPMENT. IT
 MAY BE THE MAJOR PHYSIOLOGICAL REGULATOR OF CIRCULATING PLATELETS.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- DOMAIN: TWO-DOMAIN STRUCTURE WITH AN ERYTHROPOIETIN-LIKE N-
 TERMINAL AND A SER/PRO/THR-RICH C-TERMINAL.
 CC -1- SIMILARITY: BELONGS TO THE EPO / TPO FAMILY.
 DR InterPro: IPR001323; EPO_TPO.
 DR InterPro: IPR003978; Thrombopoietin.
 DR Pfam: PF00758; EPO_TPO; 1.
 DR PRINTS: PRO1485; THROMBOPTN.
 DR PROSITE: PS00817; EPO_TPO; 1.
 KW Cytokine; Glycoprotein; Hormone; Signal.

FT CHAIN 1 23
 FT SIGNAL 24 352
 FT DISULFID 28 172
 FT DISULFID 50 106
 FT CARBOHYD 185 185
 FT CARBOHYD 197 197
 FT CARBOHYD 206 206
 FT CARBOHYD 234 234
 FT CARBOHYD 255 255
 FT CARBOHYD 332 332
 FT CARBOHYD 347 347
 FT CARBOHYD 37641 MW; 024F3B41B061PBD8 CRG64;
 SQ SEQUENCE 352 AA;

Query Match 12.5%; Score 124.5; DB 1: Length 352;
 Best Local Similarity 25.5%; Pred. No. 0.0002;
 Matches 47; Conservative 26; Mismatches 68; Indels 43; Gaps 6;

OY 12 LILSLSLPLGL-PVLGAPRLICDSRVLEKLEAKENITTCGAHCSCNMENTVDP 70

RT thrombopoietin gene".
 RN FEBS Lett. 353:57-61(1994).
 RN [5]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RX MEDLINE=95152076; PubMed=7849319;
 RA Gurney A.L., Kuang W.-J., Xie M.-H., Malloy B.E., Eaton D.L.,
 de Sauvage F.J.;
 RT "Genomic structure, chromosomal localization, and conserved
 alternative splice forms of thrombopoietin";
 RT Blood 85:981-988(1995).
 RN [6]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Liver;
 RX MEDLINE=96015174; PubMed=8537317;
 RA Kato T., Ogami K., Shimada Y., Sohma Y., Akahori H.,
 Horie K., Kokubo A., Kudo Y., Maeda E., Kobayashi K., Ohashi H.,
 Ozawa T., Inoue H., Kawamura K., Miyazaki H.;
 RT "Purification and characterization of thrombopoietin";
 RT J. Biochem. 118:229-236(1995).
 RN [7]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Placenta;
 RX MEDLINE=95122483; PubMed=7822271;
 RA Chang M., McIninch J., Basu R., Shutter J., Hsu R., Perkins C., Mar V.,
 Suggs S., Melcher A., Li L., Lu H., Bartley T., Hunt P., Martin F.,
 Smal B., Bogenberger J.;
 RT "Cloning and characterization of the human megakaryocyte growth and
 development factor (MDF) gene";
 RT J. Biol. Chem. 270:511-514(1995).
 RN [8]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 3).
 RA Im S.H., Lee W.S., Chung K.H.;
 RT "Cloning and sequencing of human thrombopoietin";
 RT Submitted (May-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: LINEAGE-SPECIFIC CYTOKINE AFFECTING THE PROLIFERATION
 AND MATURATION OF MEGAKARYOCYTES FROM THEIR COMMITTED PROGENITOR
 CELLS. IT ACTS AT A LATE STAGE OF MEGAKARYOCYTE DEVELOPMENT. IT
 MAY BE THE MAJOR PHYSIOLOGICAL REGULATOR OF CIRCULATING PLATELETS.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS; 1 (SHOWN HERE), 2/TPO-2 AND
 3/TRUNCATED; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- DOMAIN: TWO-DOMAIN STRUCTURE WITH AN ERYTHROPOIETIN-LIKE N-
 TERMINAL AND A SER/PRO/THR-RICH C-TERMINAL.
 CC -1- SIMILARITY: BELONGS TO THE EPO / TPO FAMILY.
 CC -1- DATABASE: NAME=RD Systems' cytokine source book: TPO;
 WWW="http://www.rdsystems.com/asp/g_sitebuilder.asp?bodyid=225".
 CC -----
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 CC -----
 DR EMBL: L33410; AAA59857.1;
 DR EMBL: U11025; AAA50553.1;
 DR EMBL: L36051; AAC37568.1;
 DR EMBL: L36052; AAC37566.1;
 DR EMBL: D32046; BAA06807.1;
 DR EMBL: S76771; AAB33390.1;
 DR EMBL: D32047; BAA21930.1;
 DR EMBL: U59493; AAB03392.1;
 DR EMBL: U59494; AAB03393.1;
 DR EMBL: U59495; AAB03394.1;
 DR EMBL: U17071; AAA74083.1;
 DR PIR: S45331; S45331.
 DR Gene: HGNC:11795; THPO.
 DR MIM: 600044;
 DR InterPro: IPR001323; EPO_TPO.
 DR InterPro: IPR003978; thrombopoietin.
 DR Pfam: PF00758; EPO_TPO; 1.
 DR PRINTS: PRO1485; THROMBOPTN.

DR PROSITE: PS00817; EPO_TPO; 1.
 KW Cytokine; Glycoprotein; Hormone; Signal; Alternative splicing;
 KM Polymorphism.
 FT SIGNAL 1 21
 FT CHAIN 22 353
 FT DISULFID 28 172
 FT DISULFID 50 106
 FT CARBOHYD 197 197
 FT CARBOHYD 206 206
 FT CARBOHYD 234 234
 FT CARBOHYD 255 255
 FT CARBOHYD 340 340
 FT CARBOHYD 348 348
 FT VARSPPLIC 133 136
 FT VARSPPLIC 160 198
 FT VARIANT 14 14
 FT VARIANT 116 116
 FT CONFLICT 46 46
 FT CONFLICT 76 76
 FT CONFLICT 113 113
 FT CONFLICT 131 131
 FT CONFLICT 277 277
 FT CONFLICT 346 346
 SQ SEQUENCE 353 AA; 37822 MW; F0AB5449B72E5526 CRC64;
 Query March 9.7%; Score 96.5; DB 1; Length 353;
 Best Local Similarity 26.7%; Pred. 0.093;
 Matches 46; Conservative 21; Mismatches 82; Indels 23; Gaps 6;
 QY 12 LLSLSLPIGLPVGAPRLICDSRVLYLEAKEAENITTCGAHCISLNETVYPTD 71
 Db MLLTARLTSSP---APP--ACDLRYLSKLRLSHVLSRISOCPEVHPPLTPVLLPAV 65
 QY 72 KVNYYAKRMREVRQAVYEWGGLLSAVL--RGQALLVNSQWPELQHYDKAVSGL 129
 Db DFLSGEWKTMETKADQDILGAVTLLEGVMAAGQLGPTCLISLLGSLGQVRLLLGAL 125
 QY 130 RSLTLLRLALGAKREALSPPDAASAPRLTADTFLFYVNSFNLGSLK 181
 Db 126 QSL-----LGTQ-----LPPG-----RTAHNDPNAIFLSFQHLRGKVR 161
 RESULT 13
 TPO_MOUSE
 ID TPO_MOUSE STANDARD; PRT; 356 AA.
 AC PA0226;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Thrombopoietin precursor (Megakaryocyte colony stimulating factor)
 DE (Mwelo)proliferative leukemia virus oncogene ligand (C-mpl ligand)
 DE (Mpl) (Megakaryocyte growth and development factor) (MGDF).
 GN THPO.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Kidney;
 RX MEDLINE=94261207; PubMed=8202158;
 RA Lok S., Kaushansky K., Holly R.D., Kuitper J.L., Lofton-Day C.E.,
 Oort P.J., Grant F.J., Heipel M.D., Burkhead S.K., Kramer J.M.,
 Bell L.A.N., Sprecher C.A., Blumberg H., Johnson R., Prunkard D.,
 Ching A.F.T., Mathews S.L., Bailey M.C., Forsstrom J.W., Buddle M.M.,
 Osborn S.G., Evans S.D., Sheppard P.O., Presnell S.R., O'Hara P.J.,
 Hagen F.S., Roth G.J., Foster D.C.;
 RT "Cloning and expression of murine thrombopoietin cDNA and stimulation
 of platelet production in vivo";
 RT Nature 369:565-568(1994).
 RN [2]

RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Liver;
 RA MEDLINE=94291201; PubMed=8020099;
 RA Bartley T.D., Bogenberger J., Hunt P., Li Y.-S., Lu H.-S., Martin F.,
 RA Chang M.-S., Samal B.B., Nichol J.L., Swift S., Johnson M.J.,
 RA Hsu R.-Y., Parker V.P., Suggs S., Skrine J.D., Merewether L.A.,
 RA Clogson C., Hsu E., Hokom M.M., Hornkohl A., Choi E., Pangelinan M.,
 RA Sun Y., Mar V., Kenich J., Simonet L., Jacobsen F., Xie C.,
 RA Shutter J., Chute H., Basu R., Selander L., Trollinger D., Siew L.,
 RA Padilla D., Trail G., Elliott G., Izumi R., Covey T., Crose J.,
 RA Garcia A., Xu W., del Castillo J., Biron J., Cole S., Hu M.C.-T.,
 RA Pacifici R., Ponting I., Sarris C., Wen D., Yung Y.P., Lin H.,
 RA Bosseman R.A.;
 RT "Identification and cloning of a megakaryocyte growth and development
 RT factor that is a ligand for the cytokine receptor MPL.";
 RN Cell 77:1117-1117(1994).
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RX MEDLINE=95152076; PubMed=7849319;
 RA Gurney A.L., Kuang W.-J., Xie M.-H., Malloy B.E., Eaton D.L.,
 RA "Genomic structure, chromosomal localization, and conserved
 RA alternative splice forms of thrombopoietin.";
 RT Blood 85:981-988(1995).
 CC -1- FUNCTION: LINEAGE-SPECIFIC CYTOKINE AFFECTING THE PROLIFERATION
 CC AND MATURATION OF MEGAKARYOCYTES FROM THEIR COMMITTED PROGENITOR
 CC CELLS. IT ACTS AT A LATE STAGE OF MEGAKARYOCYTE DEVELOPMENT. IT
 CC MAY BE THE MAJOR PHYSIOLOGICAL REGULATOR OF CIRCULATING PLATELETS.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: 1 (SHOWN HERE) AND 2/TPO-2, ARE
 CC PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: FOUND MAINLY IN THE LIVER, KIDNEY AND SKELETAL
 CC MUSCLE.
 CC -1- DOMAIN: TWO-DOMAIN STRUCTURE WITH AN ERYTHROPOIETIN-LIKE N-
 CC TERMINAL AND A SER/PRO/THR-RICH C-TERMINAL.
 CC -1- SIMILARITY: BELONGS TO THE EPO / TPO FAMILY.
 CC
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 CC
 CC EMBL: U34169; AAA0436.1; -
 CC PIR: S45330; S45330.
 CC MGD: MGI:101875; Thpo.
 CC InterPro: IPR001323; EPO_TPO.
 CC InterPro: IPR003978; thrombopoietin.
 CC Pfam: PF00758; EPO_TPO; 1.
 CC PRINTS: PR01485; THROMBOPTN.
 CC PROSITE: PS00817; EPO_TPO; 1.
 CC CYTOKINE; Glycoprotein; Hormone; Signal; Alternative splicing.
 KW SIGNAL 1 21
 FT CHAIN 22 356
 FT DISULFID 28 172
 FT DISULFID 50 106
 FT CARBOHYD 197 197
 FT CARBOHYD 206 206
 FT CARBOHYD 235 235
 FT CARBOHYD 249 249
 FT CARBOHYD 256 256
 FT CARBOHYD 266 266
 FT CARBOHYD 336 336
 FT CARBOHYD 351 351
 FT CARBOHYD 351 136
 FT VARSPLIC 133 136
 FT SEQUENCE 356 AA; 37835 MW; D346DBAE8392053C CRC64;
 SO
 Query Match 9.0%; Score 90; DB 1; Length 356;
 Best Local Similarity 25.1%; Pred. No. 0.39;
 Matches 44; Conservative 29; Mismatches 78; Indels 24; Gaps 6;

DB 6 L1LAAMLAVALRTLLSPAPACDPRLNKLNDLSLSRLSQCDPVDPLSIPVLLPAV 65
 OY 72 KANFYAKRMREYQOAVVEWOGALLSEAVL--RGQALVYNSQPMPEQLJHDKAVSG 129
 DB 66 DFLGCKKQYOTBSKADILGAVSLLEGMAKRGQ-----EPSCLS-----SL 111
 OY 130 RSITTLRL-ALGAQKEAISPDAASAPL--RTTADTFEKLPRVYSNFLGK 181
 DB 112 GOLSGVRLILGALGILL-----GTOLDFGRTTAKRDPALFLSIQQLRGKVR 161
 RESULT 14
 ID TPO_RAT STANDARD; PRT; 326 AA.
 AC P49745;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Thrombopoietin precursor.
 GN Thpo.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_Taxid=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=95331639; PubMed=7607561;
 RA Ogami K., Shimada Y., Sohma Y., Akahori H., Kato T., Kawamura K.,
 RA Miyazaki H.;
 RT "The sequence of a rat cDNA encoding thrombopoietin.";
 RL Gene 158:309-310(1995).
 CC -1- FUNCTION: LINEAGE-SPECIFIC CYTOKINE AFFECTING THE PROLIFERATION
 CC AND MATURATION OF MEGAKARYOCYTES FROM THEIR COMMITTED PROGENITOR
 CC CELLS. IT ACTS AT A LATE STAGE OF MEGAKARYOCYTE DEVELOPMENT. IT
 CC MAY BE THE MAJOR PHYSIOLOGICAL REGULATOR OF CIRCULATING PLATELETS.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- DOMAIN: TWO-DOMAIN STRUCTURE WITH AN ERYTHROPOIETIN-LIKE N-
 CC TERMINAL AND A SER/PRO/THR-RICH C-TERMINAL.
 CC -1- SIMILARITY: BELONGS TO THE EPO / TPO FAMILY.
 CC
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 CC
 CC EMBL: D32207; BAA06906.1; -
 CC InterPro: IPR001323; EPO_TPO.
 CC InterPro: IPR003978; thrombopoietin.
 CC Pfam: PF00758; EPO_TPO; 1.
 CC PRINTS: PR01485; THROMBOPTN.
 CC PROSITE: PS00817; EPO_TPO; 1.
 CC CYTOKINE; Glycoprotein; Hormone; Signal.
 KW SIGNAL 1 21
 FT CHAIN 22 326
 FT DISULFID 28 172
 FT DISULFID 50 106
 FT CARBOHYD 197 197
 FT CARBOHYD 206 206
 FT CARBOHYD 235 235
 FT CARBOHYD 249 249
 FT CARBOHYD 256 256
 FT SEQUENCE 326 AA; 34556 MW; F99D7E77F896FA2C CRC64;
 SO
 Query Match 8.7%; Score 86.5; DB 1; Length 326;
 Best Local Similarity 23.0%; Pred. No. 0.75;
 Matches 42; Conservative 27; Mismatches 73; Indels 41; Gaps 6;


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Db 7 LVAILLTLARL-FLSSVPPACPRLLKRLRSYLHSLSCPDVNPISIPVLPFAV 65
Qy 72 KVFNFYAKRMEVROQAVEVMOGLALISEAVL-RGQALLVNSOPWEPLQIHDKAVSGL 129
Db 66 DFLSGEKKKTQTESKADIDIGAVSLLEGVMAARGQL-----EF----- 104
Qy 130 RSLTTLRALGAQKEAI-----SPDASAPLRTITADTFERKLFRRVYSNLF 178
Db 105 SCLSSLLGQLSGQVRLILGALIGLITQLPPQG-----FTTAKHDPALFLSLQQLLRG 158
Qy 179 KTK 181
Db 159 KVR 161

RESULT 15
FACG_HUMAN
ID FACG_HUMAN STANDARD: PRT: 622 AA.
AC 015287;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Fanconi anemia group G protein (FACG protein) (DNA-repair protein
DE XRC9).
GN XRC9.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97404378; PubMed=9256465;
RA Liu N., Lamerdin J.E., Tucker J.D., Zhou Z.-Q., Walter C.A.,
RA Albata J.S., Busch D.B., Thompson L.H.;
RT "The human XRC9 gene corrects chromosomal instability and mutagen
RT sensitivities in CHO UV40 cells.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:9232-9237(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99021385; PubMed=9806548;
RA De Winter J.P., Walsflisz Q., Koolmans M.A., Van Berkel C.G.M.,
RA Bosnyak-Collins L., Alon N., Carreau M., Bender O., Demuth I.,
RA Schindler D., Pronk J.C., Arwert F., Hoehn H., Digweed M.,
RA Buchwald M., Joenje H.;
RT "The Fanconi anaemia group G gene FANCG is identical with XRC9.";
RL Nat. Genet. 20:281-283(1998).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Fibroblast, and Foreskin;
RA Lamerdin J.E., McCreedy P.M., Skowronski E., Adamson A.W.,
RA Burkhart-Schultz K., Gordon L., Kyle A., Ramirez S.,
RA Phan H., Velasco N., Ganes J., Dangnan L., Poundstone P.,
RA Christensen M., Georgescu A., Avila J., Liu S., Attik C., Andreise T.,
RA Tranhnam M., Amico-Keller G., Coetfield J., Duarte S., Lucas S.,
RA Bruce R., Thomas P., Quan G., Krommiller B., Arellano A.,
RA Montgomery M., Ow D., Nolan M., Trong S., Kobayashi A., Olsen A.O.,
RA Carrano A.V.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP CHARACTERIZATION.
RX MEDLINE=99303779; PubMed=10373536;
RA Garcia-Higuera I., Kuang Y., Nat D., Wasik J., D'Andrea A.D.;
RT "Fanconi anemia proteins FANCA, FANCC, and FANCG/XRC9 interact in a
RT functional nuclear complex.";
RL Mol. Cell. Biol. 19:4866-4873(1999).
CC -1- FUNCTION: DNA REPAIR PROTEIN THAT MAY OPERATE IN A POSTREPLICATION
CC REPAIR OR A CELL CYCLE CHECKPOINT FUNCTION. MAY BE IMPLICATED IN

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CC INTERSTRAND DNA CROSS-LINK REPAIR AND IN THE MAINTENANCE OF NORMAL
CC CHROMOSOME STABILITY. CANDIDATE TUMOR SUPPRESSOR GENE.
CC -1- SUBUNIT: BELONGS TO A MULTISUBUNIT COMPLEX COMPOSED OF FANCA,
CC FANCC AND FANCG. THE COMPLEX IS NOT FOUND IN PA PATIENTS.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (MAJOR) AND CYTOPLASMIC (MINOR).
CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN TESTIS AND THYMOS. FOUND
CC IN LYMPHOBLASTS.
CC -1- DISEASE: DEFECTS IN FANCG ARE THE CAUSE OF ONE OF THE 8
CC COMPLEMENTATION GROUPS OF FANCONI ANEMIA (FA), AN AUTOSOMAL
CC RECESSIVE DISORDER CHARACTERIZED BY PROGRESSIVE PANCYTOPEANIA, A
CC DIVERSE ASSORTMENT OF CONGENITAL MALFORMATIONS, AND A
CC PREDISPOSITION TO THE DEVELOPMENT OF MALIGNANCIES. AT THE CELLULAR
CC LEVEL, IT IS ASSOCIATED WITH HYPERSENSITIVITY TO DNA-DAMAGING
CC AGENTS, CHROMOSOMAL INSTABILITY (INCREASED CHROMOSOME BREAKAGE),
CC AND DEFECTIVE DNA REPAIR.
CC
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CC or send an email to license@sib-sib.ch).
CC
DR EMBL: U70310; AAB80802.1; -
DR EMBL: AJ007669; CAA07602.1; -
DR EMBL: AC004472; AAC07981.1; -
DR EMBL: BC000032; AAH00032.1; -
DR Genev: HGNC:3588; FANCG.
DR MIM: 602956; -
DR InterPro: IPR01440; TPR.
DR Pfam: PF00515; TPR; 2.
KW DNA repair; Nuclear protein.
SQ SEQUENCE 622 AA; 68553 MW; 4BC7475472AC3C84 CRC64;

Query Match 8.7%; Score 86.5; DB 1; Length 622;
Best Local Similarity 26.8%; Pred. No. 1.7;
Matches 51; Conservative 23; Mismatches 81; Indels 35; Gaps 7;

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Search completed: January 8, 2003, 03:43:19
 Job time : 23.4401 secs


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RESULT 5
Q9RPH5 ID Q9RPH5 PRELIMINARY; PRT; 554 AA.
AC Q9RPH5;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE RECD.
GN RECD.
OS Mycobacterium smegmatis.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1772;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MC2155;
RX MEDLINE=99412429; PubMed=10481025;
RA Griffin IV T.J., Parsons L., Leschziner A.E., Devost J.,
RA Derbyshire K.M., Grindley N.D.;
RT "In vitro transposition of tn552: a tool for DNA sequencing and
RT mutagenesis.";
RL Nucleic Acids Res. 27:3859-3865(1999).
DR EMBL: AF157643; AAD46809.1;
DR InterPro: IPR000606; Viral_helicase1.
DR Pfam: PF01443; Viral_helicase1.1;
SQ SEQUENCE 554 AA; 59516 MW; 3947B50498BD62C CRC64;

Query Match 9.5%; Score 94.5; DB 2; Length 554;
Best Local Similarity 26.7%; Pred. No. 0.89; Mismatches 56; Indels 61; Gaps 9;
Matches 50; Conservative 20;

QY 8 AMLWLILSLPLGLPVLGAP--RLICDSRVLEKLEAKENITTCGAEHCSTL--- 62
Db 72 AMLAALAA-----SPLLGQPVRLRFGDLTYLDRYWLEQY-----CDDVIALVSA 118
QY 63 NENTIVPDTKYNFYAMKMEYRQQAWEYWGCLALSL-----AVLRGALL 108
Db 119 RFGCAVDVSRFLGFCGEORAAKVAISGLTVLTGGPGTKTTVARLLALAEQAL 178
QY 109 VNSSQP-----WEPLQLHVD-----KAVSGLSLTTLRALGAKRAI 146
Db 179 AGKSPRIALAPTGKAAARLQEAIVOLEIDLDLERRRLGLHA--TLHRLGPR---- 233
QY 147 SPDDAAS 153
Db 234 --PDTSS 238

RESULT 6
Q9ROR6 ID Q9ROR6 PRELIMINARY; PRT; 623 AA.
AC Q9ROR6;
DT 01-MAR-2001 (TREMblrel. 16, Created)
DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
DE Fanconi anemia group G protein (Fanconi anemia complementation group
DE G).
GN FANCG.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FROM N.A.
RT "Sequencing and genomic structure of fangc, the murine orthologue of
RT the Fanconi anemia group G gene (FANCG).";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB;
RA van de Vugt H.J., Koomen M., Berns M.A.B., de Vries Y.,

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RA Roimans M.A., van der Weel L., Blom E., de Winter J.P., de Groot J.,
RA Schepers R.J., Hoatlin M.E., Ching Cheng N., Joenje H., Arwert F.;
RT "Characterization, expression and complex formation of murine Fancg.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF112439; AAC63198.1; -.
DR MGD: AY049715; AAL12165.1; -.
DR MGD: MGI:1926471; Fancg.
DR InterPro: IPR001440; TPR.
DR Pfam: PF00515; TPR.
DR SMART: SM00028; TPR.2;
SQ SEQUENCE 623 AA; 68505 MW; 061586EF186F74AF CRC64;

Query Match 9.4%; Score 94; DB 11; Length 623;
Best Local Similarity 25.1%; Pred. No. 1.2;
Matches 51; Conservative 25; Mismatches 65; Indels 62; Gaps 8;

QY 12 LLSLSLPLGLPVLGAPRLICDSRVLEKLEAKENITTCG-----AEHCSTL 62
Db 58 LLTLTGPAVPAVPALETLVLCNCTILRASLYQA-FTEDELTDLQGLERYLEQH--- 113
QY 63 NENTIVPDTKYNFYAMKMEYRQQAWEYWGCLALSLAEVLRGQAL--LVNSSQWPEPLQ 119
Db 114 -----HLERKSQ-----QGLKELMHVSILASSLPPELLRALHGLASLQ 151
QY 120 LHVDAVSGLSLTTLRAL-GAOKRAI-----SPDDASADPLRTTADTFPKL 168
Db 152 AVFWMDTHLDELTLTLQTLNGSCFOSSEDLILLKSWSPAESPADLIQDAESLRDV 211
QY 169 FRVYSNPLRGLKLYTGACRTG 191
Db 212 -----LTTAPACRQG 221

RESULT 7
Q8ZKZ4 ID Q8ZKZ4 PRELIMINARY; PRT; 346 AA.
AC Q8ZKZ4;
DT 01-MAR-2002 (TREMblrel. 20, Created)
DT 01-MAR-2002 (TREMblrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Periplasmic sensor in multi-component regulatory system with Tors
DE (sensory kinase) and TorR (regulator), regulates for operon.
GN TORR OR STM3825.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_TaxID=602;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LT2 / SGSC1412 / ATCC 700720;
RX MEDLINE=21534948; PubMed=11677609;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Portwiliik S., Ali J., Dante M., Du P., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Flores L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
RT LT2.";
RL Nature 413:852-856(2001).
DR EMBL: AE008878; AAL22684.1; -.
DR InterPro: IPR001761; Periplasm/PacI.
DR Pfam: PF00532; Peripla_BP_1like.1;
KW Complete proteome.
SQ SEQUENCE 346 AA; 38440 MW; E37CAB58E49FD716 CRC64;

Query Match 8.8%; Score 87.5; DB 16; Length 346;
Best Local Similarity 26.7%; Pred. No. 2.4;
Matches 44; Conservative 22; Mismatches 48; Indels 51; Gaps 9;

QY 37 RVLERYLLEAKENITTCG--CAEHCSTLNE--NITVPDTKYNFYAMKMEYRQQAWEYWG 92
Db 217 RNLIQEMLERPDANVAVAGSAIAAEAMGEGRNLTPLTIVSYL-----THOYR 267

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QY 93 GLALLSEAVLRGQALLVNSQ--PWEPLQLHVDKAVSGLSLTLRALGAQ--KEAISP 149
DB 268 GLK-----RGHILMALSDQAMQ-----GELAITOSIKVLOGQPVPEINISPP 309
QY 150 -----DASAPLRTITADTFRKLFRRYSNFKRLKLYTGEA 187
DB 310 VLITLNNADSAVRKSLSPGFRPVY-----LYQYISEA 344

RESULT 8
082ZM5 PRELIMINARY: PRT: 346 AA.
AC 082ZM5:
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-JUN-2002 (TREMBlrel. 20, Last sequence update)
DE Solite binding receptor protein.
GN STY3952.
OS Salmonella typhi.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_TaxID=601;

RN SEQUENCE FROM N.A.
RC STRAIN=CT18:
RA MEDLINE-21534947; PubMed-11677608;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebatia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connerton P.,
RA Croft A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Felwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrrell B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
RT enterica serovar Typhi CT18."
RT Nature 413:848-852(2001).
DR EMBL: AL627280; CAD03169.1;
DR InterPro: IPR001761; PeriplabP/LacI.
DR Pfam: PF00532; Peripla_BP_1.
KW Receptor; Complete Proteome.
SQ SEQUENCE 346 AA; 38546 MW; F80FBL68B8C3A8F CRC64;

Query Match 8.8%; Score 87.5; DB 16; Length 346;
Best Local Similarity 26.7%; Pred.No.2.4;
Matches 44; Conservative 22; Mismatches 48; Indels 51; Gaps 9;

QY 37 RYLERYLTAKEAENITTG--CAEHCSLNE--NITVPDFKVFNYAKRMFVROQAVEWQ 92
DB 217 RNLQEMLEHRHDANVYAGSAIAEAAMEGRULPTPLIVSYFL-----THQYR 267
QY 93 GLALLSEAVLRGQALLVNSQ--PWEPLQLHVDKAVSGLSLTLRALGAQ--KEAISP 149
DB 268 GLK-----RGHILMALSDQAMQ-----GELAITOSIKVLOGQPVPEINISPP 309
QY 150 -----DASAPLRTITADTFRKLFRRYSNFKRLKLYTGEA 187
DB 310 VLITLNNADSAVRKSLSPGFRPVY-----LYQYISEA 344

RESULT 9
09D7X0 PRELIMINARY: PRT: 454 AA.
AC 09D7X0:
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE Ribonucleoside-diphosphate reductase 2 beta chain (EC 1.17.4.1).
GN ZFP296 OR 2210018A16R1K.
OS Mus musculus (Mouse).
OC Eukaryota; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euteria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

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RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=STOMACH;
RX MEDLINE-21085660; PubMed-11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi U., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batilov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuenl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staudl F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boilelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazarrelli J., Momberts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schenbach C., Seta T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-Oka K., Wang K.H., Wetz C., Whitaker C., Wilming L.,
RA Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection."
RT Nature 409:685-690(2001).
DR EMBL: AK008746; BAB25873.1;
DR HSSP: P08153; 1ZFD.
DR MGD: MGI:1926956; Zfp296.
DR InterPro: IPR000822; Znf.C2H2.
DR Pfam: PF00096; zfp.C2H2; 5.
DR SMART: SM00355; Znf.C2H2; 5.
DR PROSITE: PS00028; ZINC_FINGER_C2H2_1; 4.
DR PROSITE: PS00157; ZINC_FINGER_C2H2_2; 4.
KW DNA-binding; Metal-binding; zinc-finger.
SQ SEQUENCE 454 AA; 48934 MW; 9012C24C9AB02000 CRC64;

Query Match 8.8%; Score 87.5; DB 11; Length 454;
Best Local Similarity 24.0%; Pred.No.3.4;
Matches 48; Conservative 24; Mismatches 81; Indels 47; Gaps 8;

QY 14 LSLSLPLGLPVLAGAPRLICDSRYLERYLTAKEAENITTG--CAEHCSLNE--NITVPDFK 72
DB 58 LQFASRPLAPSTCA--PRMPLSSKSSDRQPMWDKHDLDLTGCGKGFPLGATIANMDK 116
QY 73 VNFYAKRMFVROQAVEWQGLAL--SEAVLRGQALLVNS-----SQWEPI----- 118
DB 117 K-----QGCQLQVSPDISSESKELKAPSCLOCGROYTSPMKILCHAO 158
QY 119 -----QLHYD--KAVSGRLSTLTLRALGAQKEAISPDAAPLRTITADTFR 166
DB 159 WDHGICLYTOTHLDPTEAPLGLAEVAAASAVAVPESKPPVSSAARSPTCDVCK 218
QY 167 KLFRRYSNFKRLKLYTGE 186
DB 219 KTLSSFSN-LKVMHRSHTGE 237

RESULT 10
08ZDC8 PRELIMINARY: PRT: 323 AA.
AC 08ZDC8:
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-JUN-2002 (TREMBlrel. 20, Last sequence update)
DE Ribonucleoside-diphosphate reductase 2 beta chain (EC 1.17.4.1).
GN NRDP OR YPO2648.
OS Yersinia pestis.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Yersinia.
OX NCBI_TaxID=632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CO-92; BIOVAR ORIENTALIS;
RX MEDLINE-21470413; PubMed-11586360;

```

RA Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
 RA Prentice M.B., Sebaitia M., James K.D., Churcher C., Mungall K.L.,
 RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdano-Tarrega A.M.,
 RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
 RA Feltham T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
 RA Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
 RA Simmonds M., Skellon J., Stevens K., Whitehead S., Barrell B.G.,
 RT "genome sequence of Yersinia pestis, the causative agent of plague";
 RL Nature 413:523-527(2001).
 DR EMBL: AJ414153; CAC92889.1; -
 DR InterPro: IPR000358; RibonucL_redctase.
 DR Pfam: PF00268; ribonuc_red.sm: 1.
 DR PROSITE: PS00368; RIBRED_SMALL: 1.
 KW Oxidoreductase; Complete proteome.
 SQ SEQUENCE 323 AA; 36823 MW; 87C21F7BB9B7FD2 CRC64;
 Query Match 8.7%; Score 87; DB 16; Length 323;
 Best Local Similarity 25.2%; Pred. No. 2.4;
 Matches 34; Conservative 20; Mismatches 59; Indels 22; Gaps 5;
 QY 65 NITVPDTRKVFYAMKRMVEHQAAVEVWQGLALLSEAVLRGALLVNSQPEPIQLHYD- 123
 DB 2 NVVAPTRISAINMKIE-DDKLELVNN--RLTSNFWLPKXVPLSNDIPSWATLTPHQQ 58
 QY 124 ---KAVSGLSLTLLALGQ---KEAISPPDAASAPLRTTADTFKLFVYSNFLR 177
 DB 59 LTRVFTGLTLDTLQNTLAPALIKDAIPHEAIFSNISFMEAVHARSYSIFSTL-- 116
 QY 178 GKLLTYGECRGTG 192
 DB 117 -----CLTSD 121
 RESULT 11
 Q8T527 PRELIMINARY; PRT; 877 AA.
 AC Q8T527;
 DT 01-JUN-2002 (TREMblrel. 21, Created)
 DT 01-JUN-2002 (TREMblrel. 21, Last sequence update)
 DE ABC transporter ABCA.1.
 DE ABC transporter ABCA.1.
 GN ABCA.1.
 OS Dictyostelium discoideum (Slime mold).
 OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
 OX NCBI_TaxID=44689;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AX4;
 RA Anjard C., Loomis W.F.,
 RT "Evolution of the ABC transporter of Dictyostelium,"
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF491005; AAL99041.1; -
 SQ SEQUENCE 877 AA; 97375 MW; DBEC7C7ECB343D9 CRC64;
 Query Match 8.7%; Score 87; DB 5; Length 877;
 Best Local Similarity 27.2%; Pred. No. 8.7;
 Matches 28; Conservative 9; Mismatches 44; Indels 22; Gaps 2;
 QY 14 LSLSLPLGPGVIGCAPR---LTCDSRVLELYLEAKENITTCGAHCSL----- 62
 DB 170 VDFLSTPLGQINGAPKNEPLKMDGNSLEFNYYVNTTCNIIATCPDIATITALEK 229
 QY 63 -----NENITVPDTRKVFYAMKRMVEHQAAVEVWQGL 94
 DB 230 AVITVYSQIRNEXIPPTISYGSNAPRYPPGGAARVWGGL 272
 RESULT 12
 Q9HZM7 PRELIMINARY; PRT; 339 AA.
 AC Q9HZM7;
 DT 01-MAR-2001 (TREMblrel. 16, Created)
 DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)

DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
 DE UDP-N-acetylpyruvoylglycosamine reductase.
 GN MURB OR PA2977.
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OC Pseudomonas.
 OX NCBI_TaxID=287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AMC 15692 / PA01;
 RX MEDLINE=20437337; PubMed=10984043;
 RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
 RA Hickey M.J., Brinkman F.S.L., Hutnagle W.O., Kowalik D.V., Lagrou M.,
 RA Gader R.L., Golltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
 RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
 RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.,
 RA "Complete genome sequence of Pseudomonas aeruginosa PA01, an
 RT opportunistic pathogen";
 RL Nature 406:959-964(2000).
 DR EMBL: AE004723; AAC06365.1; -
 DR HSSP: P08373; 2MBR.
 DR InterPro: IPR003170; MurB.
 DR InterPro: IPR001575; Oxid_FAD_bind.
 DR InterPro: IPR000531; TonB_boxC.
 DR Pfam: PF02873; MurB_C; 1.
 DR Pfam: PF02873; MurB_C; 1.
 DR PROSITE: PS00430; TONB_DEPENDENT_REC_1; UNKNOWN_1.
 KW Complete proteome.
 SQ SEQUENCE 339 AA; 37627 MW; C0C8EF9F2938FE27 CRC64;
 Query Match 8.5%; Score 85; DB 16; Length 339;
 Best Local Similarity 23.0%; Pred. No. 4.1;
 Matches 42; Conservative 22; Mismatches 49; Indels 70; Gaps 8;
 QY 58 EHCISNE-NITVPDTRKVFYAMKRMVEHQAAVEVWQGLALLSEAVLRGALLV----- 109
 DB 7 EHCISLKPNTGIVGRARLAHARDE---ADVEALALARE--RLPLLVIGGGSNL 58
 QY 110 -----NSQPEP-IQLHYDVAVSGLSLTLL 136
 DB 59 LTRDVEALVLRMASQGRIVSDAASVLYEAEAGAMPVQNSLEGLAGLESLI- 117
 QY 137 RALGQKEAISPPDAASAPLRTTITA---DFFKLFVYSNFLRKLTYGECRT 190
 DB 118 -----PGTVGAAPWQNGAYGVLEKDVDSLTLA--DRODCTLREFDQACRF 163
 QY 191 GDR 193
 DB 164 GYR 166
 RESULT 13
 Q8ZHV3 PRELIMINARY; PRT; 2201 AA.
 AC Q8ZHV3;
 DT 01-MAR-2002 (TREMblrel. 20, Created)
 DT 01-MAR-2002 (TREMblrel. 20, Last sequence update)
 DE Putative siderophore biosynthesis protein.
 DE YP00778.
 GN YP00778.
 OS Yersinia pestis.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Yersinia.
 OX NCBI_TaxID=632;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CO-92 / BIOVAR ORIENTALIS;
 RX MEDLINE=21470413; PubMed=11586360;
 RA Parkhill J., Wren B.W., Thomson N.R., James K.D., Churcher C., Mungall K.L.,
 RA Prentice M.B., Sebaitia M., James K.D., Churcher C., Cerdano-Tarrega A.M.,
 RA Baker S., Basham D., Bentley S.D., Brooks K., Davis P., Dougan G.,
 RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,

RA Felwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
 RA Leathers S., Moulle S., Oyston P.C.F., Quail M., Rutherford K.,
 RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.,
 RT "Genome sequence of Yersinia pestis, the causative agent of plague."
 RL Nature 413:523-527(2001).
 DR EMBL: AJ414144; CAC89627.1; -
 DR InterPro: IPR000873; AMP-bind.
 DR InterPro: IPR001242; Condensatn.
 DR InterPro: IPR003880; Ppantne_attach.
 DR Pfam: PF00668; Condensation; 1.
 DR Pfam: PF00550; pp-binding; 2.
 DR PRINTS: PR00154; AMPBINDING; 2.
 DR PROSITE: PS00455; AMP_BINDING; 1.
 DR PROSITE: PS00012; PHOSPHOPANTETHEINE; UNKNOWN_1.
 KW Hypothetical protein: Complete proteome.
 SQ SEQUENCE 2201 AA; 246655 MW; 168E220190208D9B CRC64;

Query Match 8.5%; Score 84.5; DB 16; Length 2201;
 Best Local Similarity 25.5%; Pred. No. 49;
 Matches 48; Conservative 18; Mismatches 55; Indels 67; Gaps 9;

QY 23 LPVLGAPRR--LICDSRYLVE-----RYLLEAKENITTC----- 56
 DB 1910 LPHLPAPRLPLVCDPALVGTPEFKRQAVLSASDMQMLHKAKHQITPSCILLTCYAO 1169.
 QY 57 -----AEHCSLNEITVPTKV-----NFYAKRMEVROQAVEWOGIALISEAV 101
 DB 1970 VLAKMSESASLTINVTLLFDRKPCHPDINHMGFTSILLGCGEKGEGMLATA----- 2023
 QY 102 LKQGLLVNSSQPEPLQLHVDKAVSGLSL-----TTLRL-----ALCAQKEAISPP 149
 DB 2024 ---QRI---QOQLMRDLEREVSAAVWVRLRNQRTTHIMPEVETSAAGVADGV--P 2075
 QY 150 DAASAPL 157
 DB 2076 DSAFQAPL 2083

RESULT 14
 ID P94873 PRELIMINARY; PRT: 3722 AA.
 AC P94873:
 DT 01-MAY-1997 (TREMBLrel. 03, Created)
 DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
 DT 01-MAY-2002 (TREMBLrel. 20, Last annotation update)
 DE Alpha-aminoadipyl-cysteinyl-valine synthetase.
 GN PCBAH.
 OS Lysobacter lactamgenus.
 OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
 OC Lysobacter.
 OX NCBI_TaxID=39596;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=YK90;
 RX MEDLINE=96275949; PubMed=8737573;
 RA Kimura H., Miyashita H., Sumino Y.,
 RT "Organization and expression in Pseudomonas putida of the gene cluster
 RT involved in cephalosporin biosynthesis from Lysobacter lactamgenus
 RT YK90."
 RL Appl. Microbiol. Biotechnol. 45:490-501(1996).
 DR EMBL: D50308; BAA08846.1; -
 DR HSPF: P14687; IAMU.
 DR InterPro: IPR002106; ALCRNA_ligaseII.
 DR InterPro: IPR000873; AMP-bind.
 DR InterPro: IPR001242; Condensatn.
 DR InterPro: IPR000977; DNA_ligase.
 DR InterPro: IPR003880; Ppantne_attach.
 DR InterPro: IPR000379; Ser_estrs_site.
 DR InterPro: IPR001031; Thioesterase.
 DR Pfam: PF00501; AMP-binding; 3.
 DR Pfam: PF00668; Condensation; 3.

DR Pfam: PF00550; pp-binding; 3.
 DR Pfam: PF00975; Thioesterase; 1.
 DR PROSITE: PS00179; AA_TRNA_LIGASE_II_1; UNKNOWN_1.
 DR PROSITE: PS00075; ACP_DOMAIN; 3.
 DR PROSITE: PS00455; AMP_BINDING; 1.
 DR PROSITE: PS00697; DNA_LIGASE_AI; UNKNOWN_2.
 DR PROSITE: PS00012; PHOSPHOPANTETHEINE; UNKNOWN_2.
 KW Phosphopantetheine.
 SQ SEQUENCE 3722 AA; 411607 MW; 3597B3483463809B CRC64;

Query Match 8.5%; Score 84.5; DB 2; Length 3722;
 Best Local Similarity 20.1%; Pred. No. 97;
 Matches 39; Conservative 20; Mismatches 60; Indels 75; Gaps 7;

QY 4 HEC-PAMVLLSLPLGLPVLGAPRLICDSRYLERYLLEAKENITTCAGHCSL 62
 DB 2120 HSCFDKSMKIF-----RELQALLGATAGTLP----- 2148
 QY 63 NENITVPTKVNFYAKRMEVROQAVEV---WGLALLSEAVLRQALLVNSSQPEPL 118
 DB 2149 ---PLPATVADPSVWQROOLSDQRLDALPDYWQ-----RSLAGMPL 2187
 QY 119 QLVHDKAVSGLSRLTLLRLAGN-----KEAISPPDAASAPLRTITADTFKKLRYS 173
 DB 2188 QLPVD-----HARPAQFDYLGREIVFDVADATCQDLRVLAQTTSTFSFVLL 2234
 QY 174 NFLRGRLKLYTGEA 187
 DB 2235 AAYVLLTKAVSGQS 2248

RESULT 15
 ID Q9QVR7 PRELIMINARY; PRT: 235 AA.
 AC Q9QVR7:
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE Truncated thrombopoietin.
 DE Mus sp.
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10095;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95382808; PubMed=7654225;
 RA Wada T., Nagata Y., Nagahisa H., Okutomi K., Ha S.H., Ohnuki T.,
 RA Kanaya T., Matsumura M., Todokoro K.,
 RT "Characterization of the truncated thrombopoietin variants."
 RT Biochem. Biophys. Res. Commun. 213:1091-1098(1995).
 RL InterPro: IPR001323; EPO_TPO.
 DR InterPro: IPR003978; thrombopoietin.
 DR Pfam: PF00758; EPO_TPO; 1.
 DR PRINTS: PR01485; THROMBOPTN.
 DR PROSITE: PS00817; EPO_TPO; 1.
 SQ SEQUENCE 235 AA; 25810 MW; DABA8DC2158F7C91 CRC64;

Query Match 8.4%; Score 84; DB 11; Length 235;
 Best Local Similarity 25.0%; Pred. No. 3.2;
 Matches 24; Conservative 22; Mismatches 48; Indels 2; Gaps 1;

QY 12 LLLSLSLPLGLPVLGAPRLICDSRYLERYLLEAKENITTCAGHCSLNEITVPT 71
 DB 6 LLLAAMLAVALRLTSSPAACDPRLKLRLDSHLHSRLSQCPDVPDPLSPVLLP 65
 QY 72 KVFYAKRMEVROQAVEWOGIALISEAVL--RCQ 105
 DB 66 DPSLGEWKTQTERQSKADIIIGAVSLLLEGVMAARQ 101

Search completed: January 8, 2003, 05:13:46
 Job time : 74.8733 secs

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OM protein - protein search, using sw model

Run on: January 8, 2003, 03:39:48 ; Search time 12.9025 Seconds
(without alignments)
440.118 Million cell updates/sec

Title: US-09-813-775C-2

Perfect score: 998
Sequence: 1 MGVECPAMWLILSLSLDP.....NPLRGLKLYTGACRTGDR 193

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: Issued_Patents_AA:*
2: /cgn2_6/prodata1/1aa/5a_COMB.pep:*
3: /cgn2_6/prodata1/1aa/5b_COMB.pep:*
4: /cgn2_6/prodata1/1aa/6a_COMB.pep:*
5: /cgn2_6/prodata1/1aa/6b_COMB.pep:*
6: /cgn2_6/prodata1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	99.3	99.3	193	1	US-07-903-220-1
2	99.1	99.3	193	2	US-08-883-795A-34
3	84.6	84.8	412	4	US-09-366-009-34
4	84.3	84.5	166	1	US-08-318-193-70
5	84.3	84.5	166	4	US-09-604-871-2
6	84.3	84.5	166	5	PCT-US94-04361-37
7	83.8	84.0	165	4	US-09-604-871-1
8	83.5	83.7	165	5	PCT-US94-04361-45
9	76.1	76.3	165	5	PCT-US94-04361-38
10	75.6	75.8	165	5	PCT-US94-04361-39
11	71.0	71.1	166	5	PCT-US94-04361-44
12	70.8	70.9	166	5	PCT-US94-04361-41
13	69.6	69.7	167	5	PCT-US94-04361-40
14	68.5	68.8	167	5	PCT-US94-04361-42
15	68.6	68.7	168	5	PCT-US94-04361-43
16	18.5	18.5	36	5	PCT-US94-04361-50
17	16.6	16.6	30	5	PCT-US94-04361-28
18	15.6	15.6	30	5	PCT-US94-04361-29
19	14.8	14.8	426	3	US-08-932-823A-2
20	12.8	12.8	27	5	PCT-US94-04361-51
21	11.4	11.5	34	5	PCT-US94-04361-52
22	10.8	10.8	20	2	US-08-759-599-9
23	10.8	10.8	20	4	US-09-294-457-9
24	10.7	10.7	21	5	PCT-US94-04361-49
25	10.6	10.6	30	5	PCT-US94-04361-31
26	10.5	10.3	25	5	PCT-US94-04361-34
27	10.5	10.2	25	5	PCT-US94-04361-32

28	10.1	10.1	20	5	PCT-US94-04361-58	Sequence 58, Appl
29	98.5	9.9	25	5	PCT-US94-04361-35	Sequence 35, Appl
30	96.5	9.7	174	3	US-08-471-045-56	Sequence 56, Appl
31	96.5	9.7	174	3	US-08-469-712A-56	Sequence 56, Appl
32	96.5	9.7	174	4	US-08-446-871-56	Sequence 56, Appl
33	96.5	9.7	174	4	US-08-468-910-56	Sequence 56, Appl
34	96.5	9.7	174	4	US-08-761-907-56	Sequence 56, Appl
35	96.5	9.7	195	1	US-08-388-779A-4	Sequence 4, Appl
36	96.5	9.7	195	1	US-08-388-779A-4	Sequence 4, Appl
37	96.5	9.7	195	1	US-08-927-855-4	Sequence 4, Appl
38	96.5	9.7	353	2	US-08-330-517-2	Sequence 2, Appl
39	96.5	9.7	353	1	US-08-347-029-4	Sequence 2, Appl
40	96.5	9.7	353	1	US-08-388-779A-2	Sequence 2, Appl
41	96.5	9.7	353	1	US-08-484-246-1	Sequence 1, Appl
42	96.5	9.7	353	1	US-08-591-070A-2	Sequence 2, Appl
43	96.5	9.7	353	1	US-08-413-803-25	Sequence 25, Appl
44	96.5	9.7	353	1	US-08-321-488A-25	Sequence 25, Appl
45	96.5	9.7	353	2	US-08-414-161B-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-07-903-220-1
Sequence 1, Application US/07903220
Patent No. 5322837
GENERAL INFORMATION:
APPLICANT: Hewlett, Rodney M.
TITLE OF INVENTION: METHOD FOR THE PURIFICATION OF
TITLE OF INVENTION: ERYTHROPOIETIN AND ERYTHROPOIETIN COMPOSITION
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Paul H. Heller
STREET: Kenyon & Kenyon, One Broadway
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/903,220
FILING DATE: 19920731
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: 1248/27
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 429-1776
TELEFAX: (202) 429-0796
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 193 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-07-903-220-1

Query Match 99.3%; Score 991; DB 1; Length 193;

Best Local Similarity 99.5%; Pred. No. 2.9e-111;
Matches 192; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGVECPAMWLILSLSLPLGLVPLGAPRLICDSRYLENYLLAEAEVITTCAGHC 60
DB 1 MGVECPAMWLILSLSLPLGLVPLGAPRLICDSRYLENYLLAEAEVITTCAGHC 60

OY 61 SLNENITVPDTKVNFAKRMVEYRQOAVEWOGALLSEAVLRGALLVNSSQPMPEPLOT 120
DB 61 SLNENITVPDTKVNFAKRMVEYRQOAVEWOGALLSEAVLRGALLVNSSQPMPEPLOT 120
OY 121 HVDKAVSGRLSTLTLLRALGAQKEAISPPDASAAPLRTITADTFKRLFRVYSNFLRGKL 180
DB 121 HVDKAVSGRLSTLTLLRALGAQKEAISPPDASAAPLRTITADTFKRLFRVYSNFLRGKL 180
OY 181 KLYTGEACRTGDR 193
DB 181 KLYTGEACRTGDR 193

RESULT 2
US-08-883-795A-34
Sequence 34, Application US/08883795A
Patent No. 5985607
GENERAL INFORMATION:
APPLICANT: Delcive, Genevieve
APPLICANT: Awang, Gregor
TITLE OF INVENTION: Recombinant DNA Molecules and Expression
TITLE OF INVENTION: Vectors for Tissue Plasminogen Activator
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: BERESKIN & PARR
STREET: 40 King Street West
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5H 3Y2
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/883,795A
FILING DATE: 27-JUN-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gravelle, Micheline
REGISTRATION NUMBER: 40,261
REFERENCE/DOCKET NUMBER: 7841-062
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 364-7311
TELEFAX: (416) 364-1398
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 193 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-883-795A-34

Query Match 99.3%; Score 991; DB 2; Length 193;
Best Local Similarity 99.5%; Pred. No. 2.9e-111;
Matches 192; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DB 181 KLYTGEACRTGDR 193

RESULT 3
US-09-366-009-34
Sequence 34, Application US/09366009
Patent No. 6426042
GENERAL INFORMATION:
APPLICANT: Asada, Kiyozo
Uemori, Takashi
Ueno, Takashi
Koyama, No. 6426042uto
Hashino, Kimikazu
Kato, Ikunoshin
TITLE OF INVENTION: METHOD FOR GENE TRANSFER INTO TARGET
CELLS WITH RETROVIRUS
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: WEISER & ASSOCIATES
STREET: 230 South Fifteenth Street, Suite 500
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/366,009
FILING DATE: 02-Aug-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/809,156
FILING DATE: 13-NOV-1995
APPLICATION NUMBER: JP 294382/1995
FILING DATE: 13-NOV-1995
APPLICATION NUMBER: JP 051847/1996
FILING DATE: 08-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Weiser, Gerard J.
REGISTRATION NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 977.6507P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-875-8383
TELEFAX: 215-875-8394
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 412 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 34:
US-09-366-009-34

Query Match 84.8%; Score 846; DB 4; Length 412;
Best Local Similarity 98.8%; Pred. No. 2.8e-93;
Matches 165; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 27 GABPRILICDSRYLERYLLAKAEENITTCACBHCSENENITVPDTKVNFAKRMVEYRQO 86
DB 232 GABPRILICDSRYLERYLLAKAEENITTCACBHCSENENITVPDTKVNFAKRMVEYRQO 291
OY 87 AVEWOGALLSEAVLRGALLVNSSQPMPEPLOTLHVDKAVSGRLSTLTLLRALGAQKEAI 146
DB 292 AVEWOGALLSEAVLRGALLVNSSQPMPEPLOTLHVDKAVSGRLSTLTLLRALGAQKEAI 351
OY 147 SPDDASAAPLRTITADTFKRLFRVYSNFLRGKLKLYTGEACRTGDR 193
DB 352 SPDDASAAPLRTITADTFKRLFRVYSNFLRGKLKLYTGEACRTGDR 398

RESULT 4
US-08-318-193-70
; Sequence 70, Application US/08318193
; Patent No. 5641663
; GENERAL INFORMATION:
; APPLICANT: GARYIN, Robert T.
; APPLICANT: MALEK, Lawrence T.
; TITLE OF INVENTION: AN EXPRESSION SYSTEM FOR THE SECRETION
; OF BIOACTIVE HUMAN GRANULOCYTE MACROPHAGE COLONY
; STIMULATING FACTOR (GM-CSF) AND OTHER HETEROLOGOUS
; TITLE OF INVENTION: PROTEINS FROM STREPTOMYCES
; NUMBER OF SEQUENCES: 91
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/318,193
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,314
; FILING DATE:
; APPLICATION NUMBER: US 07/224,568
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 18740/116 CACO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 70:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 166 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-318-193-70
Query Match 84.5%; Score 843; DB 1; Length 166;
Best Local Similarity 99.4%; Pred. No. 1.5e-93;
Matches 165; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 28 APPRLCDRVLRYLLLEAKAEENITTCGAHCISLNNITVPDTRKVFYANKRMEVROOA 87
Db 1 APPRLCDRVLRYLLLEAKAEENITTCGAHCISLNNITVPDTRKVFYANKRMEVGOOA 60
QY 88 VEWOGIALLSEAVLRGQALLVNSOPWEPLQLHVDKAVSGLSRLTTLRLALGAKKEAIS 147
Db 61 VEWOGIALLSEAVLRGQALLVNSOPWEPLQLHVDKAVSGLSRLTTLRLALGAKKEAIS 120
QY 148 PPDAASAPLRTITADTFRKLFYVSNFLRGKLLKLYTGEACRTGDR 193
Db 121 PPDAASAPLRTITADTFRKLFYVSNFLRGKLLKLYTGEACRTGDR 166
RESULT 5
US-09-604-871-2
; Sequence 2, Application US/09604871
; Patent No. 6340742
; GENERAL INFORMATION:
; APPLICANT: Burg, Josef
; APPLICANT: Hilger, Bernd

APPLICANT: Josef, Hans-Peter
; TITLE OF INVENTION: ERYTHROPOIETIN CONJUGATES
; FILE REFERENCE: 1098 nonprovisional
; CURRENT APPLICATION NUMBER: US/09/604,871
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/151,454
; PRIOR FILING DATE: 1999-08-30
; PRIOR APPLICATION NUMBER: 60/147,452
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 60/142,243
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-604-871-2
Query Match 84.5%; Score 843; DB 4; Length 166;
Best Local Similarity 99.4%; Pred. No. 1.5e-93;
Matches 165; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 28 APPRLCDRVLRYLLLEAKAEENITTCGAHCISLNNITVPDTRKVFYANKRMEVROOA 87
Db 1 APPRLCDRVLRYLLLEAKAEENITTCGAHCISLNNITVPDTRKVFYANKRMEVGOOA 60
QY 88 VEWOGIALLSEAVLRGQALLVNSOPWEPLQLHVDKAVSGLSRLTTLRLALGAKKEAIS 147
Db 61 VEWOGIALLSEAVLRGQALLVNSOPWEPLQLHVDKAVSGLSRLTTLRLALGAKKEAIS 120
QY 148 PPDAASAPLRTITADTFRKLFYVSNFLRGKLLKLYTGEACRTGDR 193
Db 121 PPDAASAPLRTITADTFRKLFYVSNFLRGKLLKLYTGEACRTGDR 166
RESULT 6
PCT-US94-04361-37
; Sequence 37, Application PC/TUS9404361
; GENERAL INFORMATION:
; APPLICANT: Brigham and Women's Hospital
; APPLICANT: 75 Francis Street
; APPLICANT: Boston, MA 02115
; APPLICANT: Bun, H. Franklin
; APPLICANT: Wen, Danyi
; APPLICANT: Showers, Mark O.
; TITLE OF INVENTION: Erythropoietin Muteins With Enhanced
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/04361
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/049,802
; FILING DATE: 21-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Cimbal, Michele A.
; REGISTRATION NUMBER: 33,851
; REFERENCE/DOCKET NUMBER: 0627.336PC01
; TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 166 amino acids
TYPE: amino acid
TOPOLOGY: both
PCT-US94-04361-37

Query Match 84.5%; Score 843; DB 5; Length 166;
Best Local Similarity 99.4%; Pred. No. 1.5e-93;
Matches 165; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 28 APPRLICDSRVLYERLYLLEKAEKNITTCGAHCISLNEINTVPTKYNFYAMKMEYRQQA 87
DB 1 APPRLICDSRVLYERLYLLEKAEKNITTCGAHCISLNEINTVPTKYNFYAMKMEYRQQA 60
QY 88 VEWOGIALLSEAVLRGQALLVNSSQWPEPLQHDKAVSGLSLTLRALGAQKEAIS 147
DB 61 VEWOGIALLSEAVLRGQALLVNSSQWPEPLQHDKAVSGLSLTLRALGAQKEAIS 120
QY 148 PPDASAPLRTTTADTFKRLFRVYSNPLRGKIKLYTGACRTGDR 193
DB 121 PPDASAPLRTTTADTFKRLFRVYSNPLRGKIKLYTGACRTGDR 166

RESULT 7
US-09-604-871-1
Sequence 1, Application US/09604871
Patent No. 6340742
GENERAL INFORMATION:
APPLICANT: Burig, Josef
APPLICANT: Hilber, Bernd
APPLICANT: Josefi, Hans-Peter
TITLE OF INVENTION: ERYTHROPOIETIN CONJUGATES
FILE REFERENCE: 1098 nonprovisional
CURRENT APPLICATION NUMBER: US/09/604,871
CURRENT FILING DATE: 2000-06-28
PRIOR APPLICATION NUMBER: 60/151,454
PRIOR FILING DATE: 1999-08-30
PRIOR APPLICATION NUMBER: 60/147,452
PRIOR FILING DATE: 1999-08-05
PRIOR APPLICATION NUMBER: 60/142,243
PRIOR FILING DATE: 1999-07-02
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 165
TYPE: PRT
ORGANISM: Homo sapiens
US-09-604-871-1

Query Match 84.0%; Score 838; DB 4; Length 165;
Best Local Similarity 99.4%; Pred. No. 6.1e-93;
Matches 164; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 28 APPRLICDSRVLYERLYLLEKAEKNITTCGAHCISLNEINTVPTKYNFYAMKMEYRQQA 87
DB 1 APPRLICDSRVLYERLYLLEKAEKNITTCGAHCISLNEINTVPTKYNFYAMKMEYRQQA 60
QY 88 VEWOGIALLSEAVLRGQALLVNSSQWPEPLQHDKAVSGLSLTLRALGAQKEAIS 147
DB 61 VEWOGIALLSEAVLRGQALLVNSSQWPEPLQHDKAVSGLSLTLRALGAQKEAIS 120
QY 148 PPDASAPLRTTTADTFKRLFRVYSNPLRGKIKLYTGACRTGDR 192
DB 121 PPDASAPLRTTTADTFKRLFRVYSNPLRGKIKLYTGACRTGDR 165

RESULT 8
PCT-US94-04361-45
Sequence 45, Application PC/TUS9404361
GENERAL INFORMATION:

APPLICANT: Brigham and Women's Hospital
APPLICANT: 75 Francis Street
APPLICANT: Boston, MA 02115
APPLICANT: Bunn, H. Franklin
APPLICANT: Men, Danyl
TITLE OF INVENTION: Erythropoietin Mutelins With Enhanced
TITLE OF INVENTION: Activity
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESSES:
ADDRESSER: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/04361
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/049,802
FILING DATE: 21-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Cimbala, Michele A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 0627.336PC01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 166 amino acids
TYPE: amino acid
TOPOLOGY: both
PCT-US94-04361-45

Query Match 83.7%; Score 835; DB 5; Length 166;
Best Local Similarity 98.8%; Pred. No. 1.4e-92;
Matches 164; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 28 APPRLICDSRVLYERLYLLEKAEKNITTCGAHCISLNEINTVPTKYNFYAMKMEYRQQA 87
DB 1 APPRLICDSRVLYERLYLLEKAEKNITTCGAHCISLNEINTVPTKYNFYAMKMEYRQQA 60
QY 88 VEWOGIALLSEAVLRGQALLVNSSQWPEPLQHDKAVSGLSLTLRALGAQKEAIS 147
DB 61 VEWOGIALLSEAVLRGQALLVNSSQWPEPLQHDKAVSGLSLTLRALGAQKEAIS 120
QY 148 PPDASAPLRTTTADTFKRLFRVYSNPLRGKIKLYTGACRTGDR 193
DB 121 PPDASAPLRTTTADTFKRLFRVYSNPLRGKIKLYTGACRTGDR 166

RESULT 9
PCT-US94-04361-38
Sequence 38, Application PC/TUS9404361
GENERAL INFORMATION:
APPLICANT: Brigham and Women's Hospital
APPLICANT: 75 Francis Street
APPLICANT: Boston, MA 02115
APPLICANT: Bunn, H. Franklin
APPLICANT: Men, Danyl
TITLE OF INVENTION: Erythropoietin Mutelins With Enhanced
TITLE OF INVENTION: Activity
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:

ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/04361
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/049,802
FILING DATE: 21-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Cimbala, Michele A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 0627.336PC01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 165 amino acids
TYPE: amino acid
TOPOLOGY: both
PCT-US94-04361-38

Query Match 76.3%; Score 761.5; DB 5; Length 165;
Best Local Similarity 91.0%; Pred. No. 1e-83;
Matches 151; Conservative 7; Mismatches 7; Indels 1; Gaps 1;

QY 28 APPRLCDNSVLEERYLLEAKEAENITTCGAHCSLNENITVPDTKVFYAMKREVEVQQA 87
DB 1 APPRLCDNSVLEERYLLEAKEAENITTCGAHCSLNENITVPDTKVFYAMKREVEVQQA 60

QY 88 VEWQGLALISEAVLRQALLVNSQWPPEPQLQHVDAVSGLSLTLRALGAKREATS 147
DB 61 VEWQGLALISEAVLRQALLVNSQWPPEPQLQHVDAVSGLSLTLRALGAKREATS 119

QY 148 PPDASAAPLRTITADTFKRLFRVYSNPLRGKLTLYGECRCRGR 193
DB 120 LPPDASAAPLRTITADTFKRLFRVYSNPLRGKLTLYGECRCRGR 165

RESULT 10
PCT-US94-04361-39
Sequence 39, Application PC/TUS9404361
GENERAL INFORMATION:
APPLICANT: Brigham and Women's Hospital
APPLICANT: 75 Francis Street
APPLICANT: Boston, MA 02115
APPLICANT: Bunn, H. Franklin
APPLICANT: Wen, Danyl
TITLE OF INVENTION: Erythropoietin Mutelins With Enhanced
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/04361
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/049,802
FILING DATE: 21-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Cimbala, Michele A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 0627.336PC01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 165 amino acids
TYPE: amino acid
TOPOLOGY: both
PCT-US94-04361-39

Query Match 75.8%; Score 756.5; DB 5; Length 165;
Best Local Similarity 89.8%; Pred. No. 4e-83;
Matches 149; Conservative 9; Mismatches 7; Indels 1; Gaps 1;

QY 28 APPRLCDNSVLEERYLLEAKEAENITTCGAHCSLNENITVPDTKVFYAMKREVEVQQA 87
DB 1 APPRLCDNSVLEERYLLEAKEAENITTCGAHCSLNENITVPDTKVFYAMKREVEVQQA 60

QY 88 VEWQGLALISEAVLRQALLVNSQWPPEPQLQHVDAVSGLSLTLRALGAKREATS 147
DB 61 VEWQGLALISEAVLRQALLVNSQWPPEPQLQHVDAVSGLSLTLRALGAKREATS 119

QY 148 PPDASAAPLRTITADTFKRLFRVYSNPLRGKLTLYGECRCRGR 193
DB 120 LPPDASAAPLRTITADTFKRLFRVYSNPLRGKLTLYGECRCRGR 165

RESULT 11
PCT-US94-04361-44
Sequence 44, Application PC/TUS9404361
GENERAL INFORMATION:
APPLICANT: Brigham and Women's Hospital
APPLICANT: 75 Francis Street
APPLICANT: Boston, MA 02115
APPLICANT: Bunn, H. Franklin
APPLICANT: Wen, Danyl
TITLE OF INVENTION: Erythropoietin Mutelins With Enhanced
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/04361
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/049,802
FILING DATE: 21-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Cimbala, Michele A.

```

: REGISTRATION NUMBER: 33,851
: REFERENCE/DOCKET NUMBER: 0627.336PC01
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202) 371-2600
: TELEFAX: (202) 371-2540
: INFORMATION FOR SEQ ID NO: 44:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 166 amino acids
: TYPE: amino acid
: TOPOLOGY: both
: PCT-US94-04361-44

Query Match 71.1%; Score 710; DB 5; Length 166;
Best Local Similarity 83.7%; Pred. No. 1,6e-77;
Matches 139; Conservative 9; Mismatches 16; Indels 0; Gaps 0

Oy 28 APRRLICDSRLVRLRYLLLEAKAEANTTGCAGHCISINENTIVDTKYNFYAMRMREYQQA 87
Db 1 APRRLICDSRLVRLRYLLLEAKAEANTTGCAGHCISINENTIVDTKYNFYAMRMREYQQA 60
Oy 88 VEVWGGLALLSAVLRGQALLVNSQSPWPELDLHYDKAVSGLSLTLLRALGAQKEAIS 147
Db 61 VEVWGGLALLSAVLIRGQALLVNSQSPETLDLHYDKAVSSLSRLSLRALGAQKEAIS 120
Oy 148 PADASAAPLRTITADTFPKLFRVYSNPLRGKLTXYTGACHTGDR 193
Db 121 LPEATSAAPLRTFTVDTLCKLPRITSNPLRGKLTXYTGACRRGDR 166

RESULT 12
PCT-US94-04361-41
: Sequence 41, Application PC/TUS9404361
: GENERAL INFORMATION:
: APPLICANT: Brigham and Women's Hospital
: APPLICANT: 75 Francis Street
: APPLICANT: Boston, MA 02115
: APPLICANT: Bunn, H. Franklin
: APPLICANT: Men, Danyl
: APPLICANT: Showers, Mark O.
: TITLE OF INVENTION: Erythropoietin Mutelins With Enhanced
: NUMBER OF SEQUENCES: 59
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Sterne, Kessler, Goldstein & Fox
: STREET: 1100 New York Avenue, Suite 600
: CITY: Washington
: STATE: D.C.
: COUNTRY: U.S.A.
: ZIP: 20005-3934
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US94/04361
: FILING DATE: Herewith
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/049,802
: FILING DATE: 21-APR-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: Gimbalda, Michele A.
: REGISTRATION NUMBER: 33,851
: REFERENCE/DOCKET NUMBER: 0627.336PC01
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202) 371-2600
: TELEFAX: (202) 371-2540
: INFORMATION FOR SEQ ID NO: 41:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 166 amino acids
: TYPE: amino acid
: TOPOLOGY: both

```

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PCT-US94-04361-41
Query Match 70.9%; Score 708; DB 5; Length 166;
Best Local Similarity 82.5%; Pred. No. 2.8e-77;
Matches 137; Conservative 13; Mismatches 16; Indels 0; Gaps 0

QY 28 APPRLICDSRVLERYLLEKAEKENTTGAECNLSNENTVDDTKYNFAMKRMVEYRQQA 87
DB 1 APPRLICDSRVLERYLLEKAEKENTTGAECGRUSENTVDDTKYNFAMKRMVEYRQQA 60
QY 88 VEWVWGGLSLSEAVLRGQALVNSSQPMWPLQLHVDAKAVSGLSRLTTLRALGAQKEAIS 147
DB 61 VEWVWGGLSLSEAVLRGQALVNSSQPMWPLQLHVDAKAVSGLSRLTTLRALGAQKEAIS 120
QY 148 PDDAASAPLRTTADTFERKLFRRVYSNFTGRKIKLYTGACRTGDR 193
DB 121 PDDAQAAPLRTTADTFEKLFRVYSNFTGRKIKLYTGACRRGDR 166

RESULT 13
PCT-US94-04361-40
; Sequence 40, Application PC/TUS9404361
; GENERAL INFORMATION:
; APPLICANT: Brigham and Women's Hospital
; APPLICANT: 75 Francis Street
; APPLICANT: Boston, MA 02115
; APPLICANT: Bunn, H. Franklin
; APPLICANT: Wen, Danyl
; APPLICANT: Showers, Mark O.
; TITLE OF INVENTION: Erythropoietin Mutelins With Enhanced
; TITLE OF INVENTION: Activity
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/04361
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/049,802
; FILING DATE: 21-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Cimbalia, Michele A.
; REGISTRATION NUMBER: 33,851
; REFERENCE/DOCKET NUMBER: 0627, 336PC01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 166 amino acids
; TYPE: amino acid
; TOPOLOGY: both
;
PCT-US94-04361-40
Query Match 69.7%; Score 696; DB 5; Length 166;
Best Local Similarity 80.1%; Pred. No. 7.8e-76;
Matches 133; Conservative 14; Mismatches 19; Indels 0; Gaps 0

QY 28 APPRLICDSRVLERYLLEKAEKENTTGAECNLSNENTVDDTKYNFAMKRMVEYRQQA 87
DB 1 APPRLICDSRVLERYLLEKAEKENTTGAECGRUSENTVDDTKYNFAMKRMVEYRQQA 60

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Qy	148	PPDAAAPLRTITADDFRKLFRYYNMFGLGKLTLYGCAQCRGDR	193
Db	61	IEVWQGSLLSEALIQALLANSSQPPETLQIHIDKRAISGRSLTSLTLYLVAQGRKIMS	120
Qy	88	VEVWQGLALISEAVLRCAALLVNNSQCPWEPLOTIVDAVAGSLSTLLPALGAQKRAIS	147
Db	121	PPDTPPPAPLRTLVDFECLKLFRIYANLFRKLLTLTGEVCRKRRD	166

RESULT 14

```

PCT-US94-04361-42
1  Sequence 462, Application PC/US94/04361
2  GENERAL INFORMATION:
3  APPLICANT: Brigham and Women's Hospital
4  APPLICANT: 75 Francis Street
5  APPLICANT: Boston, MA 02115
6  APPLICANT: Bunn, H. Franklin
7  APPLICANT: Wen, Danyl
8  APPLICANT: Showers, Mark O.
9  TITLE OF INVENTION: Erythropoietin Mutains With Enhanced
10  TITLE OF INVENTION: Activity
11  NUMBER OF SEQUENCES: 59
12  CORRESPONDENCE ADDRESS:
13  ADDRESSEE: Sterne, Kessler, Goldstein & Fox
14  STREET: 1100 New York Avenue, Suite 600
15  CITY: Washington
16  STATE: D.C.
17  COUNTRY: U.S.A.
18  ZIP: 20005-3934
19  COMPUTER READABLE FORM:
20  MEDIUM TYPE: Floppy disk
21  COMPUTER: IBM PC compatible
22  OPERATING SYSTEM: PC-DOS/MS-DOS
23  SOFTWARE: PatentIn Release #1.0, Version #1.25
24  CURRENT APPLICATION DATA:
25  APPLICATION NUMBER: PCT/US94/04361
26  FILING DATE: Herewith
27  CLASSIFICATION:
28  PRIOR APPLICATION DATA:
29  APPLICATION NUMBER: 08/049,802
30  FILING DATE: 21-APR-1993
31  ATTORNEY/AGENT INFORMATION:
32  NAME: Cimbela, Michele A.
33  REGISTRATION NUMBER: 33,851
34  REFERENCE/DOCKET NUMBER: 0627,336PC01
35  TELECOMMUNICATION INFORMATION:
36  TELEPHONE: (202) 371-2600
37  TELEFAX: (202) 371-2540
38  INFORMATION FOR SEQ ID NO: 42:
39  SEQUENCE CHARACTERISTICS:
40  LENGTH: 167 amino acids
41  TYPE: amino acid
42  TOPOLOGY: both
PCT-US94-04361-42

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Query Match	68.8%;	Score 686.5;	DB 5;	Length 167;
Best Local Similarity	81.4%;	Pred. No. 1.1e-74;		
Matches 136;	Conservative 10;	Mismatches 20;	Indels 1;	Gaps 1;
QY	28	APPRICDSRYLERYLLFAKAEANETTTCCAEHCISINENTIVDTQVYNFAMKRMREYQQA	87	
Db	1	APPRICDSRYLERYLLFAKAEANETTTCCAEHCISINENTIVDTQVYNFAMKRMREYQQA	60	
QY	88	VEWOGALLSEAVLRGQALLVNSSQPEWPEQLQHVDAKAVSGSLSTTLRLAAGAKAETS	147	
Db	61	LEWOGALLSEALFRCQALPANASQPEALRLHYDKAVSGSLSTTLRLAAGAKAEP	120	
QY	148	PPDAA-SAAPLRITITADTFRKLFIRVYSNPLNRGKLKLTLYGEACRTGDR	193	
Db	121	LPDTPSAAPLRITFTVDALSKIFRTYSNPLNRGKLKLTLYGEACRRDR	167	

PCT-US94-04361-43

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1 Sequence 43, Application PC/US9404361
2 GENERAL INFORMATION:
3 APPLICANT: Brigham and Women's Hospital
4 APPLICANT: 75 Francis Street
5 APPLICANT: Boston, MA 02115
6 APPLICANT: Bumh, H. Franklin
7 APPLICANT: Wen, Danyl
8 APPLICANT: Showers, Mark O.
9 TITLE OF INVENTION: Erythropoietin Mutelins With Enhanced
10 TITLE OF INVENTION: Activity
11 NUMBER OF SEQUENCES: 59
12 CORRESPONDENCE ADDRESS:
13 ADDRESSEE: Sterne, Kessler, Goldstein & Fox
14 STREET: 1100 New York Avenue, Suite 600
15 CITY: Washington
16 STATE: D.C.
17 COUNTRY: U.S.A.
18 ZIP: 20005-3934
19 COMPUTER READABLE FORM:
20 MEDIUM TYPE: Floppy disk
21 COMPUTER: IBM PC compatible
22 OPERATING SYSTEM: PC-DOS/MS-DOS
23 SOFTWARE: Patent Release #1.0, Version #1.25
24 CURRENT APPLICATION DATA:
25 APPLICATION NUMBER: PCT/US94/04361
26 FILING DATE: Herewith
27 CLASSIFICATION:
28 PRIOR APPLICATION DATA:
29 APPLICATION NUMBER: 08/049,802
30 FILING DATE: 21-APR-1993
31 ATTORNEY/AGENT INFORMATION:
32 NAME: Gimbala, Michele A.
33 REGISTRATION NUMBER: 33,851
34 REFERENCE/DOCKET NUMBER: 0627.336PC01
35 TELECOMMUNICATION INFORMATION:
36 TELEPHONE: (202) 371-2600
37 TELEFAX: (202) 371-2540
38 INFORMATION FOR SEQ ID NO: 43:
39 SEQUENCE CHARACTERISTICS:
40 LENGTH: 168 amino acids
41 TYPE: amino acid
42 TOPOLOGY: both
43 PCT-US94-04361-43

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	Query Match	68.7%	Score 686;	DB 5;	Length 168;
	Best Local Similarity	82.1%;	Pred. No. 1.3e-74;		
	Matches 138;	Conservative 8;	Mismatches 20;	Indels 2;	Gaps 1;
QY	28	APPRICDSRYLERYLTLEAKAEANTTTGCAEHCSTENENTVDTGVNFPYAMKRMVEVOQA	87		
Db	1	APPRICDSRYLERITTEAKEGENNTMGACESCPSSENIPTDVTNVNRYAMKRMVEVOQA	60		
QY	88	VEVMOGIALLSAYLRGCALLVNSSQPMEPIQLAHDKAVSGISRLTTLRALGAQKEAHS	147		
Db	61	MEVMOGIALLSBALCGCALLANSQPSEAQLAHDKAVSGISRLTSLIRALGAQKEAIR	120		
QY	148	PPDA--SIAADPLRTTADTFPKLFVFVSNFLRGKLTKLTGEACRGTGDR	193		
Db	121	LPPDSPSSATPLRFTFAVDTLCKLFNNYSNFLGKLLTLTGEGCRRRDR	168		

Search completed: January 8, 2003, 05:16:25
Job time : 18.9025 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 8, 2003, 03:41:38 ; Search time 33.3315 Seconds
(without alignments)
112.388 Million cell updates/sec

Title: US-09-813-775c-2

Perfect score: 998

Sequence: 1 MCVHECPAMWLILSLSLP.....NFLRGKLYTGACRTGDR 193

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 118974 seqs, 19401057 residues

Total number of hits satisfying chosen parameters: 118974

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA*

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13: /cgn2_6/ptodata/1/pubppaa/US60_NEW_PUB.pep:*
14: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	84.3	84.5	166	10	US-09-853-731-2
2	84.3	84.5	166	12	US-10-014-363-2
3	84.3	84.5	169	12	US-10-014-363-4
4	84.3	84.5	174	12	US-10-014-363-3
5	84.3	84.5	174	12	US-10-014-363-5
6	83.8	84.0	165	10	US-09-853-731-1
7	83.8	84.0	165	12	US-10-014-363-1
8	28.6	28.7	60	10	US-09-864-761-48502
9	14.8	14.8	27	10	US-09-864-404-11
10	11.1	11.1	30	10	US-09-975-063-2
11	11.1	11.1	30	12	US-10-011-858-2
12	10.8	10.8	20	9	US-09-919-703-9
13	8.8	8.8	20	9	US-09-919-703-10
14	8.1	8.1	147	10	US-09-729-674-279
15	77.5	7.8	813	9	US-09-964-899-25
16	7.6	7.6	1005	10	US-09-988-117-1
17	7.6	7.6	1005	10	US-09-812-471-1
18	7.4	7.4	1005	10	US-09-812-633-1
19	7.4	7.4	136	10	US-09-764-877-1623

20	7.4	7.4	2201	12	US-10-029-907-3	Sequence 3, Appl1
21	73.5	7.4	210	10	US-09-731-872-387	Sequence 387, App
22	73.5	7.4	418	9	US-09-992-964-14	Sequence 14, Appl
23	73.5	7.4	468	10	US-09-887-879-14	Sequence 14, Appl
24	73.5	7.4	468	12	US-10-039-785-1	Sequence 11, Appl
25	7.2	7.2	224	10	US-09-242-980-11	Sequence 11, Appl
26	7.2	7.2	824	9	US-09-932-145-3	Sequence 3, Appl1
27	71.5	7.2	81	10	US-09-764-877-1947	Sequence 1947, Ap
28	71.5	7.2	311	10	US-09-191-687B-5	Sequence 5, Appl1
29	71.5	7.2	1643	9	US-09-738-626-6894	Sequence 6894, Ap
30	7.1	7.1	283	10	US-09-972-599A-55	Sequence 55, Appl
31	7.1	7.1	473	9	US-09-978-295A-400	Sequence 400, App
32	7.1	7.1	473	9	US-09-978-697-400	Sequence 400, App
33	7.1	7.1	473	9	US-09-978-192A-400	Sequence 400, App
34	7.1	7.1	473	9	US-09-999-832A-400	Sequence 400, App
35	7.1	7.1	473	9	US-09-978-189-400	Sequence 400, App
36	7.1	7.1	473	9	US-10-028-072-382	Sequence 382, App
37	7.1	7.1	473	10	US-09-758-140-2	Sequence 2, Appl1
38	7.1	7.1	473	10	US-09-796-858-34	Sequence 34, Appl
39	7.1	7.1	473	10	US-09-893-348-26	Sequence 26, Appl
40	7.1	7.1	473	10	US-09-972-599A-2	Sequence 2, Appl1
41	70.5	7.1	614	10	US-09-803-589-4	Sequence 4, Appl1
42	7.0	7.0	362	10	US-09-731-872-280	Sequence 280, App
43	7.0	7.0	489	9	US-09-992-598-138	Sequence 138, App
44	7.0	7.0	489	9	US-09-989-293A-138	Sequence 138, App
45	7.0	7.0	489	9	US-09-989-735-138	Sequence 138, App

ALIGNMENTS

RESULT 1
US-09-853-731-2
Sequence 2, Application US/09853731
Patient No. US2002037841A1
GENERAL INFORMATION:
APPLICANT: Papadimitriou, Apollon
TITLE OR INVENTION: Erythropoietin Composition
FILE REFERENCE: 20619 US
CURRENT APPLICATION NUMBER: US/09/853,731
CURRENT FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: EP/00110355.5
PRIOR FILING DATE: 2000-05-15
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 166
TYPE: PRT
ORGANISM: Homo sapiens
US-09-853-731-2

Query Match 84.5%; Score 843; DB 10; Length 166;
Best Local Similarity 99.48; Pred. No. 1.3e-79;
Matches 165; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 28 APPPLICDSRYLERYLLEAKFAENITTCAGHCNSINENITVPDTKVNFPYAKRMEVROQA 87
DB 1 APPPLICDSRYLERYLLEAKFAENITTCAGHCNSINENITVPDTKVNFPYAKRMEVROQA 60
QY 88 VEVWOGIALISEAVLRQALIVNSQPEWPELQIHDVKAIVSGLRSITLLRALGAQKEAIS 147
DB 61 VEVWOGIALISEAVLRQALIVNSQPEWPELQIHDVKAIVSGLRSITLLRALGAQKEAIS 120
QY 148 PPDASAAPLRTITADTFRKLFERYNSPLRGKLYTGACRTGDR 193
DB 121 PPDASAAPLRTITADTFRKLFERYNSPLRGKLYTGACRTGDR 166

RESULT 2
US-10-014-363-2
Sequence 2, Application US/10014363
Patient No. US20020115833A1
GENERAL INFORMATION:

APPLICANT: Burg, Josef
APPLICANT: Engel, Alfred
APPLICANT: Franze, Reinhard
APPLICANT: Hilger, Bernd
APPLICANT: Schurig, Hartmut Ernst
APPLICANT: Tischer, Wilhelm
APPLICANT: Wozny, Manfred
TITLE OF INVENTION: Erythropoietin Conjugates
FILE REFERENCE: Case 20805
CURRENT APPLICATION NUMBER: US/10/014,363
CURRENT FILING DATE: 2001-12-11
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 166
TYPE: PRT
ORGANISM: Homo sapiens
US-10-014-363-2

Query Match 84.5%; Score 843; DB 12; Length 166;
Best Local Similarity 99.4%; Pred. No. 1.3e-79;
Matches 165; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

28 APRLICDSRVLEERYLLEAKENITTCGAHCISLNIENITVPDTKVFYAMKMEYRQQA 87
1 APRPLICDSRVLEERYLLEAKENITTCGAHCISLNIENITVPDTKVFYAMKMEYRQQA 60
88 VEWOGALLSEAVLRGQALLVNSSQPWEPLQHLVDKAVSGLRSLTTLRALGAQKEAIS 147
61 VEWOGALLSEAVLRGQALLVNSSQPWEPLQHLVDKAVSGLRSLTTLRALGAQKEAIS 120
148 PPDASAAPLRTITADTFPKLFRVYSNPLRGKILKLYTGACRTGDR 193
121 PPDASAAPLRTITADTFPKLFRVYSNPLRGKILKLYTGACRTGDR 166

RESULT 3

US-10-014-363-4

Sequence 4, Application US/10014363
Patent No. US20020115833A1
GENERAL INFORMATION:
APPLICANT: Burg, Josef
APPLICANT: Engel, Alfred
APPLICANT: Franze, Reinhard
APPLICANT: Hilger, Bernd
APPLICANT: Schurig, Hartmut Ernst
APPLICANT: Tischer, Wilhelm
APPLICANT: Wozny, Manfred
TITLE OF INVENTION: Erythropoietin Conjugates
FILE REFERENCE: Case 20805
CURRENT APPLICATION NUMBER: US/10/014,363
CURRENT FILING DATE: 2001-12-11
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 169
TYPE: PRT
ORGANISM: CHO/dhfr-
US-10-014-363-4

Query Match 84.5%; Score 843; DB 12; Length 169;
Best Local Similarity 99.4%; Pred. No. 1.4e-79;
Matches 165; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

28 APRPLICDSRVLEERYLLEAKENITTCGAHCISLNIENITVPDTKVFYAMKMEYRQQA 87
4 APRPLICDSRVLEERYLLEAKENITTCGAHCISLNIENITVPDTKVFYAMKMEYRQQA 63
88 VEWOGALLSEAVLRGQALLVNSSQPWEPLQHLVDKAVSGLRSLTTLRALGAQKEAIS 147
64 VEWOGALLSEAVLRGQALLVNSSQPWEPLQHLVDKAVSGLRSLTTLRALGAQKEAIS 123
148 PPDASAAPLRTITADTFPKLFRVYSNPLRGKILKLYTGACRTGDR 193

124 PPDASAAPLRTITADTFPKLFRVYSNPLRGKILKLYTGACRTGDR 169

RESULT 4

US-10-014-363-3

Sequence 3, Application US/10014363
Patent No. US20020115833A1
GENERAL INFORMATION:
APPLICANT: Burg, Josef
APPLICANT: Engel, Alfred
APPLICANT: Franze, Reinhard
APPLICANT: Hilger, Bernd
APPLICANT: Schurig, Hartmut Ernst
APPLICANT: Tischer, Wilhelm
APPLICANT: Wozny, Manfred
TITLE OF INVENTION: Erythropoietin Conjugates
FILE REFERENCE: Case 20805
CURRENT APPLICATION NUMBER: US/10/014,363
CURRENT FILING DATE: 2001-12-11
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 174
TYPE: PRT
ORGANISM: CHO/dhfr-
US-10-014-363-3

Query Match 84.5%; Score 843; DB 12; Length 174;
Best Local Similarity 99.4%; Pred. No. 1.4e-79;
Matches 165; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

28 APRPLICDSRVLEERYLLEAKENITTCGAHCISLNIENITVPDTKVFYAMKMEYRQQA 87
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88 VEWOGALLSEAVLRGQALLVNSSQPWEPLQHLVDKAVSGLRSLTTLRALGAQKEAIS 147
69 VEWOGALLSEAVLRGQALLVNSSQPWEPLQHLVDKAVSGLRSLTTLRALGAQKEAIS 128
148 PPDASAAPLRTITADTFPKLFRVYSNPLRGKILKLYTGACRTGDR 193
129 PPDASAAPLRTITADTFPKLFRVYSNPLRGKILKLYTGACRTGDR 174

RESULT 5

US-10-014-363-5

Sequence 5, Application US/10014363
Patent No. US20020115833A1
GENERAL INFORMATION:
APPLICANT: Burg, Josef
APPLICANT: Engel, Alfred
APPLICANT: Franze, Reinhard
APPLICANT: Hilger, Bernd
APPLICANT: Schurig, Hartmut Ernst
APPLICANT: Tischer, Wilhelm
APPLICANT: Wozny, Manfred
TITLE OF INVENTION: Erythropoietin Conjugates
FILE REFERENCE: Case 20805
CURRENT APPLICATION NUMBER: US/10/014,363
CURRENT FILING DATE: 2001-12-11
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
LENGTH: 174
TYPE: PRT
ORGANISM: CHO/dhfr-
US-10-014-363-5

Query Match 84.5%; Score 843; DB 12; Length 174;
Best Local Similarity 99.4%; Pred. No. 1.4e-79;
Matches 165; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 28 APRRLICDSRYLERYLLEAKAEENITTCGAHCSLNENITVPDTKVFYAKRMEVROQA 87
      |||
Db 9 APRRLICDSRYLERYLLEAKAEENITTCGAHCSLNENITVPDTKVFYAKRMEVROQA 68
QY 88 VEWOGALLSEAVLRGQALLVNSQWPEPLQHLVDKAVSGLRSITLLRLALGAOKEAIS 147
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Db 69 VEWOGALLSEAVLRGQALLVNSQWPEPLQHLVDKAVSGLRSITLLRLALGAOKEAIS 128
QY 148 PPDAASAAPLRTITADTFRKLFRRYNSNPLRGKLTLYTGEACRTGDR 193
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Db 129 PPDAASAAPLRTITADTFRKLFRRYNSNPLRGKLTLYTGEACRTGDR 174

RESULT 6
US-09-853-731-1
; Sequence 1, Application US/09853731
; Patent No. US20020037841A1
; GENERAL INFORMATION:
; APPLICANT: Papadimitriou, Apollon
; TITLE OF INVENTION: Erythropoietin Composition
; FILE REFERENCE: 20619 US
; CURRENT APPLICATION NUMBER: US/09/853,731
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: EP/00110355.5
; PRIOR FILING DATE: 2000-05-15
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 1
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-853-731-1

Query Match      84.0%; Score 838; DB 10; Length 165;
Best Local Similarity 99.4%; Pred. No. 4.3e-79;
Matches 164; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 28 APRRLICDSRYLERYLLEAKAEENITTCGAHCSLNENITVPDTKVFYAKRMEVROQA 87
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Db 1 APRRLICDSRYLERYLLEAKAEENITTCGAHCSLNENITVPDTKVFYAKRMEVROQA 60
QY 88 VEWOGALLSEAVLRGQALLVNSQWPEPLQHLVDKAVSGLRSITLLRLALGAOKEAIS 147
      |||
Db 61 VEWOGALLSEAVLRGQALLVNSQWPEPLQHLVDKAVSGLRSITLLRLALGAOKEAIS 120
QY 148 PPDAASAAPLRTITADTFRKLFRRYNSNPLRGKLTLYTGEACRTGDR 192
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Db 121 PPDAASAAPLRTITADTFRKLFRRYNSNPLRGKLTLYTGEACRTGDR 165

RESULT 7
US-10-014-363-1
; Sequence 1, Application US/10014363
; Patent No. US20020115833A1
; GENERAL INFORMATION:
; APPLICANT: Burg, Josef
; APPLICANT: Engel, Alfred
; APPLICANT: Franze, Reinhard
; APPLICANT: Hilger, Bernd
; APPLICANT: Schurig, Hartmut Ernst
; APPLICANT: Tischer, Wilhelm
; APPLICANT: Wozny, Manfred
; TITLE OF INVENTION: Erythropoietin Conjugates
; FILE REFERENCE: Case 20805
; CURRENT APPLICATION NUMBER: US/10/014,363
; CURRENT FILING DATE: 2001-12-11
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 1
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-014-363-1
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Query Match      84.0%; Score 838; DB 12; Length 165;
Best Local Similarity 99.4%; Pred. No. 4.3e-79;
Matches 164; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 28 APRRLICDSRYLERYLLEAKAEENITTCGAHCSLNENITVPDTKVFYAKRMEVROQA 87
      |||
Db 1 APRRLICDSRYLERYLLEAKAEENITTCGAHCSLNENITVPDTKVFYAKRMEVROQA 60
QY 88 VEWOGALLSEAVLRGQALLVNSQWPEPLQHLVDKAVSGLRSITLLRLALGAOKEAIS 147
      |||
Db 61 VEWOGALLSEAVLRGQALLVNSQWPEPLQHLVDKAVSGLRSITLLRLALGAOKEAIS 120
QY 148 PPDAASAAPLRTITADTFRKLFRRYNSNPLRGKLTLYTGEACRTGDR 192
      |||
Db 121 PPDAASAAPLRTITADTFRKLFRRYNSNPLRGKLTLYTGEACRTGDR 165

RESULT 8
US-09-864-761-48502
; Sequence 48502, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 48502
; LENGTH: 60
; TYPE: PRT
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ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AF053356.1
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.93
OTHER INFORMATION: SWISSPROT HIT: P01588, EVALUE 9.00e-28
OTHER INFORMATION: EST_HUMAN HIT: AA662379.1, EVALUE 3.00e-10
US-09-864-761-48502

Query Match 28.7%; Score 286; DB 10; Length 60;
Best Local Similarity 98.3%; Pred. No. 7.3e-23;
Matches 59; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 83 VROQAEVWQGLALISEAVIRGALLVNSQPEPIQLHYDKAVSGIRSLTTLRALGAQ 142
DB 1 VGGQAEVWQGLALISEAVIRGALLVNSQPEPIQLHYDKAVSGIRSLTTLRALGAQ 60

RESULT 9
US-09-886-404-11

Sequence 11, Application US/09886404
Patent No. US20020037524A1

GENERAL INFORMATION:

APPLICANT: Medlock, Eugene

APPLICANT: Yeh, Richard

APPLICANT: Silbiger, Scott M.

APPLICANT: Elliot, Gary S.

APPLICANT: Nguyen, Hung Q.

TITLE OF INVENTION: IL-17 Like Molecules and Uses Thereof

FILE REFERENCE: 01017/37128B

CURRENT APPLICATION NUMBER: US/09/886,404

CURRENT FILING DATE: 2001-06-21

PRIOR APPLICATION NUMBER: 09/810,384

PRIOR FILING DATE: 2001-03-16

PRIOR APPLICATION NUMBER: 60/266,159

PRIOR FILING DATE: 2001-02-02

PRIOR APPLICATION NUMBER: 60/213,125

PRIOR FILING DATE: 2000-06-22

NUMBER OF SEQ ID NOS: 22

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 11

LENGTH: 27

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Epogen signal

OTHER INFORMATION: peptide

US-09-886-404-11

Query Match 14.8%; Score 148; DB 10; Length 27;
Best Local Similarity 100.0%; Pred. No. 4e-09;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MGVHECPAWMLLSLPLGLPVLG 27
DB 1 MGVHECPAWMLLSLPLGLPVLG 27

RESULT 10
US-09-975-063-2

Sequence 2, Application US/09975063
Patent No. US20020045255A1

GENERAL INFORMATION:

APPLICANT: POWELL, Jerry S.

TITLE OF INVENTION: HUMAN ERYTHROPOIETIN GENE: HIGH LEVEL

EXPRESSION IN STABLY TRANSFECTED MAMMALIAN CELLS

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dorsey & Whitney, LLP

STREET: Suite 3400, 1420 Fifth Avenue, U.S. Bank Centre

CITY: Seattle

STATE: Washington

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Wordperfect 6.7/7.8

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/975,063

FILING DATE: 10-Oct-2001

ATTORNEY/AGENT INFORMATION:

NAME: Roberts, Mark W.

REGISTRATION NUMBER: 46,160

REFERENCE/DOCKET NUMBER: 500582.03 (112893.109)

TELECOMMUNICATION INFORMATION:

TELEPHONE: 206-903-8728

TELEFAX: 206-903-8820

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 30 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-09-975-063-2

Query Match 11.1%; Score 111; DB 10; Length 30;
Best Local Similarity 83.3%; Pred. No. 3e-05;
Matches 25; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 28 APRRLCDRVLERYLLEKAEKNTTGA 57
DB 1 APRRLCDRVLERYLLEKAEKNTTGA 30

RESULT 11
US-10-011-858-2

Sequence 2, Application US/10011858
Patent No. US20020137145A1

GENERAL INFORMATION:

APPLICANT: POWELL, Jerry S.

TITLE OF INVENTION: HUMAN ERYTHROPOIETIN GENE: HIGH LEVEL

EXPRESSION IN STABLY TRANSFECTED MAMMALIAN CELLS

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dorsey & Whitney, LLP

STREET: Suite 3400, 1420 Fifth Avenue, U.S. Bank Centre

CITY: Seattle

STATE: Washington

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: MS-WORD

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/011,858

FILING DATE: 05-No. US20020137145A1-2001

ATTORNEY/AGENT INFORMATION:

NAME: Roberts, Mark W.

REGISTRATION NUMBER: 46,160

REFERENCE/DOCKET NUMBER: 500582.13

TELECOMMUNICATION INFORMATION:

TELEPHONE: 206-903-8728

TELEFAX: 206-903-8820

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 30 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 2
US-10-011-858-2

Query Match 11.1%; Score 111; DB 12; Length 30;
Best Local Similarity 83.3%; Pred. No. 3e-05;
Matches 25; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 28 APRRLCDRVLYRLYLEAKEENITGCA 57
DB 1 APRRLILDSRVLYRLYLEAKEEXITDCA 30

RESULT 12
US-09-919-703-9
Sequence 9, Application US/09919703
Patent No. US20020165129A1
GENERAL INFORMATION:
APPLICANT: KRYSTAL, Gerald
APPLICANT: RABKIN, Simon W.
TITLE OF INVENTION: Peptides and Their Use to Ameliorate
FILE REFERENCE: 50216/003004
CURRENT APPLICATION NUMBER: US/09/919,703
CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US 09/294,457
PRIOR FILING DATE: 1999-04-19
PRIOR APPLICATION NUMBER: US 08/759,599
PRIOR FILING DATE: 1996-12-05
PRIOR APPLICATION NUMBER: US 60/008,233
PRIOR FILING DATE: 1995-12-06
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 9
LENGTH: 20
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic polypeptide
US-09-919-703-9

Query Match 10.8%; Score 108; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.4e-05;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 174 NFLRGKILKLYTGACRIGDR 193
DB 1 NFLRGKILKLYTGACRIGDR 20

RESULT 13
US-09-919-703-10
Sequence 10, Application US/09919703
Patent No. US20020165129A1
GENERAL INFORMATION:
APPLICANT: KRYSTAL, Gerald
APPLICANT: RABKIN, Simon W.
TITLE OF INVENTION: Peptides and Their Use to Ameliorate
FILE REFERENCE: 50216/003004
CURRENT APPLICATION NUMBER: US/09/919,703
CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US 09/294,457
PRIOR FILING DATE: 1999-04-19
PRIOR APPLICATION NUMBER: US 08/759,599
PRIOR FILING DATE: 1996-12-05
PRIOR APPLICATION NUMBER: US 60/008,233
PRIOR FILING DATE: 1995-12-06
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10
LENGTH: 20
TYPE: PRT
ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: Synthetic polypeptide
US-09-919-703-10

Query Match 8.8%; Score 88; DB 9; Length 20;
Best Local Similarity 95.0%; Pred. No. 0.0039;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 31 RLICDSRVLYRLYLEAKEAE 50
DB 1 RLILDSRVLYRLYLEAKEAE 20

RESULT 14
US-09-729-674-279
Sequence 279, Application US/09729674
Patent No. US20010039335A1
GENERAL INFORMATION:
APPLICANT: JACOBS, Kenneth
APPLICANT: MCCOY, John M.
APPLICANT: LAVAILLE, Edward R.
APPLICANT: COLLINS-RACIE, Lisa A.
APPLICANT: EVANS, Cheryl
APPLICANT: MERBERG, David
APPLICANT: TREACY, Maurice
APPLICANT: AGOSTINO, Michael J.
APPLICANT: STEININGER II, Robert J.
APPLICANT: SPALDING, Vikki
APPLICANT: WONG, Gordon G.
APPLICANT: CLARK, Hilary
APPLICANT: FECHTEL, Kim
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
FILE REFERENCE: 6055-64X
CURRENT APPLICATION NUMBER: US/09/729,674
CURRENT FILING DATE: 2000-12-04
PRIOR APPLICATION NUMBER: 09/539,330
PRIOR FILING DATE: 2000-03-30
NUMBER OF SEQ ID NOS: 283
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 279
LENGTH: 147
TYPE: PRT
ORGANISM: Homo sapiens
US-09-729-674-279

Query Match 8.1%; Score 81; DB 10; Length 147;
Best Local Similarity 28.8%; Pred. No. 0.32;
Matches 42; Conservative 23; Mismatches 63; Indels 18; Gaps 7;

QY 17 LSLPLGLPVLCAPPRILICDSRVLYRLYLEAKEENIT--TGCARHGS--INENTTPDPT 71
DB 1 MASPSGLCVLYRLPKLILICGKTLPTLLIDAGTILVVGCSGDASKLLDDYGLVVRG 60

QY 72 KVFYAMKREYRQQAWEWOGIAL--LSEAVLR--GQALLVNSSOPWEPQLHVDKAV 126
DB 61 CLDL---HYIAMRQRNNILCNGLSLKSLAEVLYLNPLDKSLRLRCSN--WDATTLTLEDQYI 116

QY 127 SGLR---SLTTLRALCAQKRAISP 148
DB 117 YAARDAQISVALFLHLILGYPFSRNSP 142

RESULT 15
US-09-964-899-25
Sequence 25, Application US/09964899
Patent No. US2002017446A1
GENERAL INFORMATION:
APPLICANT: COHEN, Dalia et al.
TITLE OF INVENTION: Identification of Genes Involved in
FILE REFERENCE: 4-31612 A
CURRENT APPLICATION NUMBER: US/09/964,899

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; CURRENT FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: 60/236,893
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/298,309
; PRIOR FILING DATE: 2001-06-14
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 25
; LENGTH: 813
; TYPE: PRF
; ORGANISM: Homo Sapien
US-09-964-899-25

```

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Query Match          7.8%; Score 77.5; DB 9; Length 813;
Best Local Similarity 26.5%; Pred.No.7.8;
Matches 26; Conservative 19; Mismatches 36; Indels 17; Gaps 3;

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OY 39 LERYLLEAKENITTCACPHC-----SLNENITVPPTKVNFYAMKRMVEVROQAVFYWQGL 94
DB 423 LEQQLKEVRRK-----CAEEAQLISSLKRAELTSQESQISTYEELAKAREELSRLOQET 476
OY 95 ALISEAVLRGQALLVNSQPMPEPLQHLVDKAVSGLRSL 132
DB 477 AELEESVESGKAQL-----EPLQOHLQDSQOEISSM 507

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Search completed: January 8, 2003, 05:17:47
 Job time : 40.3315 secs

GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus.p2n model

Run on: January 8, 2003, 05:15:15 ; Search time 2582.65 Seconds
(without alignments)
2174.835 Million cell updates/sec

Title: US-09-813-775C-2
Perfect score: 998
Sequence: 1 MGVHCCPAMWLLLSLSLP.....NFLRCKLKLYTGACRTGDR 193

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-O/cqaz2.1/USPTO.spool/US09813775.r/unat.07012003.153122.23818/app.query.fasta_1.718
-DB=GenEmbl -OFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOECL=0 -LOOEEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=Diosune2 -TRANS=human40.cdt1 -LIST=45
-DOCALLIGN=200 -THR.SCORE=pct -THR.MAX=100 -THR.MIN=0 -ALIGN=15 -MODE=LOCAL
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-YCAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %		DB ID	Description
		Match	Length		
1	998	100.0	585	6 AX046870	AX046870 Sequence
2	991	99.3	582	6 AX025442	AX025442 Sequence
3	991	99.3	582	6 I05397	I05397 Sequence 2
4	991	99.3	788	6 AR086679	AR086679 Sequence
5	991	99.3	823	6 AR063255	AR063255 Sequence
6	991	99.3	823	6 AR179013	AR179013 Sequence
7	991	99.3	1011	6 A47505	A47505 Sequence 12
8	991	99.3	3100	6 AX451645	AX451645 Sequence
9	983	98.5	1342	6 HSERPR	X02157 Human mRNA
10	955	95.7	724	6 I05399	I05399 Sequence 4
11	899.5	90.1	1344	6 I08348	I08348 Sequence 1
12	899.5	90.1	1462	6 MACRPO	MACRPO Sequence 1
13	899.5	90.1	5107	6 A92667	A92667 Sequence 3
14	899.5	90.1	5107	6 AR158347	AR158347 Sequence
15	894.5	89.6	691	6 MACRXYTHRO	I10609 Macaca mula
16	893.5	89.5	1344	6 I07889	I07889 Sequence 1
17	862	86.4	1292	6 E00630	E00630 DNA encodin
18	849	85.1	514	6 AX150264	AX150264 Sequence
19	843	84.5	501	6 BD007423	BD007423 Cyclicall
20	843	84.5	508	6 I49875	I49875 Sequence 5
21	843	84.5	533	6 I07891	I07891 Sequence 69
22	843	84.5	551	6 I00283	I00283 Sequence 5
23	843	84.5	551	6 I07892	I07892 Sequence 6
24	843	84.5	551	6 I08350	I08350 Sequence 6
25	834	83.6	501	6 AX464420	AX464420 Sequence
26	833	83.5	501	6 AX464421	AX464421 Sequence
27	821	82.3	945	6 A47500	A47500 Sequence 7
28	821	82.3	969	6 A47497	A47497 Sequence 4
29	794.5	79.6	681	4 CATERXYTHRO	I10606 Cat erythro
30	793.5	79.5	725	4 FDU00685	UD0685 Fells domes
31	780.5	78.2	1263	4 SSC249745	AJ249745 Sus scrofa
32	778.5	78.0	1395	10 RATEPO	D10763 Rattus norv
33	774.5	77.6	681	4 DOGERYPRE	L13027 Canis fami
34	773.5	77.5	585	4 OAEERYPOA	Z24681 O.aries ery
35	769.5	77.1	688	4 PIGERYTHRO	L10607 pig erythro
36	767	76.9	679	10 RATERYTHRO	L10608 Rat erythro
37	766.5	76.8	3609	6 AX249944	AX249944 Sequence
38	761.5	76.3	1133	4 BT044762	U44762 Bos taurus
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40	759.5	76.1	689	4 SHPERYTHRO	L10610 Sheep eryth
41	751.5	75.3	98876	9 AC009488	AC009488 Homo sap
42	735.5	73.7	3211	6 I07890	I07890 Sequence 3
43	735.5	73.7	3211	6 I08349	I08349 Sequence 3
44	732.5	73.4	3601	6 AR119721	AR119721 Sequence
45	732.5	73.4	3602	6 AR086678	AR086678 Sequence

RESULT 1

ALIGNMENTS

LOCUS	AX046870	585 bp	DNA	linear	PAT 15-DEC-2000
DEFINITION	Sequence 3 from Patent WO0068376.				
ACCESSION	AX046870				
VERSION	AX046870.1	GI:11876340			
KEYWORDS					
SOURCE	chimpanzee.				
ORGANISM	Pan troglodytes				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Pan.				
AUTHORS	1 (bases 1 to 585)				
TITLE	Desauvage, F. and Jenner, D. J.				
JOURNAL	Chimpanzee erythropoietin (chpo) polypeptides and nucleic acids encoding the same				
FEATURES	Patent: WO 0068376-A 3 16-NOV-2000;				
SOURCE	GENENTECH, INC. (US)				
ORIGIN	location/Qualifiers				
BASE COUNT	115 a 185 c 168 g 117 t				
ALIGNMENT SCORES:					
Pred. No.:	2,93e-90	Length:	585		
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Percent Similarity:	100.00%	Conservative:	0		
Best Local Similarity:	100.00%	Mismatches:	0		
Query Match:	100.00%	Indels:	0		
DB:	6	Gaps:	0		

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OY	21 LeuGIyLeuProValLeuGIyAlaProProAlaTrpLeuLeuIecYAspSerArgValLeuGIu 40
Db	61 CTGGGCTCTCCAGTGTCTGGGGCCGACACAGCCTCAATCTGTGACACCCAGTCTGGAG 120
OY	41 ArgTrpLeuLeuGIuAlaLeuGIuAlaLeuIAsnIleThrTrpGIyCyAlaGIuHisCys 60
Db	121 AGGTACCTCTTGGAGGGCCAGAGAGCCGAGAAATATCAAGAGGGCTGTGGCGAACACTGC 180
OY	61 SerLeuAsnGIuAsnIleThrValProAspTrpTrpValAsnPhetrrAlaTrpLysArg 80
Db	181 AGCTTGAAATGAAATATATACTGTCTCCACACACCAAAAGTAAATTTCTATGCTTGGAAAGG 240
OY	81 MetGIuValArgGIuGIuAlaValGIuValTrpGIuGIyLeuAlaLeuLeuSerGIuAla 100
Db	241 ATGGAGGTCAAGGACAGACGGCTGTGAAGTCTGGCAGGGCCCTGGCCCTGTCTGGAAAGCT 300
OY	101 ValLeuAlaArgGIyGIuAlaLeuLeuValAsnSerSerGIuProTrpGIuProLeuGIuLeu 120
Db	301 GTCTGGCGGGCCAGAGCCCTTGTGGTCAACTTCCAGCCGTGGAGCCCTTCACACTG 360
OY	121 HisValAspLysAlaValSerGIyLeuAlaArgSerLeuThrTrpLeuAlaArgAlaLeuGIy 140
Db	361 CATGTGGATAAAGCCGTAGTGGCTTCGCAGACCTTCACCACTGTGCTTGGGGCTTGGGA 420
OY	141 AlaGIuLysGIuAlaIleSerProProAspAlaAlaIleSerAlaAlaProLeuAlaArgThrIle 160
Db	421 GCCCAGAGGAAGCCATCTCCCTCCACAGATGCGGCGCTCAGCTGCTCCACATCCGAACATC 480
OY	161 ThrAlaAspTrpPheAlaArgLysLeuPheArgValTyrSerAsnPheLeuAlaArgGIyLysLeu 180
Db	481 ACTGTGACACTTTCGCGAAACTTTCGGAATCAATCCAAATTTCCTCGGGGAAACCTG 540
OY	181 LysLeuTrpThrGIyGIuAlaLeuAlaCysArgThrGIyLysArg 193
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LOCUS	AX025442	582 bp	DNA	linear	PAT 16-SEP-2000
DEFINITION	Sequence 3 from patent FR2786104.				
ACCESSION	AX025442				
VERSION	AX025442.1	GI:10187118			
KEYWORDS					
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo. 1 (bases 1 to 582)				
AUTHORS	Haefliger, A. and Hirsch, F.				
JOURNAL	Patent: FR 2786104-A 3 26-MAY-2000; CENTRE NAT RECH SCIENT (FR)				
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ORIGIN					

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Best Local Similarity:	99.48%	Mismatches:	1
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DB:	6	Gaps:	0
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Db	61 CTGGGGCTCCCAAGTCCTGGGGGCCCCACACGCTCTCATCTGTGACACCCAGTCCTGGAG	120	
OY	41 ArgTYrLeuLeuGIuAlaAlaGIuAnIleThrGIyCySAlaGIuHisCyS	60	
Db	121 AGGTACGCTCTTGAGGCCCAAGAGCCGAGAAATATCAGACGAGGGCTGTGTAACACTGC	180	
OY	61 SerLeuAnGIuAnIleThrValProAspThrLySValAsnPherylalATrPlyArg	80	
Db	181 AGCTTGATGGAATATCATCTGCTCCAGACCCAACTTAAATTCTATGCTGGAAAGAGG	240	
OY	81 MetGIuValArgGIuAlaValGIuValTrpGIuGIyLeuAlaLeuSerGIuAla	100	
Db	241 ATGGAGTGGGGCAGCAGGCCGCTGAAAGTCTGGGAGGGCCCTGGCCCTGCTGTGGAACT	300	
OY	101 ValLeuArgGIuAlaLeuLeuValAsnSerSerGIuProTrpGIuProLeuGIuLeu	120	
Db	301 GTCGCGGGGGCCAGGCCCTGTGTGTCACGCTTCCAGCGCGTGGAGGCCCTGCACCTG	360	
OY	121 HisValAspLySAlaValSerGIyLeuArgSerLeuThrTrLeuLeuArgAlaLeuGIy	140	
Db	361 CATGTGGATTAAGCCGTCAGAGGCTTCGACGCTCAACCACTGCTGCTCGGGCTTGGA	420	
OY	141 AlaGIuLySGIuAlaIleSerProProAspAlaIleSerAlaIleProLeuArgTYrIle	160	
Db	421 GCCAGAAAGAGGCATCTCCCTCCAGATGCGGCTCTCACTGTCACATCCGACCAATC	480	


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QY 161 ThrAlaasphrPheargLysLeupheargValIyrSeranPheLeuArgLysLeu 180
Db 481 ACTGCTACACTTCCCAAACTCTTCGAGTCACTCAATTCCTCCGGGAAAGCTG 540
QY 181 LysLeuTyrThrGlyGluAlaCysArgThrGlyAspArg 193
Db 541 AAGCTGTACACAGGAGGAGGCTGCAGACAGGAGGACAGA 579

RESULT 3
LOCUS 105397 582 bp DNA linear PAT 02-DEC-1994
DEFINITION Sequence 2 from Patent EP 0267678.
ACCESSION 105397
VERSION 105397.1 GI:590970
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Beck, A.K., Withy, R.M., Zabrecky, J.R. and Masliello, N.C.
TITLE Recombinant human erythropoietin
JOURNAL Patent: EP 0267678-A1 2 18-MAY-1988:
FEATURES
SOURCE location/Qualifiers
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/organism="unknown"
BASE COUNT 113 a 181 c 170 g 118 t
ORIGIN
Alignment Scores:
Pred. No.: 1,45e-89 Length: 582
Score: 991.00 Matches: 192
Percent Similarity: 99.48% Conservative: 0
Best Local Similarity: 99.48% Mismatches: 1
Query Match: 99.30% Indels: 0
gaps: 0

US-09-813-775c-2 (1-193) x 105397 (1-582)
QY 1 MetGlyValHisGluCysProAlaTrpLeuTrpLeuLeuSerLeuLeuSerLeuPro 20
Db 1 ATGGGGGTGCACGAAATGCTCGTGGCTTCTCCCTGCTGCTGCTGCTGCTGCTGCT 60
QY 21 LeuGlyLeuProValLeuGlyAlaProProArgLeuIleCysAspSerArgValLeuGlu 40
Db 61 CTGGGCTCCAGTCCTGGGGGCCCCACACGCTCATCTGTGACAGCGGAGTCTGTGAG 120
QY 41 ArgTyrLeuLeuGluAlaLysGluAlaGluAsnIleThrThrGlyCysAlaGluHisCys 60
Db 121 AGTACTCTTTGGAGGCCAAGAGGCCGAGAAATATCACAGAGGGGCTGTGTAACACTGC 180
QY 61 SerLeuAsnGluAsnIleThrValProAspThrLysValAsnPheTyrAlaTrpLysArg 80
Db 181 AGCTTGAATGAAATATCATCTGCTCCAGACACCAAGTTAATTCTATGCTGGAAAGAG 240
QY 81 MetGluValArgGlnGlnAlaValGluValTrpGlnGlyLeuAlaLeuLeuSerGluAla 100
Db 241 ATGAGGTCTGGGCGACGAGCGGTAGAAATCTGGAGGGGCTGCGCTGCTGCGAAAGCT 300
QY 101 ValLeuArgGlyGlnAlaLeuLeuValAsnSerSerGlnProTrpGluProLeuGlnLeu 120
Db 301 GTCTGCGGGGCCAGGCCCTGTGTGTCAACTTCCAGCCCTGGAGGCCCTCTCAGCTG 360
QY 121 HisValAspLysAlaValSerGlyLeuArgSerLeuThrThrLeuLeuArgAlaLeuGly 140
Db 361 CATGTGATTAAGCGCTCAGTGGCTTGCAGCTCACCACTGTGCTTGGGGCTGTGGGA 420
QY 141 AlaGlnLysGluAlaIleSerProProAspAlaIleSerAlaIleProLeuArgThrIle 160
Db 421 GCCCAGAAGGAAGCATCTCCCTCCAGATGCGGCTCAGCTGCCACTCCGAACAATC 480
QY 161 ThrAlaAspThrPheArgLysLeuPheArgValTyrSeranPheLeuArgLysLeu 180
Db 481 ACTGCTACACTTCCCAAACTCTTCGAGTCACTCAATTCCTCCGGGAAAGCTG 540

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QY 181 LysLeuTyrThrGlyGluAlaCysArgThrGlyAspArg 193
Db 541 AAGCTGTACACAGGAGGAGGCTGCAGACAGGAGGACAGA 579

RESULT 4
LOCUS AR086679 788 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 35 from patent US 5985607.
ACCESSION AR086679
VERSION AR086679.1 GI:10013445
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Delcuve, G. and Awang, G.
TITLE Recombinant DNA molecules and expression vectors for tissue plasminogen activator
JOURNAL Patent: US 5985607-A 35 16-NOV-1999:
FEATURES
SOURCE location/Qualifiers
1..788
/organism="unknown"
BASE COUNT 145 a 264 c 228 g 151 t
ORIGIN
Alignment Scores:
Pred. No.: 2,06e-89 Length: 788
Score: 991.00 Matches: 192
Percent Similarity: 99.48% Conservative: 0
Best Local Similarity: 99.48% Mismatches: 1
Query Match: 99.30% Indels: 0
gaps: 0

US-09-813-775c-2 (1-193) x AR086679 (1-788)
QY 1 MetGlyValHisGluCysProAlaTrpLeuTrpLeuLeuSerLeuLeuSerLeuPro 20
Db 80 ATGGGGGTGCACGAAATGCTCGTGGCTTCTCCCTGCTGCTGCTGCTGCTGCTGCT 139
QY 21 LeuGlyLeuProValLeuGlyAlaProProArgLeuIleCysAspSerArgValLeuGlu 40
Db 140 CTGGGCTCCAGTCCTGGGGGCCCCACACGCTCATCTGTGACAGCGGAGTCTGTGAG 199
QY 41 ArgTyrLeuLeuGluAlaLysGluAlaGluAsnIleThrThrGlyCysAlaGluHisCys 60
Db 200 AGTACTCTTTGGAGGCCAAGAGGCCGAGAAATATCACAGAGGGGCTGTGTAACACTGC 259
QY 61 SerLeuAsnGluAsnIleThrValProAspThrLysValAsnPheTyrAlaTrpLysArg 80
Db 260 AGCTTGAATGAAATATCATCTGCTCCAGACACCAAGTTAATTCTATGCTGGAAAGAG 319
QY 81 MetGluValArgGlnGlnAlaValGluValTrpGlnGlyLeuAlaLeuLeuSerGluAla 100
Db 320 ATGAGGTCTGGGCGACGAGCGGTAGAAATCTGGAGGGGCTGCGCTGCTGCGAAAGCT 379
QY 101 ValLeuArgGlyGlnAlaLeuLeuValAsnSerSerGlnProTrpGluProLeuGlnLeu 120
Db 380 GTCTGCGGGGCCAGGCCCTGTGTGTCAACTTCCAGCCCTGGAGGCCCTCTCAGCTG 439
QY 121 HisValAspLysAlaValSerGlyLeuArgSerLeuThrThrLeuLeuArgAlaLeuGly 140
Db 440 CATGTGATTAAGCGCTCAGTGGCTTGCAGCTCACCACTGTGCTTGGGGCTGTGGGA 499
QY 141 AlaGlnLysGluAlaIleSerProProAspAlaIleSerAlaIleProLeuArgThrIle 160
Db 500 GCCCAGAAGGAAGCATCTCCCTCCAGATGCGGCTCAGCTGCCACTCCGAACAATC 559
QY 161 ThrAlaAspThrPheArgLysLeuPheArgValTyrSeranPheLeuArgLysLeu 180
Db 560 ACTGCTACACTTCCCAAACTCTTCGAGTCACTCAATTCCTCCGGGAAAGCTG 619
QY 181 LysLeuTyrThrGlyGluAlaCysArgThrGlyAspArg 193

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Db 620 AAGCTGTACACAGGAGGCGCTGCAGACAGGAGACAGA 658
RESULT 5
LOCUS AR063255 823 bp DNA linear PAT 29-SNP-1999
DEFINITION Sequence 1 from patent US 5846528.
ACCESSION AR063255
VERSION AR063255.1 GI:5992563
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 823)
AUTHORS Podsakoff, G.M. and Kurtzman, G.J.
TITLE Treating anemia using recombinant adeno-associated virus virions
JOURNAL Patent: US 5846528-A 1 08-DEC-1998;
FEATURES
source Location/Qualifiers
1. 823
BASE COUNT 159 a /organism="unknown" 275 c 233 g 156 t
ORIGIN
Alignment Scores:
Pred. No.: 2,16e-89 Length: 823
Score: 991.00 Matches: 192
Percent Similarity: 99.48% Conservative: 0
Best Local Similarity: 99.48% Mismatches: 1
Query Match: 99.30% Indels: 0
Gaps: 0
DB: 6
US-09-813-775c-2 (1-193) x AR063255 (1-823)
Qy 1 MetGlyValHisGluCysProAlaTrpLeuTrpLeuLeuSerLeuLeuSerLeuPro 20
Db 52 ATGGGGGTGCACAGAAATGCTCTGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 111
Qy 21 LeuGlyLeuProValLeuGlyAlaProProAlaGlyLeuIleCysAspSerArgValLeuGlu 40
Db 112 CTGGGCTCTCCAGTCTCTGGGCGCCGCCACACGCTCATCTGTGACAGCGCATCTCTGGAG 171
Qy 41 ArgTyrlLeuGluAlaValSerGluAlaGluAsnIleThrThrGlyCysAlaGluHisCys 60
Db 172 AGGTACTCTTGGAGGCCAAGAGGCGCGAATATCAGACAGGCGCTGTCTGAACACTGC 231
Qy 61 SerLeuAsnGluAsnIleThrValProAspThrLysValAsnPhetYrAlaTrpLysArg 80
Db 232 ACCTGAATGAGAAATATCTCTGCCAGACACCAAGTAAATTTCTATGCTCGGAAGAG 291
Qy 81 MetGluValArgGlnGlnAlaValAlaGluValTrpGlnGlyLeuAlaLeuSerGluAla 100
Db 292 ATGGAGTCTGGGACAGGCGCTAGAACTGTGGAGGCGCTGCGCTGTCTGCGAAGCT 351
Qy 101 ValLeuArgGlyGluAlaLeuLeuValAsnSerSerGlnProTrpGluProLeuGlnLeu 120
Db 352 GTCTGCGGGGCGAGGCGCTGTGGTCAACTTCTCCACGCGTGGAGCGCTCGACGCTG 411
Qy 121 HisValAspLysAlaValSerGlyLeuArgSerLeuThrThrLeuLeuArgAlaLeuGly 140
Db 412 CATGTGGAATAAAGCGCTGAGTGGCTTCGCACCTCACCACACTGCTTGGGCTCGGGA 471
Qy 141 AlaGlnLysGluAlaIleSerProProAspAlaIleSerAlaAlaProLeuArgThrIle 160
Db 472 GCCCAGAAAGAGCAATCTCCCTCCAGATCGGCGCTCAGTGTCCACTCCGAAACAATC 531
Qy 161 ThrAlaAspThrPheArgLysLeuPheArgValIlyrSerAsnPhetLeuArgLysLysLeu 180
Db 532 ACTGTGACACTTTCGCGAACTCTTCCGAGTCTACTCCAAATTTCTCTCGGGGAAAGCTG 591
Qy 181 LysLeuTyrlThrGlyGluAlaCysArgThrGlyAspArg 193
Db 592 AAGCTGTACACAGGAGGCGCTGCAGAGACAGGAGACAGA 630

RESULT 6
LOCUS AR179013 823 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 1 from patent US 6325998.
ACCESSION AR179013
VERSION AR179013.1 GI:20220568
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 823)
AUTHORS Podsakoff, G.M. and Kurtzman, G.J.
TITLE Methods of treating disease using recombinant adeno-associated virus virions administered to muscle
JOURNAL Patent: US 6325998-A 1 04-DEC-2001;
FEATURES
source Location/Qualifiers
1. 823
BASE COUNT 159 a /organism="unknown" 275 c 233 g 156 t
ORIGIN
Alignment Scores:
Pred. No.: 2,16e-89 Length: 823
Score: 991.00 Matches: 192
Percent Similarity: 99.48% Conservative: 0
Best Local Similarity: 99.48% Mismatches: 1
Query Match: 99.30% Indels: 0
Gaps: 0
DB: 6
US-09-813-775c-2 (1-193) x AR179013 (1-823)
Qy 1 MetGlyValHisGluCysProAlaTrpLeuTrpLeuLeuSerLeuLeuSerLeuPro 20
Db 52 ATGGGGGTGCACAGAAATGCTCTGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 111
Qy 21 LeuGlyLeuProValLeuGlyAlaProProAlaGlyLeuIleCysAspSerArgValLeuGlu 40
Db 112 CTGGGCTCTCCAGTCTCTGGGCGCCGCCACACGCTCATCTGTGACAGCGCATCTCTGGAG 171
Qy 41 ArgTyrlLeuGluAlaValSerGluAlaGluAsnIleThrThrGlyCysAlaGluHisCys 60
Db 172 AGGTACTCTTGGAGGCCAAGAGGCGCGAATATCAGACAGGCGCTGTCTGAACACTGC 231
Qy 61 SerLeuAsnGluAsnIleThrValProAspThrLysValAsnPhetYrAlaTrpLysArg 80
Db 232 ACCTGAATGAGAAATATCTCTGCCAGACACCAAGTAAATTTCTATGCTCGGAAGAG 291
Qy 81 MetGluValArgGlnGlnAlaValAlaGluValTrpGlnGlyLeuAlaLeuSerGluAla 100
Db 292 ATGGAGTCTGGGACAGGCGCTAGAACTGTGGAGGCGCTGCGCTGTCTGCGAAGCT 351
Qy 101 ValLeuArgGlyGluAlaLeuLeuValAsnSerSerGlnProTrpGluProLeuGlnLeu 120
Db 352 GTCTGCGGGGCGAGGCGCTGTGGTCAACTTCTCCACGCGTGGAGCGCTCGACGCTG 411
Qy 121 HisValAspLysAlaValSerGlyLeuArgSerLeuThrThrLeuLeuArgAlaLeuGly 140
Db 412 CATGTGGAATAAAGCGCTGAGTGGCTTCGCACCTCACCACACTGCTTGGGCTCGGGA 471
Qy 141 AlaGlnLysGluAlaIleSerProProAspAlaIleSerAlaAlaProLeuArgThrIle 160
Db 472 GCCCAGAAAGAGCAATCTCCCTCCAGATCGGCGCTCAGTGTCCACTCCGAAACAATC 531
Qy 161 ThrAlaAspThrPheArgLysLeuPheArgValIlyrSerAsnPhetLeuArgLysLysLeu 180
Db 532 ACTGTGACACTTTCGCGAACTCTTCCGAGTCTACTCCAAATTTCTCTCGGGGAAAGCTG 591
Qy 181 LysLeuTyrlThrGlyGluAlaCysArgThrGlyAspArg 193
Db 592 AAGCTGTACACAGGAGGCGCTGCAGAGACAGGAGACAGA 630
RESULT 7

[illegible]

Alignment Scores:	
Pred. No.:	2.75e-89
Score:	991.00
Percent Similarity:	99.48%
Best Local Similarity:	99.48%
Query Match:	99.30%
DB:	6
	Gaps:
	0

US-09-813-775C-2 (1-193) x AX451645 (1-3100)	RESULT 8		
	AX451645		
	LOCUS	3100 bp	DNA
	DEFINITION	Sequence 23 from Patent WO0224899.	linear
	ACCESSION	AX451645	
	VERSION	AX451645.1	
	KEYWORDS	GI:21698583	
	SOURCE		
	ORGANISM	synthetic construct.	
		synthetic construct	
		artificial sequences.	
	REFERENCE	1	
	AUTHORS	Abruzzese,R.V., Mehta,V. and Nordstrom,J.L.	
	TITLE	Improved system for regulation of transgene expression	
	JOURNAL	Patent: WO 0224899-A 23 28-MAR-2002;	
	JOURLINK	Valentis Inc. (US)	
	FEATURES	Location/Qualifiers	
	source	1..3100	
		/organism="synthetic construct"	
		/db_xref="taxon:32630"	
		/note="Complete nucleic acid sequence of pEP1666 plasmid."	
	BASE COUNT	656 a 913 c 856 g 675 t	
	ORIGIN		
	Alignment Scores:		
	Pred. No.:	1.01e-88	Length: 3100
	Score:	991.00	Matches: 192
	Percent Similarity:	99.48%	Conservative: 0
	Best local Similarity:	99.48%	Mismatches: 1
	Query Match:	99.30%	Indels: 0
	DB:	6	Gaps: 0

BASE COUNT	656 a	913 c	856 g	675 t
ORIGIN				

	Alignment Scores:	
Pred. No.:	1.01e-68	Length: 3100
Score:	991.00	Matches: 192
Percent Similarity:	99.48%	Conservative: 0
Best Local Similarity:	99.48%	Mismatches: 1
Query Match:	99.30%	Indels: 0
Db:	6	Gaps: 0

OY	1	MetGIyValIHISGLucSyPrOAlATrPLeuTrPLeuLeuSerLeuLeuSerLeuPro	20
Db	1	ATGGGGGTCACAGAAATGTCTCGCGGGCTGTGGCTTCTCTCCCTCTGTGCCTCCT	60
OY	21	LeuGIyLeuProValLeuGIyAlAProProArGIeunIcYSAsPSerArgValLeuJu	40
Db	61	CTGGGCCCTCCCAAGTCTCTGGCGCCCCACCAGCCCTCATCTGTGACAGCCGAATCTTGAG	12
OY	41	ArgTrIleuLeuGIyAlAlySgluaInIAcluaSnIIErrThngLyCyAlAgLuHISys	60
Db	121	AGGTAACCTCTTGAGAGCCCAAGAGGCCAGAAATATCACAGCGGCTGTGTTAACACTGC	18
OY	61	SerLeuASnGIuASnIIIErrThValProAsPTThrLyVaIASnPheTyALATrPLysArg	80
Db	181	AGCTTGATGAGAATATCATCTGTCCCAACACCAAAGTAATTCTTATGCCTGGGAAGG	24
OY	81	MetGIuValARgInGIuAlAlySIuValITrgInGIyLeuAlALeuLeuSerGIuAla	10
Db	241	ATGGAGTCCTGGGACACAGCGCGTAGAACTGTGGCAGCGCCCTGGCCCTGTGCGAAGCT	30
OY	101	ValLeuArGIyGIuAlAlyLeuLeuValASnsSerGIuProITrgLIuProLeuInIeu	12
Db	301	GTCCTCGGGGCCAGAGCCCTGTGTGCTCAACTTTCGCCAGCGGTGGAGACCCCTGAGCTG	36
OY	121	HISValAsPIySaIaValISerCIyLeuArGSerLeuTrIThrIleuLeuARgAlaleuGIy	14
Db	361	CATGTGGATMAAGCCGTATNGTGGCTTGGCAACCTCACCACTCTCTCGGGCTTGGGA	42
OY	141	AlaGIuLySGluAlaIIEserProBrAsPAAlaIsERAlaAlaIaProLeuArGrThrlIe	16
Db	421	GCCCGAAGAGAACCATCTCCCTCCAGATGAGGGCGCTCAGCTGCACCTCGAACAATC	48
OY	161	ThrAlaAsPTmrPhnearGIyLSLeuPhearGIyAlTYrSerASnpHeuARgLIyLysIeu	18
Db	481	ACTGTGCACACTTTCGGAAACTCTTCGAGCTCACTCCAATTTCTCTCGGGGAAGACTG	54
OY	181	LysIeuTYrThngLyAlaIaAcysArGrThngLyASpArg	193
Db	541	AAGCTGTACACAGGGGAGGCTTCACAGAGCAGGGGACAG 579	

OY	1	MetGIValaHISgICysProAlaIrrhLeuThrLeuLeuSerLeuLeuSerLeuPro	20
Db	417	ATGGGGGGTGCAGAAATGCTTCTGCTGGCTGTGGCTCTCTGCTCTCTCTCT	47
OY	21	LeuGIyLeuProValaLeuGIyAlaProProArGLeuIleCysAspSerArGValLeuGIu	40
Db	477	CTGGGCGCTCCAGTCTCTGGGGCGCCACACGCGCTCATCTGGACAGCGGGTCTGGAG	53
OY	41	ArgTyrrLeuLeuGIuAlaIyGLeuAlaGluAsnIleThrThrGIyCysAlaGIuHIScys	60
Db	537	AGGATATCTCCGTGGAGGCCAAGAGGCCAGAAATACAGACGGGGCTGTGCTGAACACTGC	59
OY	61	SerLeuAsnGIuAsnIleCThrValProAspThrIyValAsnPhetTyAlaTrrPysArg	80
Db	597	AGCCTGAATGAGAAATATACTGTCTCCACAGACCAAGATGAATTTCTATGCTGGAGAGG	65
OY	81	MetGIuValaArgGIuGIuAlaValaGIuValaTrrGIuGIyLeuAlaAlaLeuSerGIuAla	100
Db	657	ATGCGAGTCTGGGGCAGACGAGCGCGTGGAACTCTGGAGGGCGCTGGCCCTGTCCGAACCT	71
OY	101	ValLeuArGIyGIuAlaLeuLeuValaIAsnSerSerGIuProTrrGIuProLeuGIuLeu	120
Db	717	GTCCTGGCGGGCGAGGGCCCTGCTGTCAACTTCTCCAGCGGTGGAGACCCCTGCAGCTG	77
OY	121	HisValaIAspIyValaValSerGIyLeuArGIySerLeuTrrThrLeuLeuArGIaAlaLeuGIy	140
Db	777	CATGGGATTAAGCCGTAGTGGCTGTGGAGCCCTCACCACTCTGTCTCGGGGCTTGGGA	83
OY	141	AlaGIuIyGIuAlaIleSerProProAspAlaIleSerAlaIleAlaProLeuArGIThrIle	160
Db	837	GCCCGAAGAAGAACCATCTCCCTCCACATGGGGCTCCGCTGCCACTCCGGCACAATC	89
OY	161	ThrAlaAspThrPheArGIyLysLeuPheArGIyTyrSerAsnPheLeuArGIyLysLeu	180
Db	897	ACTGCTGACACTTCTCCGAAACTCTTCGAGATCTCACTCAATTTCTCTCGGGGAAAGCTG	95
OY	181	LysLeuTyrrThrGIyGIuAlaCysArGIrThrGIyAspArg	193
Db	957	AAGCTGACACAGGGAGGCGCTGCAGGACAGGGGACA	995

RESULT 9				
LOCUS	HSRPR	1342 bp	mRNA	linear
DEFINITION	Human mRNA for fetal erythropoietin.			
ACCESSION	X02157			
VERSION	X02157.1	GI:31229		
KEYWORDS	erythropoietin; glycoprotein hormone; hormone; signal peptide.			
SOURCE	Homo sapiens.			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
AUTHORS	1 (bases 1 to 1342)			
	Jacobs, K., Shoemaker, C., Rudesdorf, R., Neill, S.D., Kaufman, R.J.,			
	Mulsom, A., Sehra, J., Jones, S.S., Hewick, R., Fritsch, E.F.,			
	Kawakita, M., Shimizu, T. and Miyake, T.			
TITLE	Isolation and characterization of genomic and cDNA clones of human erythropoietin			
JOURNAL	Nature 313 (6005), 806-810 (1985)			
MEDLINE	85137899			
PUBMED	3838366			
COMMENT	Data kindly reviewed (24-FEB-1986) by K. Jacobs.			
FEATURES	Location/Qualifiers			
source	1..1342			

CDs	182..763	/note="erythropoietin precursor"
	/codon_start=1	
	/protein_id="CAA26094.1"	
	/db_xref="GI:31230"	
	/db_xref="SWISS-PROT:P01588"	
	/translation="MGVHECPAMLMLLSLSLDPLGLVGLGAPPRLICDSHYLERLYL	
	EAKGALNITSCAHCISLNIETVPDFTVFNRYANKRMVGQAAVEWGGALLSAVIV	
	EGKALVNSQPMPEPLQHDVHKAVSGRLSLPTLLRALRAQKEALSPDAAAPLRTIT	
	TADPFRKLFRRYSNPLNRKLLKLYGENACRTDR"	
sig_peptide	182..262	
mat_peptide	263..760	
misc_feature	/product="erythropoietin (aa 1-166)"	
misc_feature	332..334	
misc_feature	/note="glycosylation site"	
misc_feature	374..376	
misc_feature	/note="glycosylation site"	
misc_feature	509..511	
misc_feature	/note="glycosylation site"	
BASE COUNT	276 a 434 c 385 g 247 t	
ORIGIN		
Alignment Scores:		
Pred. NO.:	2.38e-88	Length: 1342
Score:	983.00	Matches: 191
Percent Similarity:	98.96%	Conservative: 0
Best Local Similarity:	98.96%	Mismatches: 2
Query Match:	98.50%	Indels: 0
DB:	9	Gaps: 0
US-09-813-775C-2 (1-193) x HSERPR (1-1342)		
OY	1 MetGIValHISGLucYSProlaIrrpleuTrrpleuleuSerleuSerleuPro 20	
Db	182 ATGGGGGGGCGACGAATGTCCTCGCGGTGGCTTCCTCCTCCCTGCGCTCCT 241	
OY	21 LeuGIleuProValLeuGIValaIrrProIrrArgLeuIleCysASpSerArgValLeu 40	
Db	242 CTGGGCGTCGCCAGTCCTCGGGCGCCGCCACACGCCCTCATCTGTGACAGCCGACTCTGGAG 301	
OY	41 ArgTrIleuLeuGIValaIlySGluAgluAsnIleThrThGlyCysAlaGluHisCys 60	
Db	302 AGGTACCTCTTGGAGCCCAAGGAGGCCAGATATACAGACGAGGCTGTGTCAMACACTGC 361	
OY	61 SerIeuASnGIuAsnIleThrValIrrAspTrIrrIlyValAsnPhetIrrAlaIrrIlyAsn 80	
Db	362 AGCTTGATAGCAATATACCTCTCCACAGCACCAAGTTAATTTCATGCTCGGAAGAG 421	

QY	81	MetGluValArgGlnGlnAlaValGluValTrpGlnGlyLeuAlaLeuLeuSerCysAla	100
Db	422	ATGGAGGTCGGGCGACCAAGCCGTAAGAAGCTTGCGAGGCGCTCGTGTGGAGAGCT	481
QY	101	ValLeuArgGlyGlnAlaLeuLeuValAsnSerSerGlnProTrpGlnProLeuGlnLeu	120
Db	482	GTCCTGCGGGGCGCAAGCCCTGTGGTCAACTTTCACAGCCGTGGGAGCCCTGCAAGCTG	541
QY	121	HisValAspPylsAlaValSerGlyLeuArgSerLeuThrThrLeuLeuArgAlaLeuGly	140
Db	542	CATGTGGATTAAGCCGTCAGTGGCCCTGGACACCTCACACACTCTGCTGGGCGCTGGGA	601
QY	141	AlaGlnIlysGluAlaIleSerProProAspAlaIleSerAlaIleProLeuArgThrIle	160
Db	602	GCCCGAAGGAAGCATCTCCCTCCAGATGGGCGCTCAGCTGCCACTCCGAACAATC	661
QY	161	ThrAlaAspThrPheArgIlysLeuPheArgValIlyrSerAspPheLeuArgIlysLeu	180
Db	662	ACTGCTGACACTTCGCCAACAATCTTCGAGAGTCATCTCCAAATTCCTCCGGGGAAAGCTG	721
QY	181	LysLeuTyrThrGlnIlyGluAlaCysArgThrGlnIlyAspArg	193
Db	722	AAGCTGTACACAGGGAGGCCCTGCAGCAGCAGGGGACAG	760

[illegible]

[illegible]

QY	121	HISValAspValValSerIcyLeuArgSerLeuThrThrLeuLeuArgAlaLeuGly	140
Db	500	CACATGGATGAAGACCATGATGCGCTTCGGACACACACACTCTGCTTCGGCGCTGGGA	559
QY	141	AAAGlnIysGluAlaIleSerProProAspAlaAlaSerAlaAlaProLeuArgThrIle	160
Db	560	GGCCGAG---GAAGCCATCTCCCTCCAGATGGCGGCTCGGCTGCCATCCGGAACATC	616
QY	161	ThrAlaAspThrPheArgIlysLeuPheArgValTyrSerAsnPheLeuArgCylsLeu	180
Db	617	ACTGCTGACACTTCTGGCAACTCTTCGAGCTCACTCAATTCTCCGGGAAGCTG	676
QY	181	LysLeuTyrThrGlyGluAlaAcysArgThrGlyAspArg	193
Db	677	AAGCTGTACACGGGAGCGCTGCAGAGAGGAGGAGCAGACA	715
RESULT 12			
LOCUS	MACEPO	1462 bp	linear PRI 04-AUG-1993
DEFINITION	Monkey (Cynomolgus) erythropoietin mRNA, complete cds.		
ACCESSION	M18189	M15818	M18188
VERSION	M18189.1	GI:342093	
KEYWORDS	erythropoietin.		
SOURCE	Monkey cDNA to mRNA.		
ORGANISM	Macaca fascicularis		
REFERENCE	Emura;Ota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Cercopithecinae; Macaca.		
AUTHORS	Lin,F.K., Lin,C.H., Lai,P.H., Browne,J.K., Eagle,J.C., Smalling,R., Fox,G.M., Chen,K.K., Castro,M. and Suggs,S.		
TITLE	Monkey erythropoietin gene: cloning, expression and comparison with the human erythropoietin gene		
JOURNAL	Gene 44 (2-3), 201-209 (1986)		
MEDLINE	87055236		
PUBMED	2877922		
COMMENT	Draft entry and computer-readable sequence for [1] kindly provided by F. K.Lin, 04-AUG-1987.		
FEATURES	Location/Qualifiers		
source	1..1462		
CDS	/organism="Macaca fascicularis" /db_xref="taxon:9541"		
	217..795		
	/note="erythropoietin precursor"		
	/codon_start=1		
	/protein_id="AAA36841.1"		
	/db_xref="GI:342094"		
	/translation="MGVHECPAMLLLSVSLPLGLPVPGAPRLICDSRVLERYLL EAKAEAVNTMGCSSESLNEMITVDPDKVNVYAKRKREYGOAAVEYWGALLSEAVL RGCAVLANSSPPPEPLDLDHDKAISGLRITTLRLALCADEAISLPDAASAPLRLITTT ADTCKLPRVYSNPLRGLKLYTGEAKRGDR"		
	217..288		
	/note="erythropoietin signal peptide"		
	289..792		
	/product="erythropoietin"		
BASE COUNT	297 a 455 c 433 g 277 t		
ORIGIN	unreported.		
Alignment Scores:			
Pred. No.:	5.26e-80	Length:	1462
Score:	899.50	Matches:	176
Percent Similarity:	95.34%	Conservative:	8
Best Local Similarity:	91.19%	Mismatches:	8
Query Match:	90.13%	Indels:	1
DB:	9	Gaps:	1
US-09-813-775C-2 (1-193) x MACEPO (1-1462)			
QY	1	MetGlyValAlaHisGluCysProAlaIrrPheLeuThrPheLeuLeuSerLeuLeuSerLeuPro	20
Db	217	ATGGGGGTGCACGATGCTCCCTCGGCTGTGGCTTCTCCTGTCTGTGCTGCCTCCCT	276

QY 21 LeuGlyLeuProValLeuGlyAlaProProAlaGlyLeuIleCysAspSerArgValLeuGlu 40
 DB 277 CTGGGCTCCCGAGTCCCGGCGCCGCCACCGCTCATCTGTGACAGCGGAGCTCTGGAG 336
 QY 41 ArgTyrLeuLeuGluAlaLysGluAlaGlnIleThrThyGlyCysAlaGlnIleCys 60
 DB 337 AGGTACCTTTGGAGGCCAAGAGGCGCGAAGATGTCAGATGGGCTGTTCGGAAGCTGC 396
 QY 61 SerLeuAsnGluAsnIleThrValProAspThrLysValAsnPheTyrAlaTrpLysArg 80
 DB 397 ACCTTGAAATGAGAAATATCATCCGTCACAGACCAAAAGTTAACTGTATGCTCGGAAGAG 456
 QY 81 MetGluValArgGlnGlnAlaValAlaGluValITrpGlnGlyLeuAlaLeuSerGluAla 100
 DB 457 ATGGAGGTGGGCGAGCAGGCTGTAGAAAGTCTGGCAGGCGCTGGCCCTGCTCAGAACTC 516
 QY 101 ValLeuArgGlyGlnAlaLeuLeuValAsnSerSerGlnProTrpGlnProLeuGlnIle 120
 DB 517 GTCTGGGCGGCGAGCGCTGTGGCCAACTCTTCCACACCTTTGAGGCCCTGCGAGCTG 576
 QY 121 HisValAspLysAlaValSerGlyLeuArgSerLeuThrThrLeuLeuArgAlaLeuGly 140
 DB 577 CACATGATGAAGACCATCATGAGCTTCCGACATCACCACCTGCTGGGCGCTGGGA 636
 QY 141 AlaGlnLysGluAlaIleSerProProAspAlaIleSerAlaAlaProLeuArgThrIle 160
 DB 637 GCCGAG--GAAGCATCTCTCCCTCCAGATGGCGCTGCTGCTCCACTCCGAACCATC 693
 QY 161 ThrAlaAspThrPheArgLysLeuPheArgValITyrSerAsnPheLeuArgGlyLysLeu 180
 DB 694 ACTGCTGACACTTCTGCAAACTCTTCCGAGTCTACTCCAAATTTCTCCGCGGGAAGCTG 753
 QY 181 LysLeuTyrThrGlyGluAlaCysArgThrGlyAspArg 193
 DB 754 AAGCTGTACACGCGGAGCGCTGACAGAGAGGAGGAGACAGA 792

RESULT 13

A92667 A92667 5107 bp DNA linear PAT 22-JAN-2000
 LOCUS DEFINITION Sequence 3 from patent WO9806437.
 ACCESSION A92667
 VERSION A92667.1 GI:6741307
 KEYWORDS
 SOURCE unidentified.
 ORGANISM unidentified.
 REFERENCE 1 (bases 1 to 5107)
 AUTHORS Murphy, J.E. and Cohen, F.
 TITLE COMPOSITIONS AND METHODS FOR POLYNUCLEOTIDE DELIVERY
 JOURNAL Patent: WO 9806437-A 3 19-FEB-1998;
 CHIRON CORP (US)
 FEATURES
 source 1..5107
 Location/Qualifiers
 /organism="unidentified"
 /db_xref="taxon:32644"
 ORIGIN
 BASE COUNT 1145 a 1463 c 1335 g 1164 t

Alignment Scores:
 Pred. No.: 2,25e-79 Length: 5107
 Score: 899.50 Matches: 176
 Percent Similarity: 95.34% Conservative: 8
 Best Local Similarity: 91.19% Mismatches: 8
 Query Match: 90.13% Indels: 1
 Gaps: 1

US-09-813-775c-2 (1-193) x A92667 (1-5107)
 QY 1 MetGlyValHisGlyCysProAlaTrpLeuTrpLeuLeuSerLeuLeuSerLeuPro 20
 DB 1710 ATGGGGGTGACAGAAATGCTCTGCTGGCTGTGGCTTCTCTCTCTCTCTCTCTCTCTCT 1769
 QY 21 LeuGlyLeuProValLeuGlyAlaProProAlaGlyLeuIleCysAspSerArgValLeuGlu 40

DB 1770 CTGGGCTCCCGAGTCCCGGCGCCGCCACCGCTCATCTGTGACAGCGGAGCTCTGGAG 1829
 QY 41 ArgTyrLeuLeuGluAlaLysGluAlaGlnIleThrThyGlyCysAlaGlnIleCys 60
 DB 1830 AGGTACCTTTGGAGGCCAAGAGGCGCGAAGATGTCAGATGGGCTGTTCGGAAGCTGC 1889
 QY 61 SerLeuAsnGluAsnIleThrValProAspThrLysValAsnPheTyrAlaTrpLysArg 80
 DB 1890 ACCTTGAAATGAGAAATATCATCCGTCACAGACCAAAAGTTAACTGTATGCTCGGAAGAG 1949
 QY 81 MetGluValArgGlnGlnAlaValAlaGluValITrpGlnGlyLeuAlaLeuSerGluAla 100
 DB 1950 ATGGAGGTGGGCGAGCAGGCTGTAGAAAGTCTGGCAGGCGCTGGCCCTGCTCAGAACTC 2009
 QY 101 ValLeuArgGlyGlnAlaLeuLeuValAsnSerSerGlnProTrpGlnProLeuGlnIle 120
 DB 2010 GTCTGGGCGGCGAGCGCTGTGGCCAACTCTTCCACACCTTTGAGGCCCTGCGAGCTG 2069
 QY 121 HisValAspLysAlaValSerGlyLeuArgSerLeuThrThrLeuLeuArgAlaLeuGly 140
 DB 2070 CACATGATGAAGACCATCATGAGCTTCCGACATCACCACCTGCTGGGCGCTGGGA 2129
 QY 141 AlaGlnLysGluAlaIleSerProProAspAlaIleSerAlaAlaProLeuArgThrIle 160
 DB 2130 GCCGAG--GAAGCATCTCTCCCTCCAGATGGCGCTGCTGCTCCACTCCGAACCATC 2186
 QY 161 ThrAlaAspThrPheArgLysLeuPheArgValITyrSerAsnPheLeuArgGlyLysLeu 180
 DB 2187 ACTGCTGACACTTCTGCAAACTCTTCCGAGTCTACTCCAAATTTCTCCGCGGGAAGCTG 2246
 QY 181 LysLeuTyrThrGlyGluAlaCysArgThrGlyAspArg 193
 DB 2247 AAGCTGTACACGCGGAGCGCTGACAGAGAGGAGGAGACAGA 2285

RESULT 14

AR158347 AR158347 5107 bp DNA linear PAT 17-OCT-2001
 LOCUS DEFINITION Sequence 3 from patent US 6251433.
 ACCESSION AR158347
 VERSION AR158347.1 GI:16220368
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 5107)
 AUTHORS Zuckerman, R.N., Dubois-Stringfellow, N., Dworki, V., Innis, M.A.,
 TITLE Polycationic polymers
 JOURNAL Patent: US 6251433-A 3 26-OCT-2001;
 FEATURES
 source 1..5107
 Location/Qualifiers
 /organism="unknown"
 ORIGIN
 BASE COUNT 1145 a 1463 c 1335 g 1164 t

Alignment Scores:
 Pred. No.: 2,25e-79 Length: 5107
 Score: 899.50 Matches: 176
 Percent Similarity: 95.34% Conservative: 8
 Best Local Similarity: 91.19% Mismatches: 8
 Query Match: 90.13% Indels: 1
 Gaps: 1

US-09-813-775c-2 (1-193) x AR158347 (1-5107)
 QY 1 MetGlyValHisGlyCysProAlaTrpLeuTrpLeuLeuSerLeuLeuSerLeuPro 20
 DB 1710 ATGGGGGTGACAGAAATGCTCTGCTGGCTGTGGCTTCTCTCTCTCTCTCTCTCTCTCT 1769
 QY 21 LeuGlyLeuProValLeuGlyAlaProProAlaGlyLeuIleCysAspSerArgValLeuGlu 40
 DB 1770 CTGGGCTCCCGAGTCCCGGCGCCGCCACCGCTCATCTGTGACAGCGGAGTCTGTGAG 1829

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OM protein - nucleic search, using frame_plus.p2n model

Run on: January 8, 2003, 03:43:33 ; Search time 209.666 Seconds
(without alignments)
2072.993 Million cell updates/sec

Title: US-09-813-775C-2
Perfect score: 998
Sequence: 1 KGVHCPAMLMILLSLSLP.....NFLRGKLYTGBCARTGDR 193

Scoring table:
BLOSUMP62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2185239 segs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:
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-DB=N.Geneseq.101002 -OFMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPT=0
-LOOPT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosump62 -TRANS=human0.cdi
-LIST=45 -DOALIGN=200 -THR_SCORE=pcr -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-NO_XUPXY -NO_MAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-NARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAEXT=0.5 -DELOP=6 -DELEX=7

Database :
N.Geneseq.101002.*
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24: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query length	DB ID	Description
1	998	100.0	585	22 AAC66882	Chimpanzee erythro
2	991	99.3	582	21 AAA46697	DNA encoding a hum
3	991	99.3	582	20 AAA46697	Human erythropoiet
4	991	99.3	616	20 AAA77361	Polynucleotide seq
5	991	99.3	616	21 AAA90393	DN encoding synthe
6	991	99.3	625	15 AA074760	Human prepro eryth
7	991	99.3	788	17 AAT31529	Human erythropoiet
8	991	99.3	788	21 AAT31529	Human EPO long cDN
9	991	99.3	823	18 AAT64847	Human erythropoiet
10	991	99.3	1015	13 AA024282	Epo:IL-3 short, re
11	991	99.3	1072	13 AA024285	Epo:IL-3 flex, rec
12	991	99.3	1158	20 AAT25701	Human erythropoiet
13	991	99.3	1245	8 AAT70360	Sequence encoding
14	991	99.3	1789	16 AAQ92296	Erythropoietin cDN
15	991	99.3	3100	24 AAB86161	Polynucleotide seq
16	991	99.3	10524	20 AAX77355	Nucleotide sequenc
17	991	99.3	10524	21 AAA90387	Plasmid pSINrep5 E
18	987	98.9	606	21 AAB07253	Human EPO cDNA seq
19	986	98.8	582	21 ABL50865	Modified erythropo
20	982	98.4	1342	7 AAN60513	CDNA of clone lamb
21	979.5	98.1	614	24 ABL59290	Nucleotide sequenc
22	977	97.9	579	22 AAT71883	Erythropoietin gen
23	977	97.9	629	24 ABL59289	Nucleotide sequenc
24	977	97.9	629	24 ABL59291	Nucleotide sequenc
25	977	97.9	6079	22 AAT71882	pe/C plasmid DNA.
26	971	97.3	1255	7 AAN60519	CDNA of clone lamb
27	968	97.0	724	9 AAN81554	EPO 140b encoding
28	943	94.5	1286	24 AAD24593	Human erythropoiet
29	941	94.3	1342	6 AAN50443	EPO clone lambda-H
30	899.5	90.1	1344	6 AAN50348	Monkey erythropoie
31	899.5	90.1	1344	19 AAV30955	Monkey erythropoie
32	899.5	90.1	5107	19 AAV21685	Vector plasmid CMV
33	871.5	87.3	681	19 AAO72942	Monkey Erythropoie
34	849	85.1	514	22 AAD06893	Human erythropoiet
35	846	84.8	994	13 AAQ24281	IL-3:Epo short, re
36	846	84.8	1239	18 AAT93879	DNA for oligopepti
37	844	84.6	370	21 ABL50864	Modified erythropo
38	843	84.5	498	21 ABL50878	Modified erythropo
39	843	84.5	501	19 AAV31031	Human erythropoiet
40	843	84.5	533	6 AAN50346	Human recombinant
41	843	84.5	533	19 AAV30963	ECERO gene used in
42	843	84.5	551	6 AAN50345	Human recombinant
43	843	84.5	551	19 AAV30970	SCEPO gene based o
44	843	84.5	1051	13 AAQ24284	IL-3:Epo flex, rec
45	838	84.0	498	21 AAA48373	Non-glycosylated e

ALIGNMENTS

RESULT 1
AAC66882
ID AAC66882 standard; cDNA; 585 BP.
XX
AC AAC66882:
XX
DT 27-MAR-2001 (first entry)
XX
DE
XX
XX Chimpanzee erythropoietin coding sequence SEQ ID NO: 3.
KM Chimpanzee; erythropoietin; EPO: hybridisation probe; gene therapy;
KW mapping; therapeutic agent; ss.
XX
XX Pan sp.
OS
PN WO200068376-A1.
XX
PD 16-NOV-2000.

XX 05-MAY-2000; 2000MO-US12370.
 XX 07-MAY-1999; 99US-0307307.
 PR 28-MAR-2000; 2000US-0307307.
 XX (GETH) GENENTECH INC.
 PA Desauvage F, Henner DJ;
 XX WPI: 2001-007393/01.
 DR
 XX Nucleic acids encoding chimpanzee erythropoietin, useful for treatment
 PT of e.g. anemia, also derived proteins, antibodies and modulators -
 XX
 PS Claim 2; Fig 2; 109pp; English.
 CC The present invention provides the coding and protein sequences of
 CC chimpanzee erythropoietin (EPO). These sequences can be used in gene
 CC therapy, to block the activity of EPO, as hybridisation probes, in
 CC genetic and chromosome mapping and as therapeutic agents.

Sequence 585 BP; 115 A; 185 C; 168 G; 117 T; 0 other;

Alignment Scores:
 Pred. No.: 3,6e-99 Length: 585
 Score: 998.00 Matches: 193
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 22 Gaps: 0

US-09-813-775C-2 (1-193) x AAC66882 (1-585)

OY 1 MetGlyValAlHisGluCysProAlaTrpLeuTrpLeuLeuSerLeuLeuSerLeuPro 20
 DB 1 ATGGGGGTGCACGAATGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 60
 OY 21 LeuGlyLeuProValLeuGlyAlaProProArgLeuIleCysAspSerArgValLeuGlu 40
 DB 61 CTGGGCTCCAGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
 OY 41 ArgTrpLeuLeuGluAlaValGluAlaGluValAsnIleThrThrGlyAlaGluHisCys 60
 DB 121 AGGTACCTTGTGAGGCCAAGAGGCCGAGAAATATCAGACGCGCTGCTCCGAAACCTGC 180
 OY 61 SerLeuAsnGluAsnIleThrValProAspTrpLysValAsnPhenylAlaTrpLysArg 80
 DB 181 ACCTGAATGAGAAATATCTACTGCTCCAGACCAAAAGTTAATTCTATGCTGGAAAGG 240
 OY 81 MetGluValArgGlnGlnAlaValGluValITrpgInGlyLeuAlaLeuSerGluAla 100
 DB 241 AAGGAGGTCAGACAGCCGCTGAGAACTGTGAGGCGCTGCTGCTGCTGCTGCTGCTG 300
 OY 101 ValLeuArgGlyAlaAlaLeuLeuValAsnSerSerGlnProTrpGluProLeuGlnLeu 120
 DB 301 GTTCCTGCGGGGCGAGCCCTGTGCTCAACTCTTCCACGCCGTGGAGGCCCTGCACTG 360
 OY 121 HisValAspLysAlaValSerGlyLeuArgSerLeuThrThrLeuLeuArgAlaLeuGly 140
 DB 361 CATGTGGAATAAGCCGCTGAGCTGCTGACAGCTCAGACAGCTGCTGCTGCTGCTGCTG 420
 OY 141 AlaGlnLysGluAlaAlaLeuSerProProAspAlaAlaSerAlaAlaProLeuArgThrIle 160
 DB 421 GCCCAAGAGGAGCATCTCCCTCCAGATGCGGCTCAGCTGCTCCATCCGAAACAATC 480
 OY 161 ThrAlaAspThrPheArgLysLeuPheArgValTyrSerAsnPhenylArgGlyLysLeu 180
 DB 481 ACTGCTGACACTTCCGCAACCTTCCGAGTCTACTCCAAATTTCTCCGCGGAAAGCTG 540
 OY 181 LysLeuTyrTrpGlyValAlaCysArgThrGlyAspArg 193
 DB 541 AAGCTGTACACAGGGAGGCTGCGAGGAGACAGGGGACAGA 579

RESULT 2
 AAA46697

ID AAA46697 standard; DNA; 582 BP.

XX AAA46697;

DT 25-SEP-2000 (first entry)

DE DNA encoding a human erythropoietin polypeptide.

KW Human; erythropoietin; EPO; inhibitor; nuclear factor-kappaB; NF-kappaB;
 KW multi-drug resistance gene; malignant hemopathy; solid tumour;
 KW malignant blood disease; leukaemia; lymphoma; solid cancer; ds.

XX Homo sapiens.

OS

FT Key Location/Qualifiers

FT CDS 1..582

FT /tag= a

FT /product= "erythropoietin"

PN WO200030587-A2.

PD 02-JUN-2000.

PF 24-NOV-1999; 99WO-FR02897.

PR 25-NOV-1998; 98FR-0014858.

XX (CNRS) CENT NAT RECH SCI.

XX Hirsch F, Haeflner A;

XX WPI: 2000-399901/34.

XX P-PSDB; AAY93638.

XX Treatment of haematological or solid tumours using an inhibitor of the

XX activation of nuclear factor-kappaB, particularly to prevent

XX development of resistance to chemotherapeutics

XX Claim 5; Page 28-29; 30pp; French.

XX The present sequence encodes a human erythropoietin (EPO) polypeptide.

XX The human growth hormone protein is used as an inhibitor of the

XX activation of nuclear factor-kappaB (NF-kappaB). The inhibitor inhibits

XX resistance gene (which contains binding sites for NF-kappaB within its

XX regulatory regions). The inhibitors are used to produce pharmaceuticals

XX which may be used in the treatment of malignant hemopathy or solid

XX tumours. The inhibitors are especially used to treat malignant blood

XX diseases (leukaemia, lymphoma) and solid cancers (of breast or ovary).

Sequence 582 BP; 113 A; 181 C; 170 G; 118 T; 0 other;

Alignment Scores:
 Pred. No.: 2,06e-98 Length: 582
 Score: 991.00 Matches: 192
 Percent Similarity: 99.48% Conservative: 0
 Best Local Similarity: 99.48% Mismatches: 1
 Query Match: 99.30% Indels: 0
 DB: 21 Gaps: 0

US-09-813-775C-2 (1-193) x AAA46697 (1-582)

OY 1 MetGlyValAlHisGluCysProAlaTrpLeuTrpLeuLeuSerLeuLeuSerLeuPro 20
 DB 1 ATGGGGGTGCACGAATGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 60
 OY 21 LeuGlyLeuProValLeuGlyAlaProProArgLeuIleCysAspSerArgValLeuGlu 40
 DB 61 CTGGGCTCCAGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120

Oy		41	Argyrilreuleuenglualalysglualaglualanlllethrthglsylsalactunhsy	60
Db		121	AGGTACTCTTTCGAGGCCCAAGAGCCCGCAAAATATACACAGGGGCTGTCTGAACATGC	180
Oy		61	SerleuensngluasnlllethrvalProasPThrLysValAsnPhetYrAlatPrLysArg	80
Db		181	AGCTTGAAATGGAATATACACTGTCCCGACACCMAAGTTAATTCTATGCTGGAAAGAG	240
Oy		81	MelGuValArggInciAlaValIgluValTrpGlnclyLeuAlaleuSerGluAla	100
Db		241	ATGGAGGTCGGGCGCAGAGCCGTAAGAAGTCGTGCAGGGCCTGGCCCTGTCGGAAGCT	300
Oy		101	ValLeuArqIgluAlalaleuLeuValAsnSerSerGlnProtRgLuPreuGlnLeu	120
Db		301	GTCCTGGGGGGCCAGGCCCTGTGGTCAACTCTTCCCACCGCGGGAGCCCTCGACGCTG	360
Oy		121	HisValaspLysAlaValSerGlyLeuArgSerLeuThrThreuleuArgAlaleuGly	140
Db		361	CATGGGATAAAGCCGTACATGGCCTTCGACGCTCACCACTCTGCTGGGCTCTGGGA	420
Oy		141	AlaGlnLysGluAlaIleSerProProaspAlaIalaSerAlaAlaProleuArrgThrile	160
Db		421	GCCCAAGAAGAGGCACTCTCCCTCCAGATCGCGGCTCAAGCTGTCTCATCTCCGAACAAC	480
Oy		161	ThrAlaaspThrPhearGlyLsleuPhearGValTySerAsnPheluArgIlyLysleu	180
Db		481	ACTCTGTACACTTTCGCCAACACTTTCGCCAGTCTACTCCAATTTCTCCGGGGAAGCTG	540
Oy		181	LysleuTyrrThrgIguAlaCySarqThrcIyAspArg	193
Db		541	AAGCTGTACACAGGGGAGGCTGTGACAGACAGGGGAGCAGA	579
RESULT		3		
AAH46972		ID	AAH46972 standard; cDNA; 582 bp.	
XX	AAH46972:			
XX	29-OCT-2001	(first entry)		
DE	Human erythropoietin (Epo) cDNA sequence.			
KW	Transgenic pig; human; erythropoietin; EPO; milk; PMSG; hcg;			
OS	chorionic gonadotrophic hormone; WAP promoter; ss.			
XX	Homo sapiens.			
FH	Key	Location/Qualifiers		
FT	CDS	1..582		
FT	/+tag= a	/product= "EPO"		
FT	sig_peptide	1..81		
FT	mat_peptide	82..579		
FT	/+tag= c			
PN	MO200159074-A1.			
PD	16-AUG-2001.			
PF	28-JUN-2000; 2000MO-KR00675.			
PR	14-FEB-2000; 2000KR-0006888.			
PA	(KORE-) REPUBLIC KOREA.			
P1	Chang W, Park J, Seong H, Min K, Yang B, Im G, Lee Y, Lee C;			
PI	Kim J.			
DR	WPI: 2001-514656/56.			
DR	P-PDB: AAB85573.			
PT	Producing transgenic porcine that secretes human erythropoietin (hEPO)			

PT	in milk, by introducing vector comprising hEPO genome into fertilized
PT	eggs of porcine to which PMSG and hCG were administered, and developing
PT	progeny
PS	Claim 4; Fig 3; 21pp; English.
XX	
CC	The invention relates to producing transgenic pigs (P) that secrete
CC	human erythropoietin (hEPO) in milk. The method involves administering
CC	PMSG and human chorionic gonadotrophic hormone (hCG) into (P), collecting
CC	fertilized eggs after mating, injecting expression vector containing a
CC	2.6 kb MAP promoter, hEPO genome and SV40 poly A DNA into male pronuclei,
CC	transplanting them in surrogate mother pig and allowing it to give birth.
CC	The method provides transgenic porcine capable of secreting hEPO in their
CC	milk, thus producing the expensive useful medicine at a low cost with
CC	stability on a large scale, giving a contribution to the improvement of
CC	human health. The present sequence represents a base sequence for a human
CC	EPO cDNA incorporated into the genome of porcine.
XX	
SQ	Sequence 582 BP; 113 A; 181 C; 170 G; 118 T; 0 other;
Alignment Scores:	
Pidm. No.:	2,06e-98
Score:	991.00
Percent Similarity:	99.48%
Best Local Similarity:	99.48%
Query Match:	99.30%
DB:	22
	Gaps: 0
US-09-813-775C-2 (1-193) x AAH46972 (1-582)	
QY	1 MetGlyValHisGlyCysProAlaTrpLeuTrpLeuLeuSerLeuSerLeuPro 20
DB	1 ATGGGGGGGCGACGAATGCTCGCGCTGTGGCTTCTCTCTCCCTGCTGCGTCCCT 60
QY	21 LeuGlyLeuProValLeuGlyAlaProProArgLeuIleCysAspSerArgValLeuGlu 40
DB	61 CTGGGCCCTCCAGCTCCTGGGGCGGCCCCAGCCGCTCATCTGTACAGCGCGAATCTCTGGAG 120
QY	41 ArgTrpLeuLeuGluValAlaLeuAlaGluValAsnIleThrThhGlyCysAlaGluHisCys 60
DB	121 AGGTACCTCTTGGAGGCCCAAGAGGCCGACAAATATACACAGGGCTGTGCTAACACTGC 180
QY	61 SerLeuAsnGluAsnIleThrValProAspThrLysValAsnPhetylAlaTrpLysArg 80
DB	181 AGCTTGAAATGAGAAATATCACTGTCGCCAGACACCAAGTAAATTGTATGATCCGGAAGAG 240
QY	81 MetGluValArgGlnGlnAlaValAlaGluValTrpGlnGlyLeuAlaLeuSerGluAla 100
DB	241 ATGGAGGTGCGGGCGACAGGGCGCTGAGAAAGTCTGGCAGGGGCTGTGCTGTGGAAACT 300
QY	101 ValLeuArgGlyGlnAlaLeuLeuValAsnSerSerGlnProTrpGlnProLeuGlnLeu 120
DB	301 GTCTCGCGGGGCCAGGCCCTGTGTGTGTCAACTCTCCAGCCGCGGGAGGCCCTTCGACATG 360
QY	121 HisValAspLysAlaValSerGlyLeuArgSerLeuThrThhLeuLeuArgAlaLeuGly 140
DB	361 CATGTCGATTAAGCGCGTACGTGGCGCTTCGAGCGCTCACACACTCTGCTTGGGGCTTGGGA 420
QY	141 AlaGlnLysGluAlaIleSerProProAspAlaIleSerAlaAlaProLeuArgThrIle 160
DB	421 GCCCAGGAAGGAGGCAATCTCCCTCCAGATGCGGGCTCAGCTGCACATTCGAGAACATTC 480
QY	161 ThrAlaAspThrPheArgLysLeuPheArgValTyrSerAsnPheLeuArgGlyLysLeu 180
DB	481 ACTGTGTGCACTTTCGCCCAACACTTTCGCCAGTCTACTCCAAATTTCCCTCCGGGGAAAGCTG 540
QY	181 LysLeuTrpThrGlyGluAlaCysArgThrGlyAspArg 193
DB	541 AAGCTGTACACAGGGGAGGCGCTCGAGACACGGGGACAGA 579
RESULT 4	
AAK77361	
AAK77361	
AAK77361 standard; DNA: 616 BP.	

XX AAX77361;
 AC 09-AUG-1999 (first entry)
 DT
 XX Polynucleotide sequence of synthetic erythropoietin.
 DE
 XX Nucleic acid identification; exogenous protein; gene sorting;
 KM growth factor; membrane receptor; sindbis virus; erythropoietin; ss.
 XX
 OS Synthetic.
 PN WO925876-A1.
 XX
 PD 27-MAY-1999.
 XX
 PF 17-NOV-1998; 98WO-US24520.
 XX
 PR 17-NOV-1997; 97US-0972218.
 XX
 PA (CYTO-) CYTOS BIOTECHNOLOGY GMBH.
 XX
 PI Bailey JE, Koller D, Orberger GH, Renner WA;
 XX
 DR WPI, 1999-357620/30.
 XX
 PT Isolating genes encoding proteins with selected properties, useful
 PT for identifying therapeutic agents or targets
 PS
 PS Disclosure: Fig 15; 136pp; English.
 CC The invention relates to the identification of a recombinant nucleic acid
 CC encoding an exogenous protein having a selected property. The method
 CC comprises preparing a population of eukaryotic host cells, culturing the
 CC cells under suitable conditions and identifying cells that contain the
 CC recombinant nucleic acid. The method is used to sort genes according to
 CC the type of proteins they express, and also to identify new ligand/
 CC receptor interactions. Typical applications of the nucleic acid and the
 CC exogenous protein are in isolation of new growth factors, cytokines,
 CC membrane receptors, cytoplasmic, organelle or nuclear proteins, all of
 CC which may be useful as therapeutic agents or therapeutic targets, e.g.
 CC apoptosis-promoting or tumour suppressing proteins, regulators of cell
 CC proliferation or metabolic processes etc. The protein can also be used to
 CC screen for specific modulators. The nucleic acid can also be used as
 CC sources of therapeutic antisense or ribozyme sequences. The method allows
 CC the protein (rather than a partial DNA sequence) to be isolated and,
 CC since a wide range of cells can be used, they can be expressed with the
 CC correct glycosylation pattern.
 CC
 SO Sequence 616 BP; 118 A; 191 C; 184 G; 123 T; 0 other;
 Alignment Scores:
 Pred. No.: 2,23e-98 Length: 616
 Score: 991.00 Matches: 192
 Percent Similarity: 99.48% Conservative: 0
 Best Local Similarity: 99.48% Mismatches: 1
 Query Match: 99.30% Indels: 0
 DB: 20 Gaps: 0
 US-09-813-775c-2 (1-193) x AAX77361 (1-616)
 QY 1 MetGlyValHisGluCysProAlaTrpLeuTrpLeuLeuSerLeuLeuSerLeuPro 20
 DB 16 ATGGGGGTGACGAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 75
 QY 21 LeuGlyLeuProValLeuGlyAlaProPheArgLeuIleCysAspSerArgValLeuGlu 40
 DB 76 CTGGGCTCCCACTGCTGGGCGCCGCCACACGCTATCTGTGACAGCCGAGTCTGGAG 135
 QY 41 ArgTyrLeuLeuGluAlaLysGluAlaGlnAsnIleThrThrGlyCysAlaGlnHisCys 60
 DB 136 AGGTACTCTTGGAGGCCCAAGAGGCCGAGAAATATCAGACAGCGGCTGTCTGACACTGC 195

QY 61 SerLeuAsnGluAsnIleThrValProAspThrLysValAsnPheTyrAlaTrpLysArg 80
 DB 196 AGCTTGAAATGAGAAATATCTACTGTCCAGACACCAAAAGTTAATTCTATCTCGAAGAG 255
 QY 81 MetGluValArgGlnGlnAlaValGluValTrpGlnGlyLeuAlaLeuSerGluAla 100
 DB 256 ATGGAGGTGGCGAGCAGGCCCTGAGAAATGCTGCGAGGCCCTGCTGCGGAAAGCT 315
 QY 101 ValLeuArgGlyGlnAlaLeuValAsnSerSerGlnProTrpGlnProLeuGlnLeu 120
 DB 316 GTCTCTGGGGCGAGGCCCTGTGTGTCACACTCTTCCACACCGTGGAGGCCCTGACGCT 375
 QY 121 HisValAspLysAlaValSerGlyLeuArgSerLeuThrThrLeuLeuArgAlaLeuGly 140
 DB 376 CATGTGATAAAGCCGCTGAGGCTTCGACAGCTCACCACCTGCTGCTGCGGCTCGGGA 435
 QY 141 AlaGlnLysGluAlaIleSerProPheAspAlaIleSerAlaAlaProLeuArgThrIle 160
 DB 436 GCCCAAGAAAGCAATCTCCCTCCAGATGCGGCTCAGCTCAGCTCAGCAACAAATC 495
 QY 161 ThrAlaAspThrPheArgLysLeuPheArgValTyrSerAsnPheLeuArgGlyLysLeu 180
 DB 496 ACTGCTGACACTTTCGCAAACTCTTCGAGTCTACTCCAAATTTCTCCGGGGAAGCTG 555
 QY 181 LysLeuTyrThrGlyGluAlaCysArgThrGlyAspArg 193
 DB 556 AAGCTGTACACAGGGAGGCTGACAGAGGAGGACAGA 594
 RESULT 5
 ID AAA90393 standard; DNA; 616 BP.
 XX
 XX AAA90393;
 AC 10-JAN-2001 (first entry)
 XX
 DR 17-NOV-2001 (first entry)
 XX
 DE DN encoding synthetic erythropoietin (EPO).
 XX
 KM Nucleic acid identification; exogenous protein; drug screening;
 KW recombinant expression; synthetic erythropoietin; EPO; ds.
 XX
 OS Synthetic.
 XX
 PN JP2000189173-A.
 XX
 PD 11-JUL-2000.
 XX
 PF 23-AUG-1999; 99JP-0236220.
 XX
 PR 17-NOV-1998; 98US-0193707.
 XX
 PR 17-NOV-1998; 98WO-US24520.
 XX
 PA (CYTO-) CYTOS BIOTECHNOLOGY GMBH.
 XX
 PI WPI, 2000-551637/51.
 XX
 DR 17-NOV-1998; 98WO-US24520.
 XX
 PT Identifying a recombinant nucleic acid to identify and isolate various
 PT cellular proteins, comprises culturing a composition comprising
 PT eukaryotic host cells and identifying a cell comprising recombinant
 PT nucleic acid
 PS
 PS Disclosure: Fig 15; 56pp; Japanese.
 XX
 XX The invention relates to the identification of a recombinant nucleic acid
 CC encoding an exogenous protein having a selected property. The method
 CC comprises preparing populations of eukaryotic host cells, where each cell
 CC comprises an expression vector encoding a different exogenous protein.
 CC The host cells are cultured under suitable conditions and the nucleic
 CC acid which encodes the exogenous protein is identified. The method is
 CC useful for the identification and isolation of proteins with a selected
 CC property. Typical applications of the nucleic acid and the exogenous
 CC protein are in isolation of new growth factors, cytokines, membrane
 CC receptors, cytoplasmic, organelle or nuclear proteins, all of which may

Db 262 ATGGAGCTGGCGACGACGCGCTGAGAGTCTGGCAGGCGCTGCTGCTGCGAAGCT 321
 Qy 101 VALLLEuArgGlyGlnAlaLeuLeuValAsnSerSerGlnProTrpGlnProLeuGlnLeu 120
 Db 322 GTTCTCGGGGCGACGCGCTGTGTGTCATCTCTCCAGCGCGGGAGCGCCCTGCGAGCTG 381
 Qy 121 HisValAspLysAlaValSerGlyLeuArgSerLeuThrLeuLeuArgAlaLeuGly 140
 Db 382 CATGTGGATTAAGCCCTCATGTGCTCCAGCTCCAGCTCCAGCTCTGCTGAGCTTGCGG 441
 Qy 141 AlAGlnLysGlnAlaLeuSerProProAspAlaAlaSerAlaAlaProLeuArgThrIle 160
 Db 442 GCCCAAGAGAAAGCCATCTCCCTCCAGATGCGGCTCCAGCTGCTCCACTCCGAAACAATC 501
 Qy 161 ThrAlaAspThrPheArgLysLeuPheArgValTyrSerAsnPhelLeuArgGlyLysLeu 180
 Db 502 ACTGCTGACACTTCCGCAAGCTCTCCAGTCTACTCCAAATTTCTCTCCGCGGAAAGCTG 561
 Qy 181 LysLeuTyrThrGlyLysAlaCysArgThrGlyAspArg 193
 Db 562 AAGCTTACACAGGGAGGATGACAGACAGGGGACAGA 600

RESULT 7

AAT31529
 ID AAT31529 standard: cDNA, 788 BP.

XX AAT31529;

DT 15-SEP-1996 (first entry)

XX Human erythropoietin cDNA.

XX Erythropoietin: EPO; anaemia; gene therapy; vector;

KW scaffold attachment region; SAR element; transgenic animal; ss.

OS Synthetic.

XX Key Location/Qualifiers

FT CDS 80..661

FT sig-peptide /*tag= a

FT mat-peptide /*tag= b

FT /*tag= 161..658

FT /*tag= c

XX W09619573-A1.

XX 27-JUN-1996.

XX 18-DEC-1995; 95WO-CA00696.

XX 19-DEC-1994; 94US-0358918.

XX (CANG-) CANGENE CORP.

XX Delcuve G;

XX WPI, 1996-309587/31.

DR P-PSDB: AAR98397.

XX Recombinant DNA molecule expressing mammalian erythropoietin

PT useful to transform cell lines, and for gene therapy, e.g. of

PT anaemia and other red blood cell disorders

PS Claim 4; Page 59; 84pp; English.

XX cDNA clone EPolong codes for human erythropoietin (EPO) (AAR88397).

CC It was obt. by chemical synthesis from component oligonucleotides.

CC A novel recombinant DNA molecule adapted for transfection of a host

CC cell comprises the EPO cDNA or genomic DNA (see also AAT31532), operably

CC linked to an expression control sequence and to 5' and 3' human

CC apolipoprotein scaffold attachment region (SAR) elements (see also

CC AAT31530-31). The SAR elements increase expression of recombinant EPO.

CC allowing stable, long-term prodn. in transfected mammalian cells.
 CC transgenic animals carrying the construct express the recombinant EPO
 CC in their milk. The EPO cDNA may also be used for the gene therapy of
 CC anaemia.

XX Sequence 788 BP; 145 A; 264 C; 228 G; 151 T; 0 other;

Alignment Scores:

Pred. No.:	3,12e-98	Length:	788
Score:	991.00	Matches:	192
Percent Similarity:	99.48%	Conservative:	0
Best Local Similarity:	99.48%	Mismatches:	1
Query Match:	99.30%	Indels:	0
DB:	17	Gaps:	0

US-09-813-775C-2 (1-193) x AAT31529 (1-788)

Qy 1 MetGlyValHisGlnCysProAlaTrpLeuThrPheLeuLeuSerLeuLeuSerLeuPro 20

Db 80 ATGGGGGTGACGAAATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 139

Qy 21 LeuGlyLeuProValLeuGlnAlaProProArgLeuIleCysAspSerArgValLeuGlu 40

Db 140 CTGGGCTCCAGCTCTGCGGCGCCGCCACCGCTCATCTGTGACAGCGAGTCTGAG 199

Qy 41 ArgTyrLeuLeuGlnAlaLysGlnAlaGlnAsnIleThrGlyCysAlaGlnHisCys 60

Db 200 AGTACCTCTTGAGAGCCAAAGAGGCGGAGAAATATCAGCAGGGGCTGTCTCAACATTTC 259

Qy 61 SerLeuAsnGlnAsnIleThrValProAspThrLysValAsnPhenylAlaTrpLysArg 80

Db 260 AGCTTGAATGAAGAAATATCTCTGCTCCAGACCAAGTTAAATTTCTATGCTCGAAGAG 319

Qy 81 MetGlnValArgGlnGlnAlaValGlnValTyrGlnGlyLeuAlaLeuSerGlnAla 100

Db 320 ATGGAGTGGGCGACAGGCGCTAGAACTGTGCGAGGCTGCTGCTGCTGCTGCTGCTG 379

Qy 101 VALLLEuArgGlyGlnAlaLeuLeuValAsnSerSerGlnProTrpGlnProLeuGlnLeu 120

Db 380 GTCTCGGGGCGACGCGCTGTGTGTCATCTCTCCAGCGGAGGCGCTGCGAGCTG 439

Qy 121 HisValAspLysAlaValSerGlyLeuArgSerLeuThrLeuLeuArgAlaLeuGly 140

Db 440 CATGTGGATTAAGCCCTCATGTGCTCCAGCTCCAGCTCTGCTGCTGCTGCTGCTGCT 499

Qy 141 AlAGlnLysGlnAlaLeuSerProProAspAlaAlaSerAlaAlaProLeuArgThrIle 160

Db 500 GCCCAAGAGAAAGCCATCTCCCTCCAGATGCGGCTCCAGCTGCTCCACTCCGAAACAATC 559

Qy 161 ThrAlaAspThrPheArgLysLeuPheArgValTyrSerAsnPhelLeuArgGlyLysLeu 180

Db 560 ACTGCTGACACTTCCGCAAGCTCTCCAGTCTACTCCAAATTTCTCTCCGCGGAAAGCTG 619

Qy 181 LysLeuTyrThrGlyLysAlaCysArgThrGlyAspArg 193

Db 620 AAGCTTACACAGGGAGGCTGACAGACAGGGGACAGA 658

RESULT 8

AAZ31999

ID AAZ31999 standard: cDNA, 788 BP.

XX AAZ31999;

DT 28-JAN-2000 (first entry)

XX Human EPO long cDNA sequence.

KW SAR element; scaffold attachment region; human; apolipoprotein B; tPA;

KW tissue plasminogen activator; protein expression; gene therapy; lysis;

KW occlusive coronary artery thrombi; transmural myocardial infarction;

KW ventricular function; congestive heart failure; acute ischaemic stroke;

KW acute massive pulmonary embolism; venous thrombosis; arterial thrombosis;

KW embolism; arteriovenous cannulae occlusion; plasminogen activator;

KM intravenous catheter clearance; blood clot; ss.
 OS Homo sapiens.
 PN US5985607-A.
 XX 16-NOV-1999.
 PD 27-JUN-1997; 97US-0883795.
 XX 19-DEC-1994; 94US-0358918.
 PR (CANG-) CANGENE CORP.
 XX Awang G, Delcuve G;
 PA WPI; 2000-012788/01.
 DR
 XX
 PT Recombinant DNA molecules encoding tissue plasminogen activator
 PT proteins, operatively linked to a scaffold attachment region, useful
 PT for the production of tissue plasminogen activator both in vivo and in
 PT vitro -
 PS
 XX Example 2; Fig 4; 49pp; English.
 CC This sequence represents the human EPO long cDNA sequence.
 CC The invention relates to a recombinant DNA molecule adapted for
 CC expression of tissue plasminogen activator (tPA). The DNA molecule
 CC comprise a sequence encoding tPA, an expression control sequence
 CC operatively linked to the tPA sequence, and at least one human
 CC apolipoprotein B scaffold attachment region (SAR) element (the SAR is not
 CC a 5' proximal apolipoprotein B SAR). The SAR element is used to increase
 CC the expression of the coding sequences. The recombinant nucleic acids may
 CC be used for the recombinant production of tPA both in vitro or in vivo
 CC (e.g. as part of a gene therapy procedure). tPA may be administered to
 CC treat and remove blood clots. It is especially useful for the lysis of
 CC occlusive coronary artery thrombi associated with evolving transmural
 CC myocardial infarction to improve ventricular function and reduce the risk
 CC of congestive heart failure. Additionally, it may be used in the
 CC management of acute massive pulmonary embolism, venous thrombosis and
 CC acute ischemic stroke. Finally, tPA may be used in treating arterial
 CC thrombosis or embolism, arteriovenous cannulae occlusion and intravenous
 CC catheter clearance. In contrast to other plasminogen activators
 CC (e.g. urokinase and streptokinase), the activity of tPA is relatively
 CC localised and (in theory) is less likely to produce systemic haemorrhagic
 CC disorders.
 XX
 SQ Sequence 788 BP; 145 A; 264 C; 228 G; 151 T; 0 other:

 Alignment Scores:
 Pred. No.: 3.12e-98 Length: 788
 Score: 991.00 Matches: 192
 Percent Similarity: 99.48% Conservative: 0
 Best Local Similarity: 99.48% Mismatches: 1
 Query Match: 99.30% Indels: 0
 DB: 21 Gaps: 0

 US-09-813-775C-2 (1-193) x AA231999 (1-788)
 QY 1 MetGlyValHisGluCysProAlaTrpLeuLeuLeuSerLeuLeuSerLeuPro 20
 Db 80 ATGGGGGTCACGAAGATGCTCGCTGGCTGGCTTCCTCGCTGCTGCTCGCT 139
 QY 21 LeuGlyLeuProValLeuGluAlaProProArgLeuLeuCysAspSerArgValLeuGlu 40
 Db 140 CTGGGGCTCCACGATCTCTGGGGCCGCCACACAGGCTATCTGTACACGCCAGTCTTGAG 199
 QY 41 ArgTyrLeuLeuGluAlaLysGluAlaGlnAsnIleThrThrGlyCysAlaGluHisCys 60
 Db 200 AGGTACCTTTGTGAGCCCAAGAGGCCCAAGAAATATCAGACGGGCTGTGCTGAACATTGC 259
 QY 61 SerLeuAsnGluAsnIleThrValProAspThrLysValAsnDheTyrAlaTrpLysArg 80
 |||||

Db	260	AGCTTGATGGAATATATCACTGTGCTCCAGACACCAAAAGTATTATTTCTATTGCTGTGAAGAGG	319
Oy	81	MetGluValArgGlnGlnAlaValGluValTyrpGlnGlyLeuAlaLeuLeuSerGluAla	100
Db	320	ATGAGAGTCGGGACAGACAGCCGTGAAGTCTGGCAGAGGCCCTGGCCCTGCTGTGGAAAGCT	379
Oy	101	ValLeuAArgGlyGlnAlaLeuLeuValAsnSerSerGlnProTrrpGluProLeuGlnLeu	120
Db	380	GTCCGCGCGGGCCAGACCCCTTGGTCAACTTCCAGCCGCTGGAGACCCCTGCACCTG	439
Oy	121	HisValAspLysAlaValSerGlyLeuLeuSerLeuThrThrLeuLeuArgAlaLeuGly	140
Db	440	CATGTGGATTAAAGCCGTAGTGGCTTGGACCTCACACACTCTGCTTGGGCTTGGGA	499
Oy	141	AlaGlnLysGluAlaIleSerProProAspAlaAlaSerAlaAlaProLeuArgThrIle	160
Db	500	GCCGAGGAAGCAAGCATCTCCCTCCAGATGCGGGCCTCAGCTGCTCCACTGCCAAATC	559
Oy	161	ThrAlaAspThrPheArgLysLeuPheArgValTyrSerAsnPheLeuArgGlyLysLeu	180
Db	560	ACTGCTGACACTTTCGCCGAAACTCTCCGACTCTACATTCATTTCTCCGCGGAAACCTG	619
Oy	181	LysLeuTyrThrGlnGlyAlaCysArgThrGlyAspArg	193
Db	620	AAGCTGTACACAGGGAGGCGCTGCAGACAGGAGGACAGA	658
RESULT 9			
AA64847	ID	AA64847 standard; cDNA: 823 BP.	
XX	XX	AA64847;	
AC	XX		
DT	XX	04-FEB-1998 (first entry)	
DE	XX	Human erythropoietin cDNA.	
KM	XX	Adeno associated virus; virion; vector: erythropoietin; muscle;	
KW	XX	anemia; renal failure; cancer; chemotherapy; antiviral therapy;	
KM	XX	haemoglobinopathy; sickle cell disease; thalassemia; gene therapy;	
ss.	XX		
OS	XX	Homo sapiens.	
FH	XX	Key	Location/Qualifiers
FT	XX	CDS	52..633
FT	XX		/*tag= a
PM	XX	W09726336-A1.	
XX	XX		
PD	XX	24-JUL-1997.	
PF	XX	17-JAN-1997; 97WO-US00980.	
PR	XX	16-JAN-1997; 97US-0785750.	
XX	XX	18-JAN-1996; 96US-0588355.	
PA	XX	(AVIG-) AVIGEN INC.	
PI	XX	Kurtzman GJ, Podsakoff GW;	
DR	XX	WPI: 1997-385339/35.	
XX	XX		
PT	XX	Adeno associated virions for expressing erythropoietin in muscle	
PT	XX	cells - useful to treat anaemia associated with chronic renal	
PT	XX	failure, cancer, cancer chemotherapy or antiviral therapy, or	
PT	XX	haemoglobinopathy	
PS	XX	Disclosure: Fig 1; 81pp: English.	
CC	XX	The cDNA sequence for human erythropoietin (EPO) is given in	
CC	XX	AA64847. A novel claimed composition includes recombinant adeno-	
CC	XX	associated virus (AAV) virions comprising an AAV vector containing	
CC	XX	a nucleic acid molecule encoding EPO operably linked to control	


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XX AAX25701;
AC 21-MAY-1999 (first entry)
DT
XX Human erythropoietin homodimer fusion gene.
DE
XX Human; erythropoietin; dimer; trimer; polymer; fusion protein; cancer;
KW biological activity; anaemia; proliferation; differentiation; ss;
KW progenitor; leucocyte; granulocyte; blood; myelosuppressed patient.
XX
OS Homo sapiens.
OS Synthetic.
XX
XX WO9902710-A1.
XX
XX 21-JAN-1999.
XX
XX 09-JUL-1998; 98WO-US13944.
XX
XX 03-FEB-1998; 98US-0018138.
XX
XX 10-JUL-1997; 97US-0890929.
XX
XX (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
XX
XX Sytkowski AJ;
XX
XX WPI; 1999-120911/10.
XX
XX P-PSDB; AAM99360.
XX
XX New fusion protein with increased activity comprising at least two
XX protein molecules - used to, e.g. treat erythropoietin related
XX deficiency states for treatment of anaemia.
XX
XX Example 1; Fig 16A-C; 119pp; English.
XX
XX This sequence represents a human erythropoietin (EPO) homodimeric fusion
XX gene. The invention relates to the production of dimeric, trimeric or
XX polymeric fusion proteins with increased biological activity. The
XX fusion proteins are used to treat or prevent protein-related deficiency
XX states, specifically, where the protein is erythropoietin (EPO;
XX AAX25689); anaemia, but also for increasing proliferation,
XX differentiation and activity of haematopoietic progenitors (e.g.
XX increasing numbers of leucocytes and granulocytes in the blood of
XX CC myelosuppressed patients) or for treating cancer and other cell growth
XX disorders.
XX
XX Sequence 1158 BP; 228 A; 352 C; 351 G; 227 T; 0 other;
XX
XX Alignment Scores:
XX Pred. No.: 5.28e-98 Length: 1158
XX Score: 991.00 Matches: 192
XX Percent Similarity: 99.48% Conservative: 0
XX Best Local Similarity: 99.48% Mismatches: 1
XX Query Match: 99.30% Indels: 0
XX DB: Gaps: 0
XX
XX US-09-813-775C-2 (1-193) x AAX25701 (1-1158)
XX
XX 1 MetGluValHisGluCysProAlaTrpLeuLeuLeuSerLeuLeuSerLeuPro 20
XX
XX 11 ATGGGGGTGACGAATGTCCTGCTGGCTGCTGCTTCTCTCCCTGCTGCTCCCT 70
XX
XX 21 LeuGluLeuProValLeuGluValAlaProProAlaGluLeuLeuLeuSerLeuLeu 40
XX
XX 71 CTTGGGCTCCAGTCTGCTGGGCGCCACACGCTCATCTGTGACAGCGCATCTCTGGAG 130
XX
XX 41 ArgTyrLeuLeuGluAlaAlaGluValaGluValaGluValaGluValaGluVala 60
XX
XX 131 AGGTACCTCTTGAGAGCCAGAGCGCCGAGATATCAGACAGCGGCTGTGTAACACTGC 190
XX
XX 61 SerLeuAaGluAaSerLeuValaProAspThrLysValaAspThrLysValaAspThr 80
XX

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DB 191 AGCTTGATGAGAAATATCATCTGCCAGACACCAAGTTAATTTCTATGCTGGAGAGG 250
XX
XX 81 MetGluValArgGlnGlnAlaValAlaGluValaTrpGlnGlyLeuAlaLeuLeuSerGluAla 100
XX
XX 251 ATGGAGGTGCGGGCAGAGGCCCTAGAGTCTGGCAGAGGCGCTGCTGTGCGAAGCT 310
XX
XX 101 ValLeuArgGlyGlnAlaLeuLeuValaAsnSerSerGlnProTrpGluProLeuGlnLeu 120
XX
XX 311 GTCTCTCGGGGCGAGGCCCTGTGGTCACACTTCCACAGCCGTGGAGAGCCCTGGAGCTG 370
XX
XX 121 HisValAspLysAlaValaSerGlyLeuArgSerLeuThrThrLeuLeuArgAlaLeuGly 140
XX
XX 371 CATGTGATTAAGCCCTGCTGAGCTTCGACCTCACCACCTGCTGGGCTGGGA 430
XX
XX 141 AlaGlnLysGluAlaAlaLeuSerProProAspAlaAlaSerAlaAlaProLeuArgThrIle 160
XX
XX 431 GCCCAAGAGGAAGCCATCTCCCTCCAGATGGGGCTCAGCTGCTCCATCCGAACAATC 490
XX
XX 161 ThrAlaAspThrPheArgLysLeuPheArgValaTyrSerAspPheLeuArgLysLeu 180
XX
XX 491 ACTGCTGACACTTTCGCCAATCTTCCGAGTCTACTCCAAATTTCTCCGGGGAAGCTG 550
XX
XX 181 LysLeuTyrThrGlyGluAlaCysArgThrGlyAspArg 193
XX
XX 551 AAGCTGTACACAGAGGAGGCTGACAGAGGAGGACAGA 589
XX
XX
XX RESULT 13
XX ID AAN70360 standard; cDNA; 1245 BP.
XX
XX AAN70360;
XX
XX 19-FEB-1991 (first entry)
XX
XX Sequence encoding human erythropoietin (EPO).
XX
XX Renal anaemia therapy; hormone; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX sig_peptide 79..159
XX FT /*tag= a
XX FT mat_peptide 160..660
XX FT /*tag= b
XX
XX EP232034-A.
XX
XX 12-AUG-1987.
XX
XX 19-JAN-1987; 87EP-0300399.
XX
XX 23-JAN-1986; 86JP-0012868.
XX
XX (SUMO) SUMITOMO CHEM IND KK.
XX (SUMI-) SUMITOMI SEIYAKU KK.
XX
XX Yanagi H, Ogawa I, Okamoto M, Hozumi T, Soga A, Yoshima T;
XX Tsutsuni M;
XX WPI; 1987-223006/32.
XX P-PSDB; AAP70256.
XX
XX Human erythropoietin prodn. - by culturing human cells, esp.
XX Namaiwa cells, transformed with DNA encoding human erythropoietin
XX
XX Disclosure: Fig 1; 22pp; English.
XX
XX A cDNA library was prepd. from the poly (A) RNA, which was isolated
XX from the erythropoietin-producing human hepatoma cell Hp-1. The cDNA
XX library was screened using the probes given in AAN70361 and AAN70362. A
XX plasmid (named as pS8-420) was isolated. The nucleotide sequence of
XX the cDNA obtained from this clone is shown in AAN70360.
XX

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XX Sequence 1245 BP; 273 A; 384 C; 351 G; 237 T; 0 other;
 Alignment Scores:
 Pred. No.: 5,83e-98 Length: 1245
 Score: 991.00 Matches: 192
 Percent Similarity: 99.48% Conservative: 0
 Best Local Similarity: 99.48% Mismatches: 1
 Query Match: 99.30% Indels: 0
 Gaps: 0

US-09-813-775c-2 (1-193) x AAN70360 (1-1245)

QY 1 MetGlyValHisGluCysProAlaTTrpLeuTTrpLeuLeuSerLeuLeuSerLeuPro 20
 |||||||
 Db 79 ATGGGGGTGCACGAATGCTGCTGGCTGCTTCTCTGCTGCTGCTGCTGCTGCT 138
 |||||||

QY 21 LeuGlyLeuProValLeuGlyAlaProProArgLeuIleCysAspSerArgValLeuGlu 40
 |||||||
 Db 139 CTGGGCTCCAGTCTGGGGCCGCCACACGCTCATCTGTGACAGCCGAGTCTGGAG 198
 |||||||

QY 41 ArgTyrLeuLeuGluAlaValSerGluAlaGluAsnIleThrThrGlyCysAlaGluHisCys 60
 |||||||
 Db 199 AGGTAACTCTTGGAGGCCAAGAGAGCCGACAAATATCACAGAGCGGCTGTGCTGAACACTGC 258
 |||||||

QY 61 SerLeuAsnGluAsnIleThrValProAspThrLysValAsnPhetYrAlaTrpLysArg 80
 |||||||
 Db 259 AGCTTGAATGAGATATCATCTGCTCCAGACACCAAGTTATTTCTATGCTGGAGAGG 318
 |||||||

QY 81 MetGluValArgGlnGlnAlaValGluValTTrpGlnGlyLeuAlaLeuSerGluAla 100
 |||||||
 Db 319 ATGAGAGTCTGGGCGACAGCGCGTGAAGTCTGGCAGCGCCCTGCTCTCGGAACCT 378
 |||||||

QY 101 ValLeuArgGlyGlnAlaLeuLeuValAsnSerSerGlnProTTrpGluProLeuGlnLeu 120
 |||||||
 Db 379 GTCTTGGGGGGCCAGCGCTTGTGTCACTTTCGCCAGCGCTGGAGACCTCTGACAGCTG 438
 |||||||

QY 121 HisValAspLysAlaValSerGlyLeuArgSerLeuThrThrLeuLeuArgAlaLeuGly 140
 |||||||
 Db 439 CATGTGATTAAGCGCTCAGTGGGCTTCGACAGCTCATCTGCTTCTCGGGCTCTGGGA 498
 |||||||

QY 141 AlaGlnIysGlnAlaIleSerProProAspAlaIleSerAlaIleProLeuArgThrIle 160
 |||||||
 Db 499 GCCCAGAAAGGACCATCTCCCTCCAGATGGCGCTCAGCTCCATCCGAAACATTC 558
 |||||||

QY 161 ThrAlaAspThrPheArgLysLeuPheArgValTyrSerAsnPhetLeuArgGlyLysLeu 180
 |||||||
 Db 559 ACTGCTACACTTTCGCCAAACTCTTCGAGTCTACTCCAAATTTCTCTCGGGGAAAGCTG 618
 |||||||

QY 181 LysLeuTyrThrGlyGlnAlaCysArgThrGlyAspArg 193
 |||||||
 Db 619 AAGCTGTACACAGGGGAGGCTGACAGGACAGGAGGACAGA 657
 |||||||

RESULT 14
 AA0922296
 ID AA0922296 standard; cDNA; 1789 BP.
 XX
 AC AA0922296:
 XX 30-OCT-1995 (first entry)
 DT
 XX Erythropoietin cDNA.
 DE
 XX Erythropoietin; anemia; gene therapy; gene transfer; red blood cell;
 KM RBC; erythrocyte; transformation; myoblast; EPO; ss.
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH CDS 625..1206
 FT /*tag= a
 XX
 PN M09513376-A.

XX
 PD 18-MAY-1995.
 XX
 XX 09-NOV-1994; 94MO-US13066.
 XX
 PF 07-OCT-1994; 94US-0320480.
 PR 10-NOV-1993; 93US-0149871.
 XX
 PA (AMGE-) AMGEN INC.
 PA (USC-) UNIV SOUTHERN CALIFORNIA.
 XX
 PI Hamamori Y, Kedes LH, Samal BB;
 DR WPL; 1995-194095/25.
 DR P-PSDB: AAR74141.
 XX
 PT Gene therapy for treatment of anaemia - and increasing red blood cell
 production by transforming red blood cells with the erythropoietin gene
 PS Disclosure; Page 38-40; 51pp; English.
 XX
 CC The cDNA sequence for human EPO is given in AA0922296. Delivery of
 CC the cDNA to target muscle cells, in vivo or in vitro, allows
 CC increased RBC prodn.
 XX
 SQ Sequence 1789 BP; 353 A; 637 C; 497 G; 302 T; 0 other;
 Alignment Scores:
 Pred. No.: 9.57e-98 Length: 1789
 Score: 991.00 Matches: 192
 Percent Similarity: 99.48% Conservative: 0
 Best Local Similarity: 99.48% Mismatches: 1
 Query Match: 99.30% Indels: 0
 Gaps: 0

US-09-813-775c-2 (1-193) x AA0922296 (1-1789)

QY 1 MetGlyValHisGluCysProAlaTTrpLeuTTrpLeuLeuSerLeuLeuSerLeuPro 20
 |||||||
 Db 625 ATGGGGGTGCACGAATGCTGCTGGCTGCTTCTCTGCTGCTGCTGCTGCTGCT 684
 |||||||

QY 21 LeuGlyLeuProValLeuGlyAlaProProArgLeuIleCysAspSerArgValLeuGlu 40
 |||||||
 Db 685 CTGGGCTCCAGTCTGGGGCCGCCACACGCTCATCTGTGACAGCGAGTCTGGAG 744
 |||||||

QY 41 ArgTyrLeuLeuGluAlaValSerGluAlaGluAsnIleThrThrGlyCysAlaGluHisCys 60
 |||||||
 Db 745 AGGTAACTCTTGGAGGCCAAGAGAGCCGAGAAATATCACAGAGCGGCTGTGTAACACTGC 804
 |||||||

QY 61 SerLeuAsnGluAsnIleThrValProAspThrLysValAsnPhetYrAlaTrpLysArg 80
 |||||||
 Db 805 AGCTTGAATGAGATATCATCTGCTCCAGACACCAAGTTATTTCTATGCTGGAGAGG 864
 |||||||

QY 81 MetGluValArgGlnGlnAlaValGluValTTrpGlnGlyLeuAlaLeuSerGluAla 100
 |||||||
 Db 865 ATGAGAGTCTGGGCGACAGCGCGTGAAGTCTGGCAGCGCTGCTCGGAAACT 924
 |||||||

QY 101 ValLeuArgGlyGlnAlaLeuLeuValAsnSerSerGlnProTTrpGluProLeuGlnLeu 120
 |||||||
 Db 925 GTCTTGGGGGGCCAGCGCTTGTGTCACTTTCGCCAGCGCTGGAGACCTCTGACAGCTG 984
 |||||||

QY 121 HisValAspLysAlaValSerGlyLeuArgSerLeuThrThrLeuLeuArgAlaLeuGly 140
 |||||||
 Db 985 CATGTGATTAAGCGCTGAGTGGGCTTCGACAGCTCATCTGCTTCTCGGGCTCTGGGA 1044
 |||||||

QY 141 AlaGlnIysGlnAlaIleSerProProAspAlaIleSerAlaIleProLeuArgThrIle 160
 |||||||
 Db 1045 GCCCAGAAAGGACCATCTCCCTCCAGATGGCGCTCAGCTCCATCCGAAACATTC 1104
 |||||||

QY 161 ThrAlaAspThrPheArgLysLeuPheArgValTyrSerAsnPhetLeuArgGlyLysLeu 180
 |||||||
 Db 1105 ACTGCTACACTTTCGCCAAACTCTTCGAGTCTACTCCAAATTTCTCTCGGGGAAAGCTG 1164
 |||||||

GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus.p2n model

Run on: January 8, 2003, 05:16:34 ; Search time 1619.26 Seconds
(without alignments)
1930.339 Million cell updates/sec

Title: US-09-813-775C-2
Perfect score: 998
Sequence: 1 MGVECPAMIMLLISLSP.....NFLRGKIKLYTGACRTGDR 193

Scoring table:
BIOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DEV=x1h
-O=/cgrn2.1/USPTO.spool/US09813775/runat_07012003_153122_23837/app.query.fasta_1.718
-DB=EST -OPMT=fastap -SUFFIX=p2n.rst -MINMATCH=0 -LOOPT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 MATRIX=BIOSUM62 TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR_SCORE=pcr -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USBR=US09813775 -GCGN_1_1_821_8runat_07012003_153122_23837 -NCPU=6 -ICPU=3
-NO_XIPYX -NO_MMAB -LARGEJURY -NEG_SCORES=0 -WAIT -LONGLOG -DEV.TIMEOUT=120
-MAIN.TIMEOUT=30 -THREDS=1 -XGAPOP=10 -YGAPOP=6 -Fgapop=6 -Fgapext=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :
EST:*
1: em_estdb:*
2: em_esthum:*
3: em_estlin:*
4: em_estlun:*
5: em_estlov:*
6: em_estlpl:*
7: em_estro:*
8: em_hlc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hlc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estlom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	443.5	44.4	567	9	AA662379
2	180	18.0	686	13	BM438685
3	159	15.9	444	10	BE663803
4	139	13.9	968	17	CNS02F50
5	117	11.7	365	13	BM279790
6	117	11.7	611	13	BM315886
7	99.5	10.0	967	12	BG475544
8	94.5	9.5	867	12	BF184120
9	94	9.4	803	13	BI648123
10	92	9.2	593	14	BM931504
11	92	9.2	657	14	BQ185758
12	91.5	9.2	800	13	BI909650
13	91	9.1	639	13	BJ528644
14	90	9.0	912	10	BE618292
15	88.5	8.9	609	9	AA538257
16	88.5	8.9	940	14	BQ684126
17	88.5	8.9	1035	17	CNS02175
18	87.5	8.8	955	13	BM006435
19	87.5	8.8	976	14	BQ642885
20	87.5	8.8	1494	11	AK008748
21	87	8.7	299	10	BE061329
22	87	8.7	814	9	AU130785
23	87	8.7	1149	13	BM048467
24	86.5	8.7	713	14	BM723615
25	86.5	8.7	770	14	BQ751539
26	86.5	8.7	809	14	BQ750964
27	86.5	8.7	1091	13	BM551902
28	86	8.6	535	14	BQ658306
29	86	8.6	606	14	BM947371
30	86	8.6	671	12	BG675678
31	86	8.6	854	13	BI600127
32	85.5	8.6	663	10	BB653289
33	85.5	8.6	1039	9	BI251034
34	85	8.5	458	9	A1030235
35	85	8.5	568	13	BI682360
36	85	8.5	641	13	BI594824
37	85	8.5	686	9	A1722105
38	84.5	8.5	644	13	BI601795
39	84.5	8.5	675	17	BH466321
40	84.5	8.5	721	17	AZ981594
41	84.5	8.5	749	12	BE916828
42	84.5	8.5	866	12	BG340812
43	84.5	8.5	874	12	BF674417
44	84.5	8.5	979	10	BB029809
45	84.5	8.5	1149	12	BG389982

ALIGNMENTS

RESULT 1
AA662379/c
LOCUS AA662379 567 bp mRNA linear EST 12-NOV-1997
DEFINITION nu93g01.s1 NCI-CGAP_P122 Homo sapiens CDNA clone IMAGE:121888 3'
similar to gb:S65458 ERYTHROPOIETIN PRECURSOR (HUMAN);, mRNA
ACCESSION AA662379
VERSION AA662379
KEYWORDS AA662379.1 GI:2616470
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 567)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/dbip/image/image.html
Seq primer: 40m13 fwd. ET from Amersham
High quality sequence stop: 375.

FEATURES
source
1. 567
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_1ib="IMAGE:1218288"
/clone_1ib="NCI-CGAP_P22"
/sex="male"
/tissue_type="normal prostate"
/lab_host="DH10B"
/note="Organ: prostate; Vector: pT73D-Pac (Pharmacia)
with a modified polylinker; 1st strand cDNA was prepared
from normal prostate bulk tissue, and was then primed with
a Not I - oligo(dT) primer. Double-stranded cDNA was
ligated to Eco RI adaptors (Pharmacia), digested with Not
I and cloned into the Not I and Eco RI sites of the
modified pT73 vector. Library is normalized, and was
constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 125 a 142 c 181 g 119 t

ORIGIN

Alignment Scores:
Pred. No.: 6 06e-41 Length: 567
Score: 443.50 Matches: 111
Percent Similarity: 89.608 Conservative: 1
Best Local Similarity: 88.804 Mismatches: 12
Query Match: 44.444 Indels: 5
DB: 9 Gaps: 1

US-09-813-775C-2 (1-193) x AA662379 (1-567)

QY 69 ProAspThrLysValAsnPheryrAlaTrpLysArgMetGluValAlaArgGlnAlaVal 88
|||||
DB 567 CCAGACACCAAGCTAA-TTCATGCTCGCAAGAAAGTGAAGT---CGGCGAGCGCCGTA 512
QY 89 GluValITrPcInGlyLeuAlaLeuSerGluAlaValLeuArgGlyGlnAlaLeu 108
|||||
DB 511 GAAGCTGGA--GGGCTGGCCCTTCTGTGCAAAAGCTGCTGCG--GGCCATGCCCTGTG 455
QY 109 ValAsnSerGlnProTrpGluProLeuGlnLeuHisValAspLysAlaValSerGly 128
|||||
DB 454 TCAACTCTTCCAGCCGCGGAGGCCCTGACCTCATGTGATAAAGCCGTCAGGGG 395
QY 129 LeuArgSerLeuThrThrLeuLeuArgAlaLeuGlyAlaGlnLysGlnAlaLeuSerPro 148
|||||
DB 394 TT--CGAGCCTACCACTGCTGGGCTGCGGAGCCGAGAAAGGAGGCACTCTCCCT 336
QY 149 ProAspAlaAlaSerAlaAlaProLeuArgThrIleThrAlaAspThrPheArgLysLeu 168
|||||
DB 335 CCGAAGGCGCCCTCAGCTGCTCAGTCCGAAACATACAGTCTGACACTTCCGCAAACTC 276
QY 169 PheArgValITrSerAsnPhelLeuArgGlyLysLeuLysLeuThrGlyGlnAlaGly 188
|||||
DB 275 TTCGGAGTCTACTCCAAATTTCTCCGGGGAAGCTGAAGCTGTACACAGGAGGCGCTGC 216
QY 189 ArgThrGlyAspArg 193
|||||
DB 215 AGGACAGGCGACAGA 201

RESULT 2
BM438685
LOCUS 686 bp mRNA linear EST 31-JAN-2002
DEFINITION Iptv01464 Liver cDNA library Ictalurus punctatus cDNA 5' similar
to Erythropeletin, mRNA sequence.
ACCESSION BM438685
VERSION 1
KEYWORDS GI:18460407
SOURCE EST.
ORGANISM channel catfish.
Ictalurus punctatus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
Ictaluridae; Ictalurus.
1 (bases 1 to 686)
Feng, J., Kuokkas, H., Kocabas, A., Li, P. and Liu, Z.
Transcriptome of channel catfish (Ictalurus punctatus): Initial
analysis of expressed sequence tags from the liver
Unpublished (2002)

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

FEATURES
source
1. 686
/organism="Ictalurus punctatus"
/db_xref="taxon:7998"
/clone_1ib="Liver cDNA library"
/note="Organ: Liver; Vector: pSport1; Site_1: NotI;
Site_2: SalI"

BASE COUNT 189 a 171 c 155 g 171 t

ORIGIN

Alignment Scores:
Pred. No.: 2 01e-10 Length: 686
Score: 180.00 Matches: 45
Percent Similarity: 51.098 Conservative: 25
Best Local Similarity: 32.858 Mismatches: 47
Query Match: 18.048 Indels: 20
DB: 13 Gaps: 3

US-09-813-775C-2 (1-193) x BM438685 (1-686)

QY 56 CysAlaGluHisCysSerLeuAsnGluAsnIleThrValProAspThrLysValAsnPh 75
|||
DB 15 TGTACAGAGGAATGACGATGCTGTACCTCTCAGAGTCTGACAGAGGATTTT 74
QY 76 TyrAlaITrPcLysArgMetGluValArgGlnGlnAlaValGluValITrPcInGlyLeuAla 95
:::
DB 75 CATGTTGGGAAAGCAAAATACAGAGGAGCAGGCTCAAGAACTGACAGACGATATGG 134
QY 96 LeuLeuSerGlnAlaValLeuArgGlyGlnAlaLeuLeuValAsnSerGlnProTrp 115
|||||
DB 135 TTGCTAAACATGSCCATTCAGCTCATAGGTCATCATCACCACACTCTGCA----- 185
QY 116 GluProLeuGlnLeuHisValAspLysAlaValSerGlyLeuArgSerLeuThrThrLeu 135
|||
DB 186 -----CTCCACCTCCACATAGAAAGCAGCATCAGAAACATTGCGAGCTCAAGCAGGTG 239
QY 136 LeuArgAlaLeuGlyAlaGlnLysGlnAlaIleSerProProAspAlaAlaSerAlaAla 155
|||||
DB 240 CTGCGACCTCCAGTATPAG-----GACTATPAG 269
QY 156 ProLeuArgThrIleThrAlaAspThrPheArg-----LysLeuPheArg 170
|||
DB 270 CCTACAAGTGTGTGGACAGAGGACACATGGAAGATCTTTCGGCTTCAGAGCTCTTCAG 329
QY 171 ValITrSerAsnPhelLeuArgGlyLysLeuLysLeuThrGlyGlnAla 187

Db	330	GTCACATCATCTTCCGTGGGAAAGTGCGCCTTTTCTCTCCCAATGCT	380
RESULT 3	BE663803	444 bp	mRNA linear EST 25-APR-2001
LOCUS	147806 MARC 4BOV Bos taurus cDNA 5'		mRNA sequence.
DEFINITION	BE663803		
ACCESSION	BE663803.1	GI:10022630	
VERSION	EST.		
KEYWORDS	Bos taurus		
SOURCE	cow.		
ORGANISM	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;		
REFERENCE	Bovidae; Bovinae; Bos.		
AUTHORS	Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T., Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitto-McKown,C.G., Pierce,G., Holt,I., Karameyeva,S., Liang,F., Quackenbush,J. and Keeler,J.W.		
TITLE	Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle genome Res. 11 (4), 626-630 (2001)		
JOURNAL	21180013		
MEDLINE	Contact: Smith TPL		
COMMENT	USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366 Fax: 402 762 4390 Email: smithemail.marc.usda.gov Single pass sequencing. Bases called and alt-trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -mismatch 12 options. PCR Primers FORWARD: AGGAACAGCTATGCACAT BACKWARD: GTTTCCTCCACTCACGACG Plate: 51 row: H column: 3 Seq primer: ATTTAGTGACCTGTAG. Location/Qualifiers 1..444 /organism="Bos taurus" /db_xref="taxon:9913" /clone_lib="MARC 4BOV" /tissue_type="pooled" /lab_host="DH10B" /note="Vector: pCMV SPORT6; Site.1: NotI; Site.2: SalI; library made from pooled tissue from day 20 and day 40 embryos."		
FEATURES	source		
BASE COUNT	110 a 85 c 142 g 106 t	1 others	
ORIGIN			
Alignment Scores:	Pred. No.: 2,83e-08	Length: 444	
Score: 159.00	Matches: 28		
Percent Similarity: 78.95%	Conservative: 2		
Best Local Similarity: 73.68%	Mismatches: 8		
Query Match: 15.93%	Indels: 0		
DB: 10	Gaps: 0		
US-09-813-775C-2 (1-193) x BE663803 (1-444)			
OY	55 glyCYsAlAglUHIscysSerLeuansngluAnsiethrValProAsphrlYsValasn	74	
Db	152 GGCTGTGCAGAAGGCTTCATCATGATGATATCATCTGTGCCAGACACCAGGTTAAC	211	
OY	75 pheTYrAlAtTrPlYsArGmetClUvAlAtAgGInGlnAlaValGlUvAlTrPcln	92	
Db	212 TTCTATGCTTGAAAGAGATGAGGTGAGTTCACGGCTCTTCTCTTGGGAA	265	
RESULT 4	CNS02F50	968 bp	DNA linear CSS 13-MAY-2000
LOCUS	CNS02F50		

[illegible]

Insert. Size selection was performed to exclude fragments <1.5kb. Library constructed and donated by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTCTGCTTAAAGTGGC and 3' end primer CGACCTGCACCTCGACGACA."

BASE COUNT 156 a 172 c 144 g 139 t
ORIGIN

Alignment Scores:

Pred. No.: 0.00315 Length: 611
Score: 117.00 Matches: 46
Percent Similarity: 34.67% Conservative: 23
Best Local Similarity: 23.12% Mismatches: 49
Query Match: 11.72% Indels: 81
DB: 13 Gaps: 6

US-09-813-775c-2 (1-193) x BM315886 (1-611)

```
OY 2 G1yValHisGluCysProAlaTTrp-----LeuTrpLeuLeuSer 15
Db 233 GGAGTGGACAGTGTGT-----TGGCCAGGCTTTCATTAAGAGCTTTGCTTACTG--- 283
OY 16 LeuLeuSerLeuProLeuGlyLeuProValLeuGlyAlaProProAlaGlyLeu11eCysasp 35
Db 284 CTGATGTGTCTGAGTGGACGCCGCTCCAGCCTGCTCCCATTAACCCCATCTGTGAC 343
OY 36 SerArgValLeuGluArgTyrLeuLeuGlu-AlaLysGluAlaGluAsn1leThrThgl 55
Db 344 CTGGCGCGCTCCGACACATTTTCATACATTCAGACT----- 386
OY 55 yCysAlaGluHisCysSerLeuAsnGluAsn1leThrValProAspThrLysValAsnph 75
Db 386 ----- 386
OY 75 eTyrAlaTrpLysArgMetGluValArgGlnGlnAlaValGluValTrrpGlnGlyLeuAl 95
Db 386 ----- 386
OY 95 aLeuLeuSerGluAlaValLeuArgGlyGlnAlaLeuLeuValAsnSerSerGlnProTr 115
Db 386 ----- 386
OY 115 pGluProLeuGlnLeuHisValAspLysAlaValSerGlyLeuArgSerLeuThrTrhLe 135
Db 387 -GAAGTGTCTGCTGCTCAGATAGATGCCATTAAGAAACATGCCAGCATCAGACAGAGT 445
OY 135 uLeuArgAlaLeuGlyAlaGlnLysGluAla1leSerProProAspAlaAlaSerAlaAl 155
Db 446 GCTCCGAAGTCTCAGCATATCCGGAATATGTA-----CCTCCAAACCATAGTGGAGA 496
OY 155 aProLeuArgThr1leThrAlaAspTrhPheArgLysLeuPheArgValTyrSerAsnph 175
Db 497 AGAAGACAGACACAGAAATATCTCGATCTCAGAGCTGTTTTCAGGTCCTCAGTCACTT 556
OY 175 eLeuArgGlyLysLeuLysLeuTyrTrhGlyGluAla-----CysArgThrGly 191
Db 557 TCTTCGGGGAAAGAGCGGTGTGCTGCCCAATGCACTGTGTGTGCACAGAGGT 611
```

RESULT 7

LOCUS

BC475544 967 bp mRNA linear EST 21-MAR-2001

DEFINITION 602491530F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4620438 5',

ACCESSION BC475544

VERSION BC475544.1 GI:13407823

KEYWORDS

SOURCE

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 967)

AUTHORS NIH-MGC <http://mgc.ncl.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: ATCC/DCMP/DRP

CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at:
<http://image.llnl.gov>
Plate: LNCM381 row: 1 column: 07
High quality sequence stop: 525.
Location/Qualifiers

FEATURES

source

```
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4620438"
/clone_id="NIH_MGC_20"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pOTB1; Site:1: XhoI; Site:2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GCCACGAC(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
```

BASE COUNT 237 a 255 c 267 g 208 t
ORIGIN

Alignment Scores:

Pred. No.: 0.639 Length: 967
Score: 99.50 Matches: 55
Percent Similarity: 37.17% Conservative: 29
Best Local Similarity: 24.34% Mismatches: 68
Query Match: 9.97% Indels: 74
DB: 12 Gaps: 12

US-09-813-775c-2 (1-193) x BC475544 (1-967)

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OY 2 G1yValHisGluCysProAlaTTrpLeu--TrpLeuLeuSerLeuLeuSerLeuPro 20
Db 363 GGCTGTGCTGCTGCTGCTGCTTTCATCAGTGTG-----CTGCCA 401
OY 21 --LeuGlyLeuProValLeu-----GlyAlaProProArg 31
Db 402 AGAGTTCACCTCCAGTACTCCAGGATCAGAGAGCCGCCCTCAGACAGATATTATC 461
OY 32 -----Leu1leCysAspSerArgValLeuGluArgTyrLeuLeu-----Glu 45
Db 462 CTTAACACTCTGCAACTCTGMAAGCTTCTCTGCCAAGAAAGTTCTGCAATGATAG 521
OY 46 AlaLysGluAlaGluAsn1leThrThrgLysAlaGlnHisCysSerLeuAsnGluAsn 65
Db 522 GTCTTAAAGTCCAAAGTCCAGCTAGCTGGAGTGTGCGAATGTG----- 566
OY 66 1leThrValProAspThrLysValAsnPheTyrAlaTrpLysArgMetGluValArgGln 85
Db 567 -----CCAGATGGGAGATATCATCTCATCTGCAGCAACAGCATGCTCCAGCAAAATAT 617
OY 86 GlnAlaValGluVal-----TrpGlnGlyLeuAlaLeuLeuSerGluAlaValLeu 102
Db 618 TCCCATGCTATTACCGTCGTCATTTGGAAAGACTTGAGCGGAGAACCCGSCAAAGACTT 677
OY 103 ArgGlyGlnAlaLeuLeuValAsnSerSerGlnProTrpGluProLeuGlnLeuHisVal 122
Db 678 CGAGGATCAACACACTTCAGAGATGGAGTGTGCATTC-----CACTGG 722
OY 123 AspLysAlaValSerGlyLeuArgSerLeuThrTrhLeu-LeuArgAlaLeuGlyAlaG 142
Db 723 GAGCAGCAGCTPACAGACAATTAATTCCTCCAAACCAATTTAATTCAGCCGACAAAGA----- 777
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```

OY 142 nlysgluAlaIleSerProAspAlaIleSerAlaIleProLeuArgThrIleThrAl 162
DB 778 -----GGGGCAAGCATCAGCCCGACACATTCATTCACCT 812
OY 162 aasphrhphearglylsleupheargValTyrSerAspPheLeuArgGlylsylsleuysle 182
DB 813 GGAAGAGTTTCACGAC-----TCCTATGACAGGAGACAGCATCAAT 854
OY 182 u-----TCCTATGACAGGAGACAGCATCAAT 854
DB 855 TACTAACATGGGTCTGGAACACACTGTTGACAAACAGAGTCTGTTGATGAGTACCT 914
OY 184 rglYgluaIaCysArg 189
DB 915 TGGAAGGCTGTGTAG 930

RESULT 8
BF184120
LOCUS 601843157F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:406367 5',
DEFINITION mRNA sequence.
ACCESSION BF184120
VERSION BF184120.1 GI:11062479
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
TITLE NIH-MGC http://mnc.nci.nih.gov/
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Clontech Laboratories, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1CM897 row: a column: 16
High quality sequence stop: 659.
Location/Qualifiers
source
1. 867
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:406367"
/clone_lib="NIH_MGC_54"
/tissue_type="from chronic myelogenous leukemia"
/lab_host="DH10B (TI phage-resistant)"
/notes="Organ: bone marrow; Vector: pDNR-LIB (Clontech);
Site_1: SfiI (ggcgccctggcgc); Site_2: SfiI (ggcgatctggcgc)
; Double-stranded cDNA was prepared from cell line RNA.
5' and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-ATTCTAGAGCGGAGCGCGCATG-dt(30)BN-3'
(Where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA)."
```

```

US-09-813-775C-2 (1-193) x BF184120 (1-867)
OY 7 ProAlaTrpLeuPhe---LeuLeuSerLeuSerLeuProLeuGlyLeuProVal 25
DB 322 CCATTCCTTGTCTGGGAGTCTGCCCTTCCTTGGAATCACTTCCTCTTTTCCCTGCA 381
OY 26 LeuGlyAlaProProArgLeuIleCysAspSerArgValLeuGluArgTyrLeuLeuGlu 45
DB 382 -----TCGGTTTGTGCCAGCGCTGCTGCTGCTGCTGCATTCATTCACG 423
OY 46 AlAlaYgluaIaGluAsnIleThrTrpGlyCysAlaGluHisSerSerLeuAsnGluAsn 65
DB 424 CTAGCGGATGAGAACTCAGAGTGCAGGCTTCATTCATTAATGAATTCGCGGA 483
OY 66 IleThrValProAspThrIleValAspPheTyrAlaTrpLysArgMetGluValArgGln 85
DB 484 CTACAGGCTGCTGATACACAAATGATTTGTTTGTGG-----ATTGAAACCGAGAT 537
OY 86 GlAlaValaIgluValTrp 91
DB 538 AAGGAAAGATAGTTTGG 555

RESULT 9
BF184123
LOCUS 603278441F1 NCI_CGAP_Mam3 Mus musculus cDNA clone IMAGE:5318674 5',
DEFINITION mRNA sequence.
ACCESSION BF184123
VERSION BF184123.1 GI:15562359
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
TITLE NIH-MGC http://mnc.nci.nih.gov/
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-r@mail.nih.gov
Tissue Procurement: Lohar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM1808 row: a column: 11
High quality sequence stop: 802.
Location/Qualifiers
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1. 803
/organism="Mus musculus"
/strain="129, C57BL/6J.FVB/N"
/db_xref="taxon:10090"
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/clone_lib="NCI_CGAP_Mam3"
/tissue_type="tumor, gross tissue"
/dev_stage="10 months"
/lab_host="DH10B"
/notes="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigators
providing samples: Lohar Hennighausen/Chu-Xia Deng, NIH
Reference for transgenic model: Xu et al., Nature Genetics
22, 37-43 (1999)."
```

Alignment Scores:

Pred. No.:	2.06	Length:	867
Score:	94.50	Matches:	26
Percent Similarity:	50.00%	Conservative:	17
Best Local Similarity:	30.23%	Mismatches:	34
Query Match:	9.47%	Indels:	9
DB:	12	Gaps:	3

Alignment Scores:

Pred. No.:	2.1	Length:	803
Score:	94.00	Matches:	51
Percent Similarity:	37.44%	Conservative:	25

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Db	417	AAGGGGAGNtAACCCTTGAGGCCATGTGGTATGAGGCATCAGGACCCCGCACTGA	358		
Oy	102	-----	LeuArgIylAlaLeuLeuValAsnSerSer	112	
Db	357	GAACAACCTTTTCGGCACCTGGCTGTCTCCCGACAGCAGCAGCACTTCTGAAATCCAAGC	298		
Oy	113	GINPOTRPGJUPRO--LeugInLeuHISValAspLyAlaValSerLyleu-----A	130		
Db	297	CAAGCTCAGAAACCCGAGACCAAGGTCGGCCCCCTTAGGGCTCCCGCTCAATATTCCC	238		
Oy	130	TgSerLeuThrLeuLeuArgAlaLeuAlaGlInLySglAlaLalSerProprio	149		
Db	237	GAGTTCAGAAGCTCAAAATAGACCATTTAGGGCCCTCGAACGAGGAATCCAGCCTCC	179		
RESULT 13					
BUSJ28644/c	BUS28644	639 bp	mRNA	linear	EST 09-AUG-2002
DEFINITION	BUS28644 MF01SSB cDNA Oryzias latipes CDNA clone MF01SSB03E16 5'				
ACCESSION	BUS28644				
VERSION	BUS28644.1	GI:22187456			
KEYWORDS	EST.				
SOURCE	Japanese medaka.				
ORGANISM	Oryzias latipes				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Acanthopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percormorpha; Atherinomorpha; Belontiiformes; Adrianchthyidae; Oryziinae; Oryzias.				
AUTHORS	Kohara,Y., Shin-I,T., Kimura,T., Narita,T., Jindo,T. and Takeda,H.				
JOURNAL	Medaka EST Project in Takeda's lab				
COMMENT	Unpublished (2001)				
	Contact: Tadasu Shin-i				
	National Institute of Genetics Information				
	1111 Yata, Mishima, Shizuoka 411-8540, Japan				
	Tel: 81-559-81-6856				
	Fax: 81-559-81-6855				
	Email: tshini@genes.nig.ac.jp.				
FEATURES	location/Qualifiers				
source	1..639				
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	/strain="Hd-IR"				
	/db_xref="taxon:8090"				
	/clone_id="MF01SSB03E16"				
	/seq="mixture of female and male"				
	/tissue_type="whole embryo"				
	/dev_stage="segmentation stage 20 - 25"				
BASE COUNT	175 a 137 c 228 g 97 t				2 others
ORIGIN					
Alignment Scores:					
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Percent Similarity:	37.31%	Conservative:	21		
Best Local Similarity:	26.42%	Mismatch:	60		
Query Match:	9.12%	Indels:	61		
DH:	13	Gaps:	9		
US-09-813-775C-2 (1-193) x BUS28644 (1-639)					
Oy	5	GlucYs-----ProAlaTrp-----LeuTrpLeuLeuLeuSerLeuLeu	17		
Db	546	GAAGTGTGACCTCCACTTTCGGCCCGCTTCCTTCCTTCGCTTCATGCTTCATTCGTCACAG	487		
Oy	18	SerLeuProLeuGlyLeuProValLeuLcylAlaProPargLeuIlacYaspsrArg	37		
Db	486	TCAATCTCCTTGGGGGCTTCTCTCTTCACCTCCTCCTCCTCAT-----	445		

LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
OY 38	valleugluarGTYrLeuLeuclunlaalysgluaiaaunllethrthGlycysla	445	-----	445							
OY 58	gluHiscysSerLeuAsnGluAsnIleThrValProAspThrIysValAsnPheTyrAla	444	: : : : :	409							
OY 78	trpIysaIgmGtGluValaIargGlnGlnaIaValGluValItrpGlnGlyLeuAlaLeuLe	408	-----CTCCGTCAGGATTCCTCCTCAG--TGGTGTGGATTCGTCACAGCT	367							
OY 97	uSerGluAlaValLeuArGlyGlnAlaIleuLeuLeuValAsnSerSerGlnProTpgIuPr	366	CATTGAGTTCAATCCCTTCACAGG--GCCCCAGTTGTGAATCCACTTCCCCACAGCTTCT	310							
OY 117	oleuGlnIleuHis-----ValAspIysAlaValSerIlyLeuArGserLeuThrThrLe	309	CCTCACCGTTTATTAATTTGTCTACGCGCGGTGTCTGTCTCAAAATTACAGCTTTTCCCGCG	250							
OY 135	uLeuArGAlaLeuGlyAlaGlnGlnIysGluAlaIleSerProPro-----AspAlaAl	249	AGTCAAAAGCCGTCACGCGACCATACCGCACCCCTGCCCGCGGCTCCCGCGGTGC	190							
OY 152	aSerAlaIaIaProLeuArGThrIleThr-----AlaAspThrPh	189	CACCGCGTCCTCCATGGCGCGATACCGATGCGGTCTTCCACTGAGAAATTCACACACTT	130							
OY 165	eArGlysLeuPheArGValItyrSerAsnPheLeuArG	129	CAGTCTTCTCTACAGCATCCGACGAGGTGCTCAAA	93							
RESULT 14	BE618292	912 bp	mrna	linear	EST 20-OCT-2000						
LOCUS	60146267001 NIH_MGC_67	Homo sapiens	cdna	clone	IMAGE:3866248 5'						
DEFINITION	mrna sequence.	BE618292									
ACCESSION	BE618292.1	GI:9889230									
VERSION	EST.										
KEYWORDS	human.										
SOURCE	Homo sapiens										
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;										
REFERENCE	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.										
AUTHORS	1 (bases 1 to 912)										
TITLE	NIH-MGC http://mgc.nci.nih.gov/.										
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)										
COMMENT	Unpublished (1999)										
	Contact: Robert Strausberg, Ph.D.										
	Email: cgapbs-remail.nih.gov										
	Tissue Procurement: ATCC										
	CDNA Library Preparation: Life Technologies, Inc.										
	DNA Sequencing by: Incyte Genomics, Inc.										
	Clone distribution: MGC clone distribution information can be										
	found through the I.M.A.G.E. Consortium/LNL at:										
	http://image.lnl.gov										
	Plate: LMA9610 row: k column: 17										
	High quality sequence stop: 671.										
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	/db_xref="taxon:9606"										
	/clone="IMAGE:3866248"										
	/clone_lib="NIH_MGC_67"										
	/tissue_type="retinoblastoma"										
	/lab_host="DH10B (phage-resistant)"										
	/note="Organ: eye; Vector: pCMV-SPORT6; Site:1: NotI;										
	Site:2: SalI; Cloned unidirectionally. Primer: oligo dT.										
	Average insert size 1.75 kb. Library constructed by Life										
	Technologies."										
BASE COUNT	180 a 316 c 264 g 152 t										

	Type	L #	Hits	Search Text	DBs	Time Stamp	Comments	Error Definition	Errors
1	BRS	L1	5796	erythropoietin	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/01/08 19:34			0
2	BRS	L2	3	1 same chimpanzee	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/01/08 19:36			0
3	BRS	L3	0	2 same chimeric	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/01/08 19:37			0
4	BRS	L4	1	desauvage adj frederic.in.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/01/08 19:38			0
5	BRS	L5	14	henner adj dennis.in.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/01/08 19:39			0
6	BRS	L6	4	5 and 1	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/01/08 19:39			0

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COST IN U.S. DOLLARS
SINCE FILE
ENTRY
SESSION
TOTAL
0.21
0.21

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FILE 'AGRICOLA' ENTERED AT 19:45:10 ON 08 JAN 2003

=> s erythropoietin
L1 69950 ERYTHROPOIETIN

=> s 11 (p) chimpanzee
L2 5 L1 (P) CHIMPANZEE

=> duplicate remove
ENTER L# LIST OR (END):12

Duplicate preference is 'MEDLINE', CAPLUS'
KEEP DUPLICATES FROM MORE THAN ONE FILE? Y/(N):n

L3
L3 5 DUPLICATE REMOVE L2 (0 DUPLICATES REMOVED)

=> d 13 1-5 1b1b abs

L3 ANSWER 1 OF 5 CAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2002:736286 CAPLUS
DOCUMENT NUMBER: 137:257948

TITLE: ***Chimpanzee***
(CHEPO) (CHPO)

INVENTOR(S):
Desauvage, Frederic; Henner, Dennis J.
- immunoadhesins for use in regulating erythropoiesis

PATENT ASSIGNEE(S):

Genentech, Inc., USA
PCT Int. Appl., 120 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO. KIND DATE APPLICATION NO. DATE

WO 2002074807 A2 20020926 WO 2002-US4773 20020214

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN,

CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP,

KR, KZ, LC, LK, LR, LS, LT, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZM, ZW, AM, AZ,

BY, BG, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG,

PRIORITY APPLN. INFO.:

US 2001-813775 A 20010320

AB The present invention is directed to immunoadhesins comprising
chimpanzee
erythropoietin (CHEPO) polypeptides. The

immunoadhesins have an enhanced in vivo half-life compared to the corresponding CHEPO polypeptide and retains CHEPO bio. activity. Also provided herein are nucleic acid mols. encoding such immunoadhesins, vectors and host cells comprising those nucleic acid sequences, and methods using and compns. comprising the CHEPO immunoadhesins.

L3 ANSWER 2 OF 5 CAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2000:814616 CAPLUS
DOCUMENT NUMBER: 134:1044
TITLE: ***Chimpanzee***
INVENTOR(S): Desauvage, Frederic; Henner, Dennis J.
PATENT ASSIGNEE(S): Genentech, Inc., USA
SOURCE: PCT Int. Appl., 109 pp.
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO. KIND DATE APPLICATION NO. DATE
WO 2000068376 A1 20001116 WO 2000-US12370 20000505

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, FI, GB, GD, GE, GH, GM, GU, HR, HU, ID, IL, IN, IS, JP, KE, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, BF, BJ, CF, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SF, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG
EP 117285 A1 20020206 EP 2000-928879 20000505
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO
JP 2002543784 T2 20021224
PRIORITY APPLN. INFO.:
US 1999-307307 A 19990507
US 2000-287594P P 20000328
US 2000-552265 A 20000419
WO 2000-US12370 W 20000505

AB The present invention is directed to novel ***chimpanzee***
erythropoietins and to nucleic acid mols. encoding those polypeptides. Also provided herein are vectors and host cells comprising those nucleic acid sequences, chimeric proteins comprising the ***erythropoietins*** of the present invention fused to heterologous protein sequences, antibodies which bind to the proteins of the invention, and to methods for producing the proteins of the invention. Agonists and antagonists of ***erythropoietin*** may be used to modulate erythropoiesis.

REFERENCE COUNT: 8
THERE ARE 8 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT
L3 ANSWER 3 OF 5 CAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1999:708637 CAPLUS
DOCUMENT NUMBER: 131:335812
TITLE: Monoclonal antibodies with reduced immunogenicity
INVENTOR(S): Taylor, Alexander H.
PATENT ASSIGNEE(S): Smithkline Beecham Corporation, USA
SOURCE: PCT Int. Appl., 122 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO. KIND DATE APPLICATION NO. DATE
WO 9955369 A1 19991104 WO 1999-US9131 19990428
W: CA, JP, US
RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE

CA 2327505 AA 19991104 CA 1999-2327505 19990428
EP 1073464 AI 200104 EP 1999-918862 19990428
JP 2002512776 T2 20020508 JP 2000-545566 19990428
US 2002062009 AI 20020523 US 1998-83367P P 19980428
US 1999-300970 B1 19990428
WO 1999-US9131 W 19990428
AB Antibodies having reduced immunogenicity comprising non-human antigen-specific donor antibody and non-human primate acceptor framework. Random cDNA cloning and sequence anal. of VH and V.kappa. of ***chimpanzee*** and cynomolgus were performed, and engineered murine monoclonal antibodies (contg. ***chimpanzee*** or cynomolgus framework) specific for interleukin 5, integrin, and ***erythropoietin*** receptor were prepd. for treating asthma, vascular diseases and hematopoietic disorders resp. REFERENCE COUNT: 1 THERE ARE 1 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 4 OF 5 CAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1970:505985 CAPLUS
DOCUMENT NUMBER: 73:105985
TITLE: Anti-human follicle stimulating hormone; complete cross-reactivity with three other human glycoprotein tropic hormones, luteinizing hormone, human chorionic gonadotropin, and thyrotropin
AUTHOR(S): Rosen, Saul W.; Schlaft, Sheldon; Roth, Jesse Nat. Inst. Arthritis and Metab. Dis., Nat. Inst. of Health, Bethesda, MD, USA
SOURCE: Protein Polypeptide Horm., Proc. Int. Symp. (1969), Meeting Date 1968, 396-7. Editor(s): Margoulies, M. Excerpta Med. Found.: Amsterdam, Neth.
CODEN: 22AMAE
DOCUMENT TYPE: Conference
LANGUAGE: English
AB Addn. of excess rabbit or guinea pig anti-human FSH sera to FSH-131I pptd. 70-85% of the radioactivity; nonimmune sera pptd. 6% of the radioactivity. Excess unlabeled FSH displaced 95% of the antibody-bound radioactivity into the supernatant. Displacement curves of FSH-131I from anti-FSH by various FSH preps. were superimposable when the abscissas were adjusted for varying FSH content. Plasma from postmenopausal patients, patients with gonadal insufficiency due to the Turner syndrome or Klinefelter syndrome, and patients with gonadotropin-producing bronchogenic carcinomas showed curves of displacement superimposable over a 4-20 fold range of diln. Human LH, HCG (human chorionic gonadotropin), and TSH displaced FSH-131I from anti-FSH. LH-131I and HCG-131I were bound as strongly as FSH-131I by anti-FSH sera and the curves of displacement of LH-131I from anti-FSH by LH and SFH were quant. identical. Human growth hormone, bovine ACTH, ovine FSH, human ***erythropoietin***, arginine vasotocin, human .alpha.-acid glycoprotein, bovine thyroglobulin, human ceruloplasmin, bovine fetuin, human orosomucoid, and blood group A and B substances did not displace FSH-131I from anti-FSH. Plasma from rabbits, guinea pigs, dogs, cats, hogs, goats, sheep, burros, and horses, including some aged and some castrate females, failed to displace FSH-131I. Displacement of human FSH-131I from anti-human FSH was produced by sera from the higher apes (***chimpanzee***, gorilla, orangutan, gibbon) but not by sera from rhesus, pigtail, Java, or African green monkeys, or from black apes, baboons, or drills. These data suggested that the pituitary glycoprotein tropic hormones and chorionic gonadotropin in man, and possibly in the social apes, share common antigenic sites.

L3 ANSWER 5 OF 5
MEDLINE
ACCESSION NUMBER: 68092392
DOCUMENT NUMBER: 68092392 Pubmed ID: 6073630
TITLE: ***Erythropoietin*** response to renal stress in the
AUTHOR: Murphy G P, Mirand E A, Wade J C, Melby E C
SOURCE: INVESTIGATIVE UROLOGY, (1967 Nov) 5 (3) 234-8.
Journal code: 0374747. ISSN: 0021-0005.
United States
Journal: Article; (JOURNAL ARTICLE)
LANGUAGE: English

FILE SEGMENT:
ENTRY MONTH:
ENTRY DATE:

Priority Journals
196802
Entered STN: 19900101
Last updated on STN: 19900101
Entered Medline: 19680215

=> d h1s

(FILE 'HOME' ENTERED AT 19:44:43 ON 08 JAN 2003)

FILE 'MEDLINE', CAPLUS, BIOSIS, EMBASE, SCISEARCH, AGRICOLA' ENTERED AT 19:45:10 ON 08 JAN 2003

L1 69950 S ERYTHROPOIETIN
L2 5 S L1 (P) CHIMPANZEE
L3 5 DUPLICATE REMOVE L2 (0 DUPLICATES REMOVED)

=> s chimeric
L4 105699 CHIMERIC

=> s l3 (p) l4
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'L27' (P) L18'
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'L29' (P) L19'
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'L31' (P) L20'
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'L33' (P) L21'
L5 2 L3 (P) L4

=> d l5 1-2 ibib abs

L5 ANSWER 1 OF 2 CAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2002:736286 CAPLUS
DOCUMENT NUMBER: 137:257948

TITLE: Chimpanzee erythropoietin (CHEPO) - immunoadhesins for
use in regulating erythropoiesis
INVENTOR(S): Desauvage, Frederic; Henner, Dennis J.
PATENT ASSIGNEE(S): Genentech, Inc., USA
SOURCE: PCT Int. Appl., 120 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO. KIND DATE APPLICATION NO. DATE

WO 2002074807 A2 20020926 WO 2002-US4773 20020214
AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, FL, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KP, KR, KZ, LC, LK, LR, LS, LT, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, BG, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG
PRIORITY APPLN. INFO.: US 2001-813775 A 20010320

AB The present invention is directed to immunoadhesins comprising chimpanzee erythropoietin (CHEPO) polypeptides. The immunoadhesins have an enhanced in vivo half-life compared to the corresponding CHEPO polypeptide and retains CHEPO biol. activity. Also provided herein are nucleic acid moles encoding such immunoadhesins, vectors and host cells comprising those nucleic acid sequences, and methods using and compns. comprising the CHEPO immunoadhesins.

L5 ANSWER 2 OF 2 CAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2000:814616 CAPLUS
DOCUMENT NUMBER: 134:1044

TITLE: Chimpanzee erythropoietin and cDNA and methods of

modulate erythropoiesis

Desauvage, Frederic; Henner, Dennis J.

Genentech, Inc., USA

PCT Int. Appl., 109 pp.

CODEN: PIXXD2

Patent

English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.

KIND DATE

APPLICATION NO. DATE

WO 2000068376 A1 20001116 WO 2000-US12370 20000505

AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, GU, HA, HE, HI, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, PU, RO, RU, SD, SE, SG, SI, SK, SL, ST, TM, TR, TT, TZ, UA, UG, US, VZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GN, GW, ML, MR, NE, SN, TD, TG

EP 117285 A1 20020206 EP 2000-928879 20000505

JP 2002543784 T2 20021224 JP 2000-616342 20000505

US 1999-307307 A 19990507 US 2000-287594P P 20000328 US 2000-552265 A 20000419 WO 2000-US12370 W 20000505

AB The present invention is directed to novel ***chimpanzee*** polypeptides. Also provided herein are vectors and host cells comprising those nucleic acid sequences, ***chimeric*** proteins comprising the ***erythropoietins*** of the present invention fused to heterologous protein sequences, antibodies which bind to the proteins of the invention, and to methods for producing the proteins of the invention. Agonists and antagonists of ***erythropoietin*** may be used to modulate erythropoiesis.

REFERENCE COUNT: 8 THERE ARE 8 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

=> d his

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FILE 'MEDLINE', CAPLUS, BIOSIS, EMBASE, SCISEARCH, AGRICOLA' ENTERED AT

19:45:10 ON 08 JAN 2003

L1 69950 S ERYTHROPOIETIN

L2 5 S L1 (P) CHIMPANZEE

L3 5 DUPLICATE REMOVE L2 (0 DUPLICATES REMOVED)

L4 105699 S CHIMERIC

L5 2 S L3 (P) L4

L6 0 EPILOPE ADJ TAG

=> s epitope adj tag

L7 1837 EPILOPE TAG

=> s epitope tag

L8 0 L7 AND L5

=> s L7 and L5

L9 2 IMMUNOGLOBULIN

=> s immunoglobulin

IN IS NOT A RECOGNIZED COMMAND

The previous command entered was not recognized by the system.

For a list of commands available to you in the current file, enter
"HELP COMMANDS" at an arrow prompt (= >).

=> s immunoglobulin L10 719573 IMMUNOGLOBULIN

=> s 15 (p) 110
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FIELD CODE - 'AND' OPERATOR ASSUMED 'L28 (p) L66'
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FIELD CODE - 'AND' OPERATOR ASSUMED 'L30 (p) L67'
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
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PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'L34 (p) L69'
L11 0 L5 (p) L10

=> s 19g or 19g1 L12 340314 IGG OR IGG1

=> s 112 and 15 L13 0 L12 AND L5

=> d his

(FILE 'HOME' ENTERED AT 19:44:43 ON 08 JAN 2003)

FILE 'MEDLINE', CAPLUS, BIOSIS, EMBASE, SCISEARCH, AGRICOLA' ENTERED AT
19:45:10 ON 08 JAN 2003

L1 69950 S ERYTHROPOIETIN
L2 5 S L1 (p) CHIMPANZEE
L3 5 DUPLICATE REMOVE L2 (0 DUPLICATES REMOVED)
L4 105699 S CHIMERIC
L5 2 S L3 (p) L4
L6 0 S EPILOPE ADJ TAG
L7 1837 S EPILOPE TAG
L8 0 S L7 AND L5
L9 2 S IMMUNOGLOBU
L10 719573 S IMMUNOGLOBULIN
L11 0 S L5 (p) L10
L12 340314 S IGG OR IGG1
L13 0 S L12 AND L5

=> log y
COST IN U.S. DOLLARS
SINCE FILE ENTRY TOTAL

FULL ESTIMATED COST
SINCE FILE ENTRY TOTAL

DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)
SINCE FILE ENTRY TOTAL

CA SUBSCRIBER PRICE
ENTRY TOTAL

STN INTERNATIONAL LOGOFF AT 19:50:27 ON 08 JAN 2003

